DEX-0113 B9

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
22 February 2001 (22.02.2001)

PCT

(10) International Publication Number
WO 01/12659 A2

(51) International Patent Classification[7]: C07K 14/00

(21) International Application Number: PCT/IB00/01496

(22) International Filing Date: 18 August 2000 (18.08.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/149,499 18 August 1999 (18.08.1999) US
60/156,503 28 September 1999 (28.09.1999) US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:
US 60/156,503 (CIP)
Filed on 18 August 1999 (18.08.1999)

(71) Applicant *(for all designated States except US)*: GERMAN HUMAN GENOME PROJECT [DE/DE]; Fraunhofer Patentstelle, Leonrodstrasse 68, 80636 Munich (DE).

(72) Inventor; and
(75) Inventor/Applicant *(for US only)*: WIEMANN, Stefan [DE/DE]; Grosse Lachstrasse 30a, 69207 Sandhausen (DE).

(74) Agent: CARPMAELS & RANSFORD; 43 Bloomsbury Square, London WC1A 2RA (GB).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
— *Without international search report and to be republished upon receipt of that report.*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN DNA SEQUENCES

(57) Abstract: Novel human cDNA sequence of a clones, the encoded protein sequence of a clones, antibodies and variants thereof, are provided. The disclosed sequence of a clones find application in a number of ways, including use in profiling assays. In this regard, various assemblages of nucleic acids or proteins are provided that are useful in providing large arrays of human material for implementing large-scale screening strategies. The disclosed sequence of a clones may also be used in formulating medicaments, treating various disorders and in certain diagnostic applications.

WO 01/12659 A2

HUMAN DNA SEQUENCES

Background of the Invention

Current methods for testing pharmacological substances rely on a three-stage testing approach to drug development. First, candidate compounds are typically screened in some sort of *in vitro* system, like inhibition of cancer cell growth. Candidates are then tested in an animal model, as a first approximation of systemic effects, including efficacy and toxicity. Compounds that still show promise after these initial *in vivo* screens, finally are tested in humans. Again, human testing typically occurs in three phases: toxicity; preliminary efficacy; and efficacy. The entire process can take more than a decade and cost hundreds of millions of dollars. Aside from the monetary costs and protracted time scale, moreover, current testing regimes waste the lives of countless laboratory animals and needlessly endanger the lives of human subjects.

A need exists, therefore, for more sophisticated drug screening techniques that can be done rapidly *in vitro*. These screening techniques ideally will be reflective of systemic and/or organ-specific responses, so that they provide a reliable indicator of action in a human body. Current techniques, however, tend to utilize only a single or limited number of markers, thus answering only very simple questions that are of questionable medical import. For example, a typical *in vitro* assay may ask whether a lead compound binds a particular receptor, which has been implicated in a certain disorder. It is presumed that such binding is indicative of therapeutic usefulness, but it does not even purport to address systemic effects.

Not only are screening techniques for efficacy inadequate, the available toxicity screens likewise are inadequate. Toxicity, on a first level, is usually measured by animal testing. Aside from the complications related to *in vivo* versus *in vitro* testing, such screens are insufficient because of differences in metabolism, uptake, etc., relative to humans. Thus, improved methods would be not only be *in vitro*-based, they would also be more "human."

With the increasing miniaturization of screening assays and the growing availability of targets for pharmaceutical intervention, there is increasing interest in developing arrays containing large numbers of these targets that can be assayed simultaneously. If such an

array contains a large enough population of targets, it can be used to essentially mimic the systemic response. In other words, the array becomes an *in vitro* surrogate for the human body. The more refined the array, the more accurate the predictive capability. In theory, an array could be constructed that can detect all of the known human expression products simultaneously, thereby, providing a very reliable indicator of the human response to a given compound. These arrays offer advantages over the present *in vitro* screening systems in that they can assay large numbers of responses simultaneously. They are superior to animal testing because they are more "human" and, thus, more predictive of human responses.

In order to construct such arrays, however, the field is in need of further human targets. Advantageously, such targets will be provided with additional physiologically relevant information, such as whether the target is expressed in a particular tissue and whether it is related to a known functional class of targets. In this way, the artisan can focus as needed, for example, on tissue-specific effects or target class-specific effects, thereby providing information useful in evaluating efficacy and/or toxicity.

In addition to a need for pharmacological screening targets, there is a need for further pharmacological substances. These substances can be used in the formulation of medicinal compositions and in treating a wide variety of disorders.

The present invention responds to the aforementioned and other needs in the field by providing a population of novel targets useful, *inter alia*, in the profiling and medicinal contexts described above.

Summary of the Invention

It is an object of the invention, therefore, to provide a set of human cDNA clones. Further to this object, the invention provides sequences of human cDNA clones that were isolated from libraries generated from different human tissues.

It is another object of the invention to provide assemblages of targets useful in profiling matrices for screening pharmacological test compounds. According to this object, assemblages comprising different populations of human nucleic acids, proteins and antibodies are provided. In different embodiments, cDNA library-specific assemblages and target-family-specific targets are provided.

It is a further object of the invention to provide a database of human nucleotide and protein sequences. Further to this object, novel human nucleotide and protein sequences are provided in electronic form. In one embodiment, one or more of these sequences is provided in a searchable database.

It is still another object of the invention to provide biologically active target molecules useful in treating or detecting human disorders. Further to this object, the invention provides nucleic acid and protein molecules that have the capacity to affect disease etiology or symptoms or correlate with known disease states. Also further to this object, a database is provided which comprises the disclosed molecules in electronic form.

It is still a further object of the invention to provide polypeptides encoded by the human cDNA clones disclosed herein. Further to this object, the invention provides antibodies and fragments thereof that are capable of binding to a specific portion of these polypeptides.

It is yet another object of the invention to provide pharmaceutical compositions which comprise an effective amount of a pharmaceutical agent, wherein the pharmaceutical agent is selected from the group consisting of one or more polypeptides contemplated by the invention, variants or functional derivatives thereof, and antibodies thereto; and a physiologically acceptable carrier or excipient.

It is still another object of the invention to provide expression vectors comprising one or more human cDNA clones disclosed herein or fragments thereof; and optionally a promoter operably linked to the cDNA clone or fragment thereof. Further to this object, the invention provides methodology for recombinantly producing a desired peptide, comprising expressing in a host cell a peptide encoded by a human cDNA clone disclosed herein.

Detailed Description

The invention results from a need in the art for new human nucleic acids and proteins. This need arises in several contexts. First, there is a need to identify targets for therapeutic intervention. Second, there is a need to identify molecules that may be adversely affected in a therapeutic context, thereby resulting in toxicity. Knowledge of these molecules will aid in

the design of new medicaments with enhanced efficacy and decreased toxicity. Finally, the need encompasses human nucleic acids and proteins that have medicinal applicability in their own right.

In view of these needs, the present inventors set out to isolate and sequence human cDNAs from tissue-specific libraries. In this way, they represent subsets of molecules likely to be targets for therapeutic intervention or for avoiding toxicity. In addition, the inventors divided the molecules into various sub-categories, based on suspected functionality, structural similarity etc, which are of interest from a pharmacological perspective. These molecules are disclosed in provisional application serial nos. 60/149,499 and 60/156,503, filed August 18, 1999, and September 28, 1999, respectively, both of which are hereby incorporated by reference in their entirety.

GENERAL DESCRIPTION OF THE INVENTIVE MOLECULES

The present invention provides novel polynucleotide molecules that, in some instances, have similarities with known molecules. The inventive DNAs were cloned from five different human cDNA libraries. In addition to these DNA molecules, the invention provides their protein translations and antibodies derived from them. The inventive DNA and protein sequences are show individually, below. The inventive nucleic acids also include the complements of these DNA sequences, as well as their RNA counterparts. Methods of producing the molecules also are provided. Further, the invention provides methods for detecting all or part of the molecules and of detecting polynucleotides encoding all or part of the molecules.

The inventive molecules derive from five cDNA libraries: human fetal brain; human fetal kidney; human mammary carcinoma; human testis; and human uterus. For convenience, each sequence bears a designation that indicates from which library it is derived. In particular, these designations are: "hfpbr" for human fetal brain; "hfkd" for human fetal kidney; "hmcf" for human mammary carcinoma; "htes" for human testis; and "hute" for human uterus. The individual libraries were constructed and screened as described below in the examples.

The protein and DNA molecules of the invention are variously described herein as "target" molecules or "inventive" molecules. The sequences and other information pertinent to the nucleic acid and protein molecules of the invention are shown, below.

Interpreting the data disclosed with the Table and cDNA sequences, below:

The table and data below provide the coding sequences of the inventive cDNAs as well as the protein sequences and other useful information, as set out below.

Grouping

The clones were assigned to the following fourteen functional and/or tissue-derived groups:

1. Cell Cycle
2. Cell Structure and Motility
3. Differentiation/Development
4. Intracellular Transport and Trafficking
5. Metabolism
6. Nucleic Acid Management
7. Signal Transduction
8. Transmembrane Protein
9. Transcription Factors
10. Brain derived
11. Kidney derived
12. Mammary Carcinoma derived
13. Testes derived
14. Uterus derived

Description of Clone Files

The individual clone files are structured in the same pattern. The Sections are separated by paragraphs.

1. Clone Name

The clone names are deciphered with reference to the following example: DKFZphfkd2_24e23, wherein the code represents:

- producer of library ("DKFZ") (for convenience, this reference may be eliminated)
- a "p" for "plasmid cDNA library" (for convenience, this reference may be eliminated)
- library name (e.g. hfbr = human fetal brain; hfkd = human fetal kidney; hmcf = human mammary carcinoma; htes = human testes; hute = human uterus)
- an underscore ("_") to separate library information from plate information
- plate number (e.g. "16")
- plate coordinates (letter first; e.g. "f14")

2. Group

3. Introduction

short review of the similarities, function of the protein and possible applications

4. Short Information

specifications about the cDNA (who sequenced, completeness of the cDNA, similarity, who sequenced, chromosomal localisation, length of cDNA, localisation of poly A tail and polyadenylation signal)

5. cDNA-Sequence

6. BLASTn Results

search results of blasting the cDNA sequence against all public databases

7. Medline Entries

information about genes/proteins similar to the novel cDNA (if available)

8. Putative Encoded Protein Information

specifications about the encoded protein (ORF: length and localisation of the reading frame)

9. Protein Sequence

10. BLASTp Results

search results of blasting the protein sequence against all public databases

11. Pedant Information

output of fully automated annotation: summarises peptide information, homologies, patterns as follows:

[Length]

- length of the protein = number of amino acid residues

[MW]

- molecular weight of the protein

[pI]

- isoelectric point

[HOMOL]

- shows protein with closest similarity to the cDNA-encoded protein

[FUNCAT]

- functional information according to a catalogue developed by Munich Information center for Protein Sequences (MIPS)

[BLOCKS]

- Blocks are multiply aligned ungapped segments corresponding to the most highly conserved regions of proteins. The blocks for the Blocks Database are made automatically by looking for the most highly conserved regions in groups of proteins documented in the Prosite Database. The Prosite pattern for a protein group is not used in any way to make the Blocks Database and the pattern may or may not be contained in one of the blocks representing a group. These blocks are then calibrated against the SWISS-PROT database to obtain a measure of the chance distribution of matches. It is these calibrated blocks that make up the Blocks Database. The WWW versions of the Prosite and SWISS-PROT Databases that are used on this server are located at the ExPASy World Wide Web (WWW) Molecular Biology Server of the Geneva University Hospital and the University of Geneva. World Wide Web URL http://blocks.fhcrc.org/blocks/about_blocks.html/ is the entry point to the database.

- here Blocks segments found in the analysed protein sequences are displayed

[SCOP]

Nearly all proteins have structural similarities with other proteins and, in some of these cases, share a common evolutionary origin. The scop database provides a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known, including all entries in Brookhaven National Laboratory's Protein Data Bank (PDB). It is available as a set of tightly linked hypertext documents which make the large database comprehensible and accessible. In addition, the hypertext pages offer a panoply of representations of proteins, including links to PDB entries, sequences, references, images and interactive display systems. World Wide Web URL http://scop.mrc-lmb.cam.ac.uk/scop/ is the

entry point to the database. Existing automatic sequence and structure comparison tools cannot identify all structural and evolutionary relationships between proteins. The scop classification of proteins has been constructed manually by visual inspection and comparison of structures, but with the assistance of tools to make the task manageable and help provide generality. Proteins are classified to reflect both structural and evolutionary relatedness. Many levels exist in the hierarchy, but the principal levels are family, superfamily and fold. The exact position of boundaries between these levels are to some degree subjective. Scop evolutionary classification is generally conservative: where any doubt about relatedness exists, we made new divisions at the family and superfamily levels.

- - here SCOPE segments found in the analysed protein sequences are displayed

[EC]

ENZYME is a repository of information relative to the nomenclature of enzymes. It is primarily based on the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided. World Wide Web URL http://www.expasy.ch/enzyme/ is the entry point to the database.

- here EC-number and name of enzymes with similarity to the analysed protein sequences are displayed

[PIRKW]

- functional information according to the Protein Information Resource (PIR) database catalogue developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JIPID).

[SUPFAM]

- information according to the Protein Information Resource (PIR) database catalogue of protein superfamilies developed by Munich Information Center for Protein Sequences (MIPS), the National Biomedical Research Foundation (NBRF) and the International Protein Information Database in Japan (JIPID).

[PROSITE]

please refer to 12. PROSITE Motifs

[PFAM]

please refer to 13. PFAM Motifs

[KW]

- overall 2dimensional folding information

- 3D indicates that the proteins is similar to a protein of which a 3 dimensional structure is known

- overall structural information

[]

The last PEDANT-block depicts information about the folding structure of the protein generated by PREDATOR. PREDATOR is a secondary structure prediction program. It takes as input a single protein sequence to be predicted and can optimally use a set of unaligned sequences as additional information to predict the query sequence. The mean prediction accuracy of PREDATOR is 68% for a single sequence and 75% for a set of related sequences. PREDATOR does not use multiple sequence alignment. Instead, it relies on careful pairwise local alignments of the sequences in the set with the query sequence to be predicted.

World Wide Web URL http://www.embl-heidelberg.de/argos/predator/predator_info.html is the entry point to the database.

- H = helix, E = extended or sheet, _ = coil, T = transmembrane, B = beta

- x indicates a low-complexity region with repeat-like structure which is omitted in all BLAST searches

12. PROSITE Motifs

PROSITE is a database of protein families and domains. It consists of biologically significant sites, patterns and profiles that help to reliably identify to which known protein family (if any) a new sequence belongs. World Wide Web URL http://www.expasy.ch/prosite/ is the entry point to the database. A description of the prosite consensus patterns is also provided, below.

13. PFAM Motifs

PFAM (protein families) is a large collection of multiple sequence alignments and hidden

Markov models covering many common protein domains. World Wide Web URL http://www.sanger.ac.uk/Pfam/ is the entry point to the database.

Deposit of Clones

Clones were deposited as a pool with the American Type Culture Collection under accession number __________, from which each clone comprising a particular polynucleotide is obtainable. Each clone has been transfected into separate bacterial cells (E. coli) in this composite deposit.

The clones may also be obtained from the Resource Center of the German Human Genome Project (Heubner Weg 6, 14059 Berlin, GERMANY). The Resource Center library numbers are slightly different that those presented here, but may be readily obtained by the following key or with the assistance of Resource Center personnel.

The library name becomes a number: brain (hfbr2) becomes 564; kidney (hfkd2) becomes 566; mammary carcinoma (hmcfl) becomes 727; testis (htes3) becomes 434;and uterus (hute1) becomes 586. Next, the plate number is converted to two digits (e.g., "2" becomes "02") and is moved behind the plate coordinate, and the underscore is dropped. The following examples are helpful:

Listed Number	Resource Center Number
DKFZphfbr2_16f21	DKFZp564F2116
DKFZphfkd2_1j9	DKFZp566J091
DKFZphmcfl_1c23	DKFZp727C231
DKFZphtes3_14g5	DKFZp434G0514
DKFZphute1_17k7	DKFZp586K0717

The libraries were constructed using two commercially available vectors. The brain (hfbr2 designations) and kidney (hfkd2 designations) libraries utilize pAMP 1 from Life Technologies and are maintained in XL-2Blue (Strategene); the uterus (hute1), testes (htes3) and mammary carcinoma (hmcfl) libraries are constructed in pSPORT1, also from Life Technologies, and are maintained in DH10B (LifeTechnologies). In addition to the following techniques, consultation with the commercial literature available on these clones will make evident all of the housekeeping techniques needed to propagate and isolate the individual constructs. All inserts may be excised with a NotI/SalI digestion. Alternatively, universal primers, flanking the cloning region, may be used to amplify the inserts using PCR methods.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. Methods of probe design are presented below.

Oligonucleotide probes may be labeled with γ-^{32}P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other, non-radioactive labeling techniques can also be used. Unincorporated label typically is removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe can be quantified by measurement in a scintillation counter. Preferably, specific activity of the resulting probe generally should be approximately $4X10^6$ dmp/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 μl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 50 - 100 μg/ml (for XL-2Blue strains 25 μg/ml tetracycline should also be used). The culture should preferably be grown to saturation at 37°C., and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μg/ml (for XL-2Blue strains 25 μg/ml tetracycline should also be used)and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them. The filter is then preferably incubated at 65°C. for 1 hour with gentle agitation in 6 x SSC (20 x stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to $1X10^6$ dpm/mL. The filter is then preferably incubated at 65°C. with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2 x SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2 x SSC/0.1% SDS at room

temperature with gentle shaking for 15 minutes. A third wash with 0.1 x SSC/0.5% SDS at 65°C. for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Alternatively, clones may be grown as described above, and PCR used to isolate the insert DNAs. Methods of PCR are described below and are otherwise well known .

ERROR SCREENING

The DNA sequences found herein derive from individual clones, which are publicly available, as noted above. Thus, the skilled artisan will recognize that any specific sequence disclosed herein readily can be screened for errors by resequencing a particular fragment, in both directions (*i.e.*, by sequencing both strands). Alternatively, error screening can be performed by amplifying and/or cloning any of the inventive DNAs, using for example RT-PCR, and sequencing the resulting amplified product. In the event that there is a sequencing error, reference should be made to the deposited clone as the correct sequence.

USES AND BIOLOGICAL ACTIVITIES OF THE INVENTIVE MOLECULES

The inventive molecules and their derivatives are susceptible to a wide variety of uses, based on functional and/or structural properties. The skilled worker will appreciate, based on the biological activities detailed below, and discussed with regard to the individual sequences disclosed below, that the inventive molecules will find usefulness in numerous therapeutic and diagnostic applications.

The DNA molecules, especially the potassium salts thereof, can be used as fertilizer supplements due to their high nitrogen and phosphorus contents. Since the DNAs are of defined length, they are also useful in gel electrophoresis as molecular weight markers. Due to their similarity with known molecules, certain of the DNA molecules and their variants and derivatives may be used in any number of different diagnostic procedures and therapeutic applications. They may also be used to make the encoded proteins.

The proteins themselves have many possible uses. They may be used as a nutritional supplement for humans, animals and even for laboratory use as, for example, medium for bacterial cultures. Moreover, since the proteins are of defined, known sizes, they may be used as molecular weight markers for gel electrophoresis and gel filtration. Because they are of defined sequences, they also have use in microsequencing and protein fingerprinting applications.

Expression Profiling Applications

Given their known tissue expression and functional associations, assemblages of the inventive proteins (or corresponding antibodies) and nucleic acids are particularly suited to expression profiling applications. Expression profiling generally entails constructing an array of indicators that signal the presence of a particular RNA or protein expression product. Such arrays can be used to evaluate, for example, pharmacological effectiveness and toxicity. In particular, expression profiles from such arrays can be generated from cells treated with known compounds, having known properties, and these profiles can be compared to profiles of unknowns to evaluate similarities and differences, which can be correlated with efficacy or toxicity.

Additional uses of profiling include diagnosis, tracking development, and ascertaining signaling and metabolic pathways. For examples of references describing profiling and its uses, see Farr *et al.*, U.S. Patent 5,811,231 (1998); Seilhamer *et al.*, U.S. Patent 5,840,484 (1998); Rine *et al.*, U.S. Patent No. 5,777,888 (1998); WO 97/27317; WO 99/05323; WO 99/09218; and WO 99/14369. For a device for implementing such techniques, see Lipshutz *et al.*, U.S. Patent No. 5,856,174 (1999) and Anderson et al., U.S. Patent No. 5,922,591 (1999).

In one embodiment, a subset of the inventive DNAs will be arrayed on a substrate, like a gene chip, a filter or a 96-well plate. Test samples containing cells are maintained in the presence of a label capable of incorporation into nascent mRNA. Samples are treated with test and control compounds, which will induce mRNA expression in the sample, resulting in incorporation of label. Whole mRNA is isolated and applied to the array such that it hybridizes with the DNAs contained therein. After washing, the amount of hybridization is quantified and a profile is generated. These steps are repeated with various control and test compounds, thereby generating a library of profiles, which can be used to ascertain the relationships relevant to pharmacological efficacy or toxicity.

The matrices used in such profiling, however, need not be limited to those utilizing DNAs. Rather, other nucleic acids, like RNAs and protein nucleic acids (PNAs), as well as the inventive proteins and antibodies corresponding to the inventive proteins may also be employed. Hence, for example, antibodies could form the array and the samples could be treated in order to label nascent proteins. Whole proteins then would be isolated and applied to the antibody matrix. Developing the resulting signal would result in a protein expression profile, which is useful in essentially the same manner as the nucleic acid profile. A protein matrix could be used, for example, in evaluating antibody responses to pharmaceutical agents in order to eliminate possible cross-reactivity.

Moreover, where nucleic acids are used in the matrix, it is often beneficial to use variants (as defined below) of the molecules described herein. This can be used to account for genetic variations that are of little or no consequence to the function of the resultant gene product. Hence, they can account for wobble or conservative amino acid variations that do not perturb function, like variations in some of the protein motifs elucidated below. Thus, each position in the matrix can employ multiple nucleic acid probes that account for a series of variants.

Expression profiling may also be done, in another embodiment, using two-dimensional protein gels in which the inventive proteins are detected. The resultant profiles can be used in the same way as described.

Matrices useful for profiling may be constructed based on different criteria. Of course, the more relevant profiles will take into account expression of most human genes, preferably all of them. In certain situations, however, it is advantageous to look at a smaller subset. For example, if one were concerned about fetal neural toxicity, a fetal brain-specific matrix might be chosen. On the other hand, if one were interested in targeting mammary carcinoma tissue, a corresponding matrix could be used. Thus, matrices may be constructed using all of the sequences available from a tissue-specific library.

* * *

The following discussion relates to some of the various functional and structural groupings that would be of interest to the artisan wishing to construct profiling matrices. Of course, the artisan will also recognized that these functional descriptions may find additional applicability in the therapeutic and diagnostic applications discussed below.

Cell Cycle

A proliferating cell must coordinate replication and chromosomal separation to ensure that the genome is replicated completely, and that a single copy is correctly inherited by each daughter cell. The cell cycle is the coordinated series of events that achieves these aims. Many of the key events are initiated by a family of conserved Seiren/threonine protein kinases, the cyclin-dependent kinases (CDKs), that are activated by the cyclin family of proteins (cyclins A-H). In turn, the cyclin-CDK complexes are modulated by other protein kinases or phosphatases, and by binding specific inhibitor proteins. The enormous variety of ways in which CDK activity can be regulated allows the cell to respond to internal signals generated by preceding events in the cell cycle and to external growth signals.

The somatic cell cycle is divided into four phases: DNA replication (S phase) and chromosome separation (M phase) are separated by gap phases (G1 and G2). At specific control points the decision to begin the next stage (DNA synthesis or mitosis) is carefully regulated.

Cdc2, the primary kinase, is especially required for the G1-S transition and S phase. Cdc4 and Cdc6 are involved at the restriction point, where the cell can decide to proliferate or arrest (G1<->G0) and Cdc7 is a CDK activating kinase (CAK) as well as a subunit of TFIIH.

The Cyclin-CDK complexes are regulated in various ways. One is through phosphorylation by CDK activating kinases (CAK), like the Y15 kinase (Wee1) and dephosphorylation by CDK associated phosphatases (CAP), like Cdc25A a member of the Cdc25 family (Cdc25A, B and C).

An other way of regulation occurs through two classes of CDK inhibitors (CKI), the INK4 proteins p15, p16, p18, and p19, who negatively regulates the cyclin D CDK complexes and second the p21 family with p21, p27, and p57.

The cell cycle is also regulated through ubiquitin-mediated proteolysis involving the destruction of both cyclins and CDK inhibitors by the 26S proteasome, that requires an ubiquitin conjugating enzyme (UBC) and an ubiquitin ligase. The instability is conferred by PEST regions (cyclin D and E) or a ten amino acid region in the amino terminus (degradation box) in the A- and B-type cyclins.

All these modifications play an important role for the cellular localization, because only the nuclear CDK-cyclin complexes are functional for cell cycle. During G1 phase of the cell cycle, cyclines A, E and D are synthesized and bind to their cyclin-dependent kinase (CDK) partners. CDK complexes containing cyclins A, E and D1 are then imported into and concentrated within nuclei. Cdk6- cyclin D3 has been localized to both cytoplasmic and nuclear compartments, although only the nuclear complex is active. As cells enter S phase, cyclin A and cyclin E complexes remain within the nucleus, whereas cyclin D1 relocalizes to the cytoplasm for proteolysis at the onset of S phase. Like Cdk2-cyclin A, Cdc2-cyclin A is nuclear and remains so until it is degraded during mitosis. By contrast, as a result of ongoing nuclear import and more rapid re-export, cyclin B1, which binds to Cdc2 upon synthesis during S phase, is predominantly cytoplasmic. Cdc2-cyclin B2 is also cytoplasmic, although this might occur through anchoring of the complex to some cytoplasmic constituent. At prophase, phosphorylation of cyclin B1 promotes accumulation of Cdc2-cyclin B1 in the nucleus, whereas cyclin B2 remains in the cytoplasm until nuclear envelope breakdown.

Two crucial regulators of Cdc2-cyclin B-Wee1 and Cdc25C exist and are responsible for the G2 to M control point. Wee1 is a nuclear protein throughout the cell cycle, whereas Cdc25C binds to 14-3-3 proteins during interphase and remains predominantly cytoplasmic. In some systems Cdc25C, like cyclin B1, rushes precipitously into the nucleus just before entry into mitosis.

The 110-kDa retinoblastoma (tumor suppressor) protein (RB), a pRB-family member is an important regulator of cell-cycle progression and differentiation. Like the E2F family (E2F1-5) or DP family (DP1-3) of transcription activators, RB suppresses inappropriate proliferation by arresting cells in G1 by repressing the transcription of genes required for the transition into S phase. Before the cell proceeds into S phase, RB becomes phosphorylated at multiple sites by the cyclin dependent protein kinases (CDKs) and loses its transcriptional repressing activity. Phosphorylation of RB during late G1 phase results in the dissociation of the E2F-RB repressor complex which allows S-phase specific genes to be transcribed. Cyclin E is the evolutionary conserved target for E2F and interacts together with CDC2 in late G1.

For a proliferating cell it is vital that only undamaged DNA is replicated because if DNA damage is substantial, its replication can lead to chromosome loss or rearrangement.

Thus, we find a G1<->S checkpoint in late G1 that requires tumor suppressor p53. A p53-dependent G1 arrest is effected by the cyclin dependent kinase inhibitor p21 through higher expression levels that inhibits almost all cyclin CDK complexes.

The kinase responsible for phosphorylating the unidentified kinetochore component in metaphase may be a member of the MAP kinase family and appears to be the proto oncogene c-MOS, a cytostatic factor (CSF) in meiosis.

Several categories of proteins are coded for by clones of the invention within the overall group of "Cell cycle"and include, among others, the following:

Tumor suppressors (e.g. N33): Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. The N33 gene has been reported by OMIN OMIN (Online Mendelian Inheritance in Man at http://www.ncbi.nlm.nih.gov/htbin-post/Omin) to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) prostate cancer suppression (OMIN *601385). Clones in this category include: fbr2_2k14.

C-TAK1 Cdc25c associated protein kinase: Cdc25C is a protein kinase that controls entry into mitosis by dephosphorylation of Cdc2. Cdc25C function is regulated by phosphorylation, too. Serine 216 phosphorylation of Cdc25C mediates the binding of 14-3-3 protein to Cdc25C. C-TAK1 (Cdc twenty-five C associated protein kinase) phosphorylates Cdc25C on serine 216 in vitro. Alterations in the gene coding for the above protein kinase has been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with Pancreatic cancer (OMIN *60278). Clones in this category include: tes3_7j3.

Cell structure and motility

One of the major differences between prokaryotes and eukaryotes is the ability of the eukaryotic cell to adopt very different shapes dependent on its function during the differentiation process. Animal cells vary from being round to extended cylindric forms like motorneurons or muscle cells. In humans, more than 100 different cell types can be distinguished, each having a characteristic shape. The form of a cell often is closely related to

its capacity to move. Some completely differentiated cells like fibroblasts can still change their form actively, thereby migrating. Other cell types serve as motor elements - "macroscopically" like muscle cells or "microscopically" like ciliated epithelia. Such tasks are fulfilled by a big class of proteins; on the one hand responsible for maintenance of cell structure and contacting neighbor cells or the intercellular matrix and on the other hand for cell motility. These topics cannot be regarded separately: The motility apparatus e.g. must be fixed in the cytoskeleton. Three different types of filaments can be distinguished: Actin filaments, tubulin filaments and intermediate filaments, each present in almost all types of cells.

Actin filaments (F-actin) are built up of monomers (G-Actin). In muscle cells, actin, myosin, for both of which several paralogous genes are known, as well as many more proteins are constituents of the contractile apparatus.

The "thin" and "thick filaments" in a muscle cell consist mainly of actin and myosin, respectively.

Several different proteins are responsible for the anchoring of the actin filaments in the Z-disks (e.g. alpha-actinin and desmin) or at the end of the myofibers in the cell membrane.

Troponin I, -C, -T and Tropomyosin - associated with actin - confer the Ca++-dependent triggering of contraction.

Length of the sarcomere is controlled by the giant protein titin.

In smooth muscle, there is no troponin. Contraction activity is controlled by phosphorylation / dephosphorylation of myosin by a specialized kinase instead. Contractile fibers are not organized in sarcomeres.

Apart from contributing to muscle contraction, the actomyosin system is responsible for many other motions at cellular level, e.g. the amoeboid movement of pseudopodia or the fission of cells at the end of mitosis by a contractile ring.

Besides this, actin fibers fulfill structural tasks like maintenance of the shape of stereocilia or microvilli. Here, actin filaments are connected by proteins like fimbrin. But not

only specialized structures like the mentioned ones contain actin fibers. There is a network covering the complete cell volume with F-actin as a major constituent. Whereas the actin filaments in the structures mentioned above are relatively stable, this F-actin is highly dynamic. Management of the network structure and turnover is achieved by connecting proteins like alpha-actinin, fimbrin or fill-in; turnover is regulated by gelsolin, villin, and different capping- and fragmentation-proteins.

Microtubules are built up of alpha-beta tubulin heterodimers. Turnover of filaments is achieved by building-in and releasing of monomers with different time constant rates at both ends. The resulting cycle is called "treadmilling". Thirteen strings of tubulin duplets build up one subfiber, whereas one fiber contains two or three of those. A complete axoneme consists of 9 radial and 2 central fibers. This "9+2" - structure is the basis both of flagella, their basal bodies and centrioles. In flagella, several additional structures like radial elements exist. Nexin connects the fibers and dyneine is the motor ATPase which shifts the fibers relative to each other. Several genetic diseases like the Cartageneric syndrome are caused by deficiencies of distinct proteins in cilia.

Besides this, microtubules are abundant in all types of cells. They are part of a delivery system for organelles, e.g. in the golgi apparatus. A further very important system based on microtubules is the mitotic spindle, it is organized by the centrosomes. Besides many other components, the major part of a centrosome are two centrioles which are built up of nine microtubule-triplets. Most remarkably, new centrioles are not synthesized de novo but generated by duplication of old ones.

Cytoplasmic microtubules are associated with many different proteins. Two major classes are known: The MAPs ("microtubule-associated proteins", with molecular masses between 200 and 300 kD) and the much smaller tau-Proteins with a MW between 60 and 70 kD. These proteins regulate the treadmill-process and the interaction with other structures in the cell.

Besides actin and myosin the so-called intermediate filaments constitute a third class of filaments. In contrast to the former two groups, they do not participate in motility, nor are they dynamic structures subject to a vivid turnover. The most important ones are

neurofilaments (in neurons), keratin filaments (mainly in epithelial cells), and vimentin filaments (in many sorts different cell types).

The biological function of both the cytoskeleton as well as contractile apparatus of a cell does not end at the cell membrane. Cells must be embedded in the extracellular matrix, all cells of a muscle must act as one single mechanical unit and epithelia must resist macroscopic mechanical forces. Hence, cell adhesion and the extracellular matrix are closely connected to the cytoskeleton. Vincullin is one of the proteins which serve as an anchor for intracellular fibers (actin). Different types of desmosomes and tight junctions connect neighbor cells with intercellular fibers. On the inside, cytoplasmic plaques connect them to the cytoskeleton. These structures, on the one hand, serve as mechanical elements whereas gap junctions, on the other hand, connect cells metabolically.

The extracellular matrix consists of a network of proteins, glycoproteins and polysaccharides. Different proteins are present in relation to different mechanical demands:. Elastin is found in tissues with high elasticity (lungs, heart) whereas collagen, a more hard-wearing protein, is found in tendons and ligaments. Fibronectin is an extracellular protein highly important for cell adhesion.

Reference: Murray J *et al* (1992): Cell Motil Cytoskeleton 22: 211-223.

Within the overall group of Cell Structure and Motility several categories of proteins are coded for by clones of the invention:

Collagen alpha chain proteins: Proteins with the typical (xxG)n repeat of collagen proteins and Pfam von Willebrand factor type A domain(s) suggest they are collagen alpha chains. These proteins can find application in modulation of connective tissue, bone and cartilage development and maintainance. OMIN reports collagen alpha chains have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Osteogenesis imperfecta, type I (OMIN #166200); 2) Osteogenesis imperfecta congenita (OMIN #166210); 3) Alport Syndrome, X-linked (OMIN #301050); 4) Thrombastenia of Glanzmann and Naegeli (OMIN *273800); 5) Ehlers-Danlos Syndrome, Type VII (OMIN #130060); 6) Marfan Syndrome (OMIN #154700); 7) Alport Syndrome, Autosomal Recessive (OMIN #203780); 8) Alpha-2-Deficient Collagen Disease (OMIN 203760); 9) Goodpasture Syndrome (Omin 233450); 10) Osteogenesis Imperfecta,

progressively deforming, with normal sclerae (OMIN #259420); 11)) Ehlers-Danlos Syndrome, Type VII Autosomal Recessive (OMIN *225410); and 12)) Osteogenesis imperfecta, Type IV (OMIN #166220). OMIN reports that von Willebrand factor type A domains have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases:: 1) Hemophilia A (OMIN *306700); 2) Von Willebrand Disease (OMIN *193400); 3) Giant Platelet Syndrome (OMIN *231200); 4) Thrombastenia of Glanzmann and Naegeli (OMIN *273800); 5) Congenital Thrombotic Diseasae due to protein C deficiency (OMIN #176860); 6) Polycystic Kidney Disease 1 (OMIN *601313); 7) Nephrogenic Diabetes Insipidus (OMIN *304800); 8) Factor V Deficiency (OMIN *227400); and 9) Dentatorubral-Pallidoluysian Atrophy (Omin *125370). Clones in this category include: fbr2_2b5.

Radial spokehead protein: Radial spokehead proteins, e.g., Chlamydomonas reinhardtii radial spokehead protein of flagella or axoneme and the Strongylocentrotus purpuratus sea urchin spermatozoa protein p63, and human proteins with similarity thereto are important for the maintenance of a planar form of sperm flagellar beating. The human protein(s) can find application in modulating the structure of the human spermatozoa radial spoke head and modulation of sperm motility in men (e.g., in sterility). Clones in this category include: tes3_15i5.

Ankyrins: Ankyrins are peripheral membrane proteins which interconnect integral proteins with the spectrin-based membrane skeleton. Thus these proteins are involved in coupling of cyto skeleton and cell membrane. OMIN reports that Ankyrins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Heriditary Spherocytosis (OMIN *182900); 2) Hemolytic Poikilocytic Anemia due to reduced ankyrin binding sites (OMIN 141700); 3) Atypical Elliptocytosis (OMIN 225450); 4) Autosomal recessive spherocystosis (OMIN #270970); 5) Werner Syndrome (OMIN *277700); and 6) Rhesus-unlinked type Elliptocytosis (OMIN #130600). Clones in this category include: tes3_1817.

FGD1-related F-actin binding protein (Farbin/FGD1): FGD1-related F-actin-binding protein (Farbin/FGD1) is a novel F-actin-binding protein. The gene locus fgd1 seems to be responsible for faciogenital dysplasia or Aarskog-Scott syndrome. (OMIN 305400). Frabin binds F-actin and shows F-actin-cross-linking activity. Overexpression of frabin in Swiss 3T3 cells and COS7 cells induces cell shape change and c-Jun N-terminal kinase activation, as

described for FGD1. Because FGD1 has been shown to serve as a GDP/GTP exchange protein for Cdc42 small G protein, it is likely that frabin is a direct linker between Cdc42 and the actin cytoskeleton. Cdc42p is an esin yeast, Cdc42p transduces signals to the actin cytoskeleton to initiate and maintain polarized growth and to mitogen-activated protein morphogenesis. In mammalian cells, Cdc42p regulates a variety of actin-dependent events and induces the JNK/SAPK protein kinase cascade, which leads to the activation of transcription factors within the nucleus. Clones in this category include: tes3_72k15.

Paramyosins: Paramyosin is a major structural component of thick filaments and invertebrate muscle. Paramyosins are promising antigens for immunization against several parasites, such as Schistosoma mansoni. Clones in this category include: tes3_7b22.

Tuftelin: Tuftelin/enamelin are matrix proteins of the teeth. As other proteins involved in calcification, these proteins are also expressed in the uterus matrix. The new protein can find application in modulation of tissue-calcification, especially the uterus. As reported by OMIN, tuftelin has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with amelogenesis imperfecta (OMIN *600087). Clones in this category include: ute1_19g22.

Cell Adhesion Regulator (CAR1): CAR1 is involved in the regulation of cell-cell adhesion. OMIN reports the association (as potentially diagnostic, therapeutic, causative, and/or related, etc...) of CAR1 with tumor suppression by the reduction of tumor invasion (OMIN *116935). Clones in this category include: ute1_24j6.

Differentiation/Development

Almost every multicellular organism originates from meiotic cell divisions and the recombination of a paternal and a maternal set of chromosomes. After fertilization of the egg, all cells of a body originate from this one cell. Thus the cells of the developing body are initially genetically alike. But phenotypically they become very different. They are specialized to a certain cell type and arranged in an organized pattern to a certain type of tissue and the whole structure has the well-defined shape of an organ. All these features are determined by the DNA sequence of the genome, which is reproduced in every cell. Each cell acts on the genetic instructions given to a certain time and at a certain place of development and plays its individual part in the multicellular organism. Cell differentiation may be divided into three general steps: cell cycle exit, apoptosis protection and tissue specific gene

expression. These processes are coordinated to provide the final and unique tissue characteristics.

An animal cell that has achieved a certain level of development is said to be determined. This differentiation of a cell may be irreversible and in that case the cell may be renewed only by simple duplication. Other cells are renewed by means of stem cells which are immortal (e.g. stem cells of the bone marrow, epidermal stem cells). The genetic control of development is extensively studied in non-vertebrates and vertebrates. The classical animal model is the fruit fly Drosophilia and the modern model is the transgenic mouse. Animal transgenesis has proven to be useful for physiological as well as physiopathological studies. Besides the approach based on the random integration of a DNA construct in the mouse genome, gene targeting can be achieved using totipotent embryonic stem cells for targeted transgenesis. Transgenic mice are than derived from the embryonic stem cells. This allows the introduction of null mutations in the genome (so-called knock-out) or the control of the transgene expression by the endogeneous regulatory sequence of the gene of interest (so-called knock-in). Mice can be created that express wild-type genes, mutant genes, marker genes or cell lethal genes in a tissue specific manner. These animal models allow to follow changes in tissue and organ development and lead to a better understanding of the cellular function of many genes or to the generation of animal models for human diseases. Fundamental problems in immunology, onset and development of cancer, regulation in fatty acid metabolism, aspects of cardiovascular function, control of the central nervous system development, analysis of reproductive development and function are only some examples of research interests.

The final stage of cell differentiation is growth arrest. In animal tissues with rapid cell turnover terminally differentiated cells undergo programmed cell death. The cells have the ability to kill themselves by activating an intrinsic cell suicide program when they are no longer needed or have become seriously damaged. The execution of this program is termed apoptosis. Apoptosis is of importance for development and homeostasis of animals. The key components of this program have been conserved in evolution from worms (C. elegans) to insects (Drosophilia) to humans. The roles of apoptosis include the sculpting of structures during development, deletion of unneeded cells and tissues, regulation of growth and cell number, and the elimination of abnormal and potentially dangerous cells. In this way

apoptosis provides "quality control mechanism" that limits the accumulation of harmful cells, such as virus-infected cells and tumor cells. On the other hand inappropriate apoptosis is associated with a wide variety of diseases, including AIDS, neuro-degenerative disorders and ischemic stroke. Because it is now clear that apoptosis is a result of an active, gene-directed process, it should be eventually possible to manipulate this form of cell death by developing drugs that interact with its recently identified mechanisms of action. Inducers of cell differentiation, cell cycle arrest and apoptosis might be the novel molecular targets for new anticancer agents in addition to the signaling pathways for growth factors and cytokines.

Proteins, factors, receptors and genes of importance in apoptosis:

Proteases:

- Calpain, an intracellular cysteine protease, exact role unknown.

- Caspase-1 to Caspase-11, a family of proteases synthesized as an inactive proenzyme. Targets of the activated enzymes include: poly(ADP-ribose) polymerase, DNA-dependent protein kinase, U1 ribonucleoprotein, nuclear laminins and cytoskeleton components (actin).

- Granzyme B, a serine protease released by cytotoxic T-cells.

Receptors:

- CD 95 (synonyms: Fas, APO-1), a receptor protein of the TNF-receptor family which includes TNF-R1 and TNF-R2 with the common characteristic of a 70 amino acid cytoplasmic domain.

- FADD (synonym: MORT-1), a cytoplasmic protein

- DR-3 (synonym: APO-3) a member of the TNF-receptor-family

- DR-4 and DR-5

Genes:

- ced-3, ced-4 and ced-9 encode the general apoptotic and antiapoptotic program in Caenorhabditis elegans. Apaf-3 is the mammalian homologue of ced-3.

- Bcl-2 / Bcl-xL / Bax / Bcl-xS / Bak: a large gene family that can either inhibit or promote apoptosis.

- Cytokine response modifier A, a cowpox virus gene whose gene product inhibits caspases.

Others:

- Caspase-activated DNase (CAD) and its inhibitor (ICAD), causes DNA fragmentation in the nucleus

- Ceramide, a complex lipid that acts as a second messenger.

- c-Jun N-terminal kinase (JNK) is a proline-directed kinase

- p53 protein, is essential for the induction of apoptosis as a response to chromosomal damage.

- RAIDD, a death signal-transducing protein.

- Receptor interacting protein (RIP) is an accessory protein with a death domain and a serine/threonine kinase activity.

- Sphingomyelinase, an enzyme that hydrolyzes the complex lipid sphingomyelin to ceramide.

- Tumor necrosis factor (TNF) is a type -II membrane protein

- TNF-receptor associated factor (TRAF2), is an accessory protein that can bind to both TNF-R1 and TNF-R2.

Within the overall group of Differentiation/Development, several categories of proteins are coded for by clones of the invention:

Interleukins (e.g. Interleukin-7): Interleukin precursors related to interleukin-7, for example, are expected to act as new growth factors for human B lineage cells. Additionally,

these proteins should induce the gene rearrangement of the T-cell receptor repertoire, leading to thymocyte commitment, and subsequently induce both cytotoxic T-cell- and lymphocyte-activated killer cells These interleukins could find clinical application in a variety of conditions of hematolymphopoietic failure and different tumours, because of its recruitment of B cell lineage cells, cytotoxic T-cell- and lymphocyte-activated killer cells. (OMIN *146660). Clones in this category include: tes3_35e21.

Testis-specific Y-encoded proteins: The TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. Proteins of the TSPY-SET-NAP1L1 family represent proteins closely related to TSPY. These proteins seem to be involved in early spermatogenesis. Clones in this category include: fbr2_2d15.

Intracellular transport and trafficking

Eukaryotic cells rely for their viability on the partitioning of many basic cellular processes into membrane-bounded organelles. These are the nucleus, endoplasmic reticulum (ER), Golgi apparatus, endosomes, lysosomal compartments, mitochondria and peroxisomes. Most molecules destined for the lysosome, cell surface and outside the cell are routed through the ER and Golgi, which together with the vesicular intermediates between them, comprise the secretory pathway (Palade 1975). In the ER and Golgi compartments proteins are sorted, modified and often assembled into complexes *en route* to their final destination. Incorrectly assembled proteins are retained in the ER until they fold correctly or are targeted for degradation. Additional proteins are translocated into and function within the lumenal spaces of organelles or are secreted. Thus a large proportion of proteins synthesized require targeting to membranes either for insertion into or transport across them. A major purpose of this is growth. The secretory pathway is dependent on an intact cytoskeleton and also closely linked to general metabolism by affecting ribosome biogenesis (Mizuta and Warner, 1994). A huge number of proteins is required for targeting, translocation and sorting of newly synthesized proteins.

The first step in sorting is the recognition of cis-acting targeting or signal sequences that organelle-targeted proteins contain. This is carried out by cytosolic targeting factors and/or receptors on the membrane to which the protein is targeted. In some cases the primary

sequences are extremely degenerate, with only the overall character being conserved (hydrophobicity for an ER signal sequence, helical amphiphilicity for mitochondrial targeting sequence (Kaiser *et al.*, 1987; Lemire *et al.*, 1989). Following the targeting step, proteins are either inserted into or transported across the membrane (translocated) through a proteinaceous apparatus (termed the translocon). The translocon include or recruit motors to drive the translocation process in the correct direction (Schatz and Dobberstein, 1996).

Defined intracellular protein transport steps:

• ER

- targeting to the ER

- translocation into the lumen of the ER, and, depending on the presence of certain signals in the peptide sequence transport through the golgi complex

• Mitochondria

- targeting

- translocation

• Peroxisomes

• The general secretory pathway

- protein modification, assembly and quality control in the ER

- vesicle-mediated trafficking

- vesicle docking and fusion

- transport through the golgi apparatus and sorting at the trans-golgi

- transport to the cell surface

- transport routes to the lysosome

• Endocytosis

• Specialized protein transport routes

• Protein export from the cytoplasm

References: Palade, G (1975) Science 189:347-358; Mizuta et al. (1994) Mol Cell Biol 14: 2493-2502; Kaiser *et al.* (1987) Science 235: 312-317; Lemire *et al.* (1989) J Biol Chem 264: 20206-20215; Schatz et al. (1996) Science 271: 1519-1526.

<u>Rab proteins</u>

In eukaryotic cells the compartmentalisation of processes is a prerequisite for a tight regulation of processes and activities. The cells contain a highly dynamic set of membrane compartments that are responsible for packaging, sorting, secreting, and recycling proteins

and other molecules. Trafficking between organelles within the secretory pathway occurs as vesicles derived from a donor compartment fuse with specific acceptor membranes, resulting in the directional transfer of cargo molecules. This process is tightly controlled by the Rab/Ypt family of proteins (reviewed by Novick and Zerial, 1997), a branch of the superfamily of small GTPases. Rab proteins regulate a variety of functions, including vesicle translocation and docking at specific fusion sites. Rabs may also play critical roles in higher order processes such as modulating the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998).

Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide array of distinct cellular processes.

The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination with a SNAP-25 molecule, coalesce into an elongated -helical bundle (Poirier et al., 1998 ; Sutton et al., 1998), which may lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999). In this regard, Rab proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997).

Concomitant with the SNARE cycle, Rab proteins undergo a intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the membrane upon forming a complex with a cytosolic GDP-dissociation

inhibitor (GDI). This cytosolic intermediate is then recycled onto a newly forming vesicle, most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-6, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal Ca2+-binding C2 domains, implicating these effectors in synaptic vesicle localization or docking in response to Ca2+ influx (Wang et al., 1997). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A

homolog, interacts with the exocyst (Guo et al., 1999), a complex of seven or more subunits that is assembled at sites of vesicle fusion along the plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a Zn2+-finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

References: Dascher et al. (1991) Mol. Cell. Biol. 11, 872-885; Echard et al. (1998). Science. 279, 580-585; Geppert et al. (1998) Annu. Rev. Neurosci. 21, 75-95; Guo et al. (1999). EMBO J. 18, 1071-1080; Kato et al. (1996) J. Biol. Chem. 271, 31775-31778; Novick et al. (1997) Curr. Opin. Cell Biol. 9, 496-504; Peterson (1999) Curr. Biol. 9, 159-162; Poirier et al. (1998) Nat. Struct. Biol. 5, 765-769; Vitale et al. (1998) EMBO J. 17, 1941-1951; Wang et al. (1997) Nature. 388, 593-598; Yang et al. (1999) J. Biol. Chem. 274, 5649-5653.

Within the overall group of Intracellular Transport and Trafficking several categories of proteins are coded for by clones of the invention.

Rab proteins:

Rab1B is essential for the intracellular transport of nascent low density lipoprotein (LDL) receptor. It is discussed as a universal mediator of endoplasmatic reticulum to Golgi transport of membrane glycoproteins in mammalian cells. . Clones in this category include: fbr2_2i17, fbr2_3b16.

Rab10 appear concentrated on membranes in the perinuclear region. Rab 10 has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases as reported by OMIN: 1) Choroideremia (OMIN *303199); and 2)RETT Syndrome (OMIN 312750). Clones in this category include: fbr2_62I19.

In mice, Rab17 shows epithelial cell specificity. Rab 17 is discussed as candidate gene for the mouse mutations ln (leaden), Tw (twirler), and ax (ataxia). Cloned from a brain cDNA library, the new putative Rab-protein is expected to be involved in vesicle trafficking within neuronal cells. These proteins can find application in modulating the transport of vesicles inside neuronal cells, which are essential for development of functional dendritic processes... Clones in this category include: fbr2_41m15.

Ankyrin G: The ankyrin 3 gene encodes a novel ankyrin, which is expressed in multiple tissues, with very high expression at the axonal initial segment and nodes of Ranvier of neurons in the central and peripheral nervous systems. Ankyrin G shows several tissue-specific alternative mRNA processing. The different ankyrin G proteins participate in maintenance/targeting of ion channels and cell adhesion molecules to nodes of Ranvier and axonal initial segments. Ankyrin G has been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with Werner disease (OMIN *277700). Clones in this category include: fkd2_24p5.

Zn-T-transporters: The Zn-T-transporters are membrane proteins that facilitates sequestration of zinc in endosomal vesicles. In the brain, ZnT-3 mRNA seems to be involved in the accumulation of zinc in synaptic vesicles. Zinc (Zn) is an essential element in normal development and metabolism. Recent studies show that in Alzheimer's disease, Zn functions as a double-edged sword, affording protection against Alzheimer's amyloid beta peptide (the major component of senile plaques) at low concentrations and enhancing toxicity at high concentrations by accelerated aggregation of the amyloid beta peptide. These proteins can find application in modulation of Zinc transport in neuronal cells, thus providing means for a modulation of Alzheimer's amyloid beta peptide plaque formation. (OMIN *602878, *602095). Clones in this category include: fbr2_62f10.

Metabolism

This group includes proteins which are involved in the uptake and consumption of nutrients, and enzymes which are part of the biochemical pathways for energy metabolism or

which are involved in the supply of building blocks of nucleic acids, proteins (NTPs, dNTPs, amino acids) for DNA/RNA and protein synthesis, and fatty acids (membranes), to allow for the generation of higher order structures. This group constitutes the most important and largest group in prokaryotes and lower eukaryotes. The higher the evolutionary level of an organism is, however, the more other protein classes like 'signal transduction', 'cell cycle' and 'differentiation and development' increase in importance and number of representatives.

Proteins involved in the metabolism of energy and compounds (here: other than nucleic acids or proteins) are usually the products of house keeping genes, they are often constitutively and/or ubiquitously expressed.

Several categories of proteins are coded for by clones of the invention within the overall group of Metabolism:

NAT1, ARD1: In yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1. NAT1 controls full repression of the silent mating type locus HML, sporulation and entry into G0. ARD1 is involved in the assembly of the NAT 1-complex. These can find application modulating NAT assembly and action and therefore could be important in metabolism of drugs and environmental mutagens.(OMIN *108345). Clones in this category include: fbr2_3g8.

Apolipoprotein E receptor: In LDL-receptors the class A domains form the binding site for LDL and calcium. The acidic residues between the fourth and sixth cysteines are important for high-affinity binding of positively charged sequences in LDLR's ligands. These proteins can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins. In normal individuals, chylomicron remnants and very low density lipoprotein (VLDL) remnants are rapidly removed from the circulation by receptor-mediated endocytosis in the liver. In familial dysbetalipoproteinemia, or type III hyperlipoproteinemia (HLP III), increased plasma cholesterol and triglycerides are the consequence of impaired clearance of chylomicron and VLDL remnants because of a defect in apolipoprotein E. Accumulation of the remnants can result in xanthomatosis and premature coronary and/or peripheral vascular disease. OMIN reports that apolipoprotein has associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Familial hypercholesterolemia (OMIN 143890); 2) Familial combined hyperlipidemia (OMIN 144250); and 3) Alzheimer disease. (OMIN #104300). Clones in this category include: fbr2_62017.

Ubiquitin carboxyl-terminal hydrolases: Ubiquitin carboxyl-terminal hydrolases (EC 3.1.2.15) (UCH) (deubiquitinating enzymes) are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquinated proteins. OMIN reports that Ubiquitin-specific proteases have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Lung carcinoma (OMIN *603486); 2) x-linked retinal diseases (OMIN *300050); 3) oncogenesis (OMIN *300050);4) ovarian cancer (OMIN *300050). Clones in this category include: fbr2_78k24; htes3_27d1.

Phosphoserine signature (phosphoglucomutases, phosphomannomutase): These proteins take part in the conversion of hexose phosphates. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following disease: Fanconi-Bickel Syndrome (OMIN #227810). Clones in this category include: fkd2_24b15.

NADH ubiquinone oxidoreductase: NADH:ubiquinone oxidoreductase is the first enzyme in the respiratory electron transport chain of mitochondria. It is a a membrane-bound multi-subunit protein. The bovine heart enzyme contains about 40 different polypeptides. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following disease: Brancio-oto-renal syndrome (OMIN *6601445). Clones in this category include: fkd2_3o17.

Transketolases: Transketolase requires thiamin pyrophosphate as cofactor and shows a wide specificity for both reactants, e.g. converts hydroxypyruvate and R-CHO into CO(2) and R-CHOH-CO-CH(2)OH. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: Wernicke-Korsakoff Syndrome (OMIN *277730). Clones in this category include: tes3_17l17.

Fatty acid-CoA synthetases/ligases: These proteins contain AMP-binding domain signature(s), which is present in enzymes which act via an ATP-dependent covalent binding of AMP to their substrate. This domain is found in several CoA synthetases, such as acetate-CoA ligase (EC 6.2.1.1), long-chain-fatty-acid-CoA ligase (EC 6.2.1.3), bile acid-CoA ligase. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic,

causative, and/or related, etc...) with the following diseases: 1) Alport syndrome , mental retardation and elliptocytosis (OMIN *300157); 2) Adrenoleukodystrophy (OMIN *300100). Clones in this category include: tes3_35k17.

ADP/ATP or Adenine Nucleotide Translocataors: These proteins contain mitochondrial energy transfer signature(s) and are most abundant in mitochondria. In its functional state, it is a homodimer of 30-kD subunits embedded asymmetrically in the inner mitochondrial membrane. The dimer forms a gated pore through which ADP is moved from the matrix into the cytoplasm.. OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) cardiomyopathy (OMIN *103220); 2) myopathy (OMIN *103220); 3)Progressive external ophthalmoplegia (OMIN *601227). Clones in this category include: tes3_35n12.

Carboxylesterases: OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1)hepatic carboxylesterase with detoxification of foreign compounds (OMIN *114835); 2) non-Hodgkin lymphoma (OMIN *114835); 3) B-cell chronic lymphocytic leukemia (OMIN *114835); 4) rheumatoid arthritis (OMIN *114835). Clones in this category include: tes3_35n9.

Heat shock proteins: OMIN reports that these proteins have associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1)27 kd heat shock protein has been correlated with thermotolerance in response to environmental challenges and developmental transitions. (OMIN *6021295). Clones in this category include: utel1_23e13.

Nucleic acid management

The genetic information is stored in the form of nucleic acids in all organisms. Two kinds of nucleic acids exist, DNA and RNA. Whereas the more stable DNA in most organisms constitutes the storage form of the genetic information, the labile RNA and in particular mRNA is an intermediate used for the temporal expression of specific genes.

In eukaryotes, DNA is usually a double stranded linear molecule consisting of two antiparallel strands and made up of a deoxyribose, a phosphorus backbone and the four bases A, C, G, and T. The DNA of some organisms has a ring structure. The structure of DNA was

unraveled years ago by Watson and Crick. DNA is directional molecule determined by the C-atoms of the sugar.

The most important processes dealing with nucleic acids are:

- replication (e.g. DNA polymerases, Telomerase)
- transcription (RNA polymerases)
- RNA processing (maturation - splicing and degradation)
- in addition, enzymes and proteins exist which require a nucleic acid (mostly RNA) in the active center to be functional (ribozymes - e.g. RNase, Ribosomal proteins)

The DNA of a cell is replicated in the S-phase of the cell cycle. Several enzymes carry out the task of doubling this nucleic acid. As all steps of the cell cycle, also the process of replication is tightly regulated. The enzyme DNA polymerase and several other proteins are involved in this process. Whereas many prokaryotes do have only one origin of replication (i.e., the starting point of the replication cycle), in eukaryotic DNAs (chromosomes) multiple such start points exist. The switch from the synthesis (S) phase to the subsequent G2 or M phases of the cell cycle are dependent on the completion of the replication. This makes clear, that a number of proteins are involved in the replication itself as well as in the control of the process. Since most eukaryotic chromosomes are linear structures, additional proteins and enzymes are necessary to make sure that the structure is maintained through successive generations. This includes those proteins necessary to build the three dimensional structure of chromosomes (e.g. histones) and the structural network of the nucleus and nucleolus (including the defined localization of transcriptionally active genes in the vicinity of nucleoli) but also such enzymes as telomerase which guarantees the integrity of the chromosomal ends.

The expression of genes is usually performed in two steps. First a messenger RNA (mRNA) is produced (transcribed) in one to many copies and second this mRNA is translated into the protein product. The regulation of transcription is discussed under the separate heading 'transcription factors', but also the classes 'signal transduction', 'development', 'cell cycle' and others are affected as the expression of certain genes determines the fate of a cell or organism.

The primary transcript (hnRNA - heterogeneous nuclear RNA) is a single stranded one-to-one copy of the gene as it is located on the chromosome. Before a protein can be translated, already during transcription the process of maturation is initiated. Firstly, a 5' cap structure is enzymatically and covalently added to the RNA, blocking the 5' end of the RNA.

Second, when the RNA polymerase has terminated polymerization, the enzyme poly A polymerase adds varying numbers of adenine residues to the 3' end of the transcript. This enzyme recognizes the sequence AAUAAA or AUUAAA (+ some minor variations), cuts the RNA 10 - 30 nucleotides downstream and adds the A residues. The size of the poly A sequence affects the stability of the RNA. Finally, in the process of splicing, the introns present on the genomic level and also present in the hnRNA are spliced out by a multi-protein complex consisting of several proteins and RNAs. The finally maturated mRNA is exported to the cytoplasm where it is translated with help of the ribozymes.

The half life of RNA is usually much shorter than that of DNA. Usually, the mRNA is degraded shortly after synthesis, to guarantee a very defined window of expression of a given gene. This regulation is necessary to specifically maintain or change the set of proteins present at any time in a cell. Specific regions in the 3'UTR (untranslated region) determine the stability of the mRNA in the cytoplasm before it is degraded by RNases, enzymes consisting both of protein and RNA.

References: Watson and Crick (1953) Nature **171**: 737-738.

Several categories of proteins are coded for by clones of the invention within the overall group of "Nucleic acid management"and include, among others, the following:

<u>RNA helicases including DEAD/H box helicases</u>: RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. DEAD box proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by with the following disease processes and/or genes: 1) ataxia-telangiectasia gene: "A human gene (DDX10) encoding a putative DEAD-box RNA helicase at 11q22-q23" *Genomics* 33:199-206, 1996, Savitsky et al., (OMIN *601235); 2) hematopoetic tumors: "Cloning and expression of a murine cDNA homologous to the human RCK/P54, a lymphoma-linked chromosomal breakpoint 11q23", Gene 166:293-6, 1995, Seto et al. (OMIN *600326); 3) dermatomyositis: a) "The major dermatomyositis-specific Mi-2 autoantigen is a presumed helicase involved in transcriptional activation."

Arthritis Rheum. 38: 1389-1399, 1995, Seelig et al. (OMIN *603277); b) "Two forms of the major antigenic protein of the dermatomyositis-specific Mi-2 autoantigen." (Letter), *Arthritis Rheum.* 39: 1769-1771, 1996., Seelig et al. (OMIN *603277); c) "The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activities", *Cell* 95: 279-289, 1998. Zhang et al. (OMIN *603277); 4) Muscular Dystrophy, Pseudohypertrophic Progressive Duchenne and Becker Types (OMIN *310200); 5) Mucopolysaccharidosis Type IVA (OMIN *253000); 6) Albinism I (OMIN *203100); 7) Wilms Tumor 1 (OMIN *194070); 8) Spinocerebellar Ataxia 7 (OMIN *164500). Clones in this category include: fbr2_23b10, fbr2_3cl8, fbr2_6o17, fbr2_82i24, and tes3_14h21.

<u>Inorganic pyrophosphatase</u>: Inorganic pyrophosphatase (EC 3.6.1.1) (PPase) is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed as the product of the many biosynthetic reactions that utilize ATP. All known PPases require the presence of divalent metal cations, with magnesium conferring the highest activity. Clones in this category include: fbr2_64a15.

<u>DNA-damage –inducible protein (dinP) or Proteins induced by DNA-Damage</u>: The dinB/P pathway is a second SOS-pathway in E.coli. Genes related to this seem to be involved in modulating DNA repair and mutagenesis. Clones in this category include: fbr2_72b18.

<u>Proteins with myc-type, helix-loop-helix dimerization domain signature(s)</u>. This helix-loop-helix domain mediates protein dimerization has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers. Therefore, these proteins could be novel DNA-binding proteins. Clones in this category include: fbr2_72l12.

<u>Cytosolic ribosomal proteins L36</u>: L36 seems to be part of the eukaryotic ribosomal peptidyl transferase center and can find application in modulation of ribosome assembly, maintenance and activity. Clones in this category include: fkd2_3b2.

<u>Ribonuclease H</u>: Ribonuclease H proteins are RNA modificating proteins and have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases as reported by OMIN: 1) Adenomatous Polyposis of the Colon (OMIN

*175100); 2) Retinoblastoma (OMIN *180200) ; and 3) Von Hippel-Lindau Syndrome (OMIN *193300). Clones in this category include: phtes3_15j3.

Signal transduction

Cells in higher order organisms need to continuously communicate with its environment especially with other cells of the same organism in order to maintain the function and specialization of the whole system these cells are part of. This important task of communication is performed with help of cell-surface receptors which receive and transmit signals from outside into the cell.

G-proteins

The largest known family of cell-surface receptors is that of the G-protein-coupled receptors, which mediate the transmission of diverse stimuli such as neurotransmitters, glycopeptides, hormones, peptides, odorant molecules, and photons. The functional unit of these receptors is composed of the receptor molecule itself (GPCR) which is anchored in the cytoplasma membrane with seven membrane spanning domains, the heterotrimeric G-protein which is composed of α and $\beta\gamma$-subunits (Gα and G$\beta\gamma$), and the effectors that interact with Gα and / or G$\beta\gamma$. In particular, the dissociated Gα and G$\beta\gamma$ can regulate the activities of a number of effector molecules such as adenylate cyclases, phopholipase C isoforms, ion channels, and tyrosine kinases, resulting in a variety of cellular functions. The process of signal transduction must be tightly regulated and reversible in order to avoid overstimulation, to achieve signal termination, and render the receptor responsive to subsequent stimuli [Iacovelly L. et al., (1999) *FASEB J.* **13**, 1-8, Hamm, H.E. (1998) *J. Biol. Chem.* **273**, 669-672].

G-proteins are GTPases that, upon binding of GTP change their conformation which in return unmasks structural motives, in particular the so called effector loop, which can mediate the interactions to target proteins, or effectors, for the GTPases. This ability enables the GTPases to cycle between active, GTP-bound and inactive, GDP bound conformations and in the process to function as molecular traffic lights in a multitude of signal transduction pathways. The most important of these signal transduction pathways that are regulated with help of G-proteins are that of the phospholipase C / protein kinase C and that of the adenylate cyclase / protein kinase A.

The cycling of GTPases is tightly regulated by three main classes of proteins: The exchange of hydrolyzed GDP for a fresh GTP is facilitated by guanosine nucleotide exchange factors (GEFs), the hydrolysis of GTP to GDP is sped up by GTPase-activating proteins (GAPs), and the dissociation of GDP from the GTPases is inhibited by GDP dissociation inhibitors (GDIs) [Tapon and Hall (1997) *Curr.Opin. Cell. Biol.* **9**, 86-92, Van Aelst and D-Souza-Schorey (1997) *Genes Dev.* **11**, 2295-2322].

SOC-family

A conserved motif that was originally identified in proteins that negatively regulate the signaling action of cytokines was termed SOCS box, the Suppressor Of Cytokine Signaling. Based on homology, five distinct structural protein classes have been identified since that carry this motif. The function of most of these proteins is presently not known. Common to the proteins is only the SOCS box which is located near the C-terminus of the respective peptides. Recently, the SOCS box has been demonstrated to induce binding of proteins to elongins B and C which could target the proteins (and bound substrates) to the proteasomal protein degradation pathway (Kamura, T. *et al.* (1998) *Genes Dev.* **12**, 3872-3881; Zhang, J.-G. *et al.* (1999) *Proc. Natl. Acad. Sci. USA* **96**, 2071-2076).

The class where the SOCS box was originally described contains several members (SOCS-1-SOCS-7 and CIS). In addition to the SOCS box, these proteins also contain a SH2 (Src-homology 2) domain and a variable N-terminus. These SOCS proteins appear to form part of a classical negative feedback loop that regulates cytokine signal transduction. Upon cytokine stimulation, expression of SOCS proteins is rapidly induced and the proteins inhibit further cytokine action. The mode of action of the SOCS proteins is variable. While SOCS-1 binds and inhibits the JAK (Janus kinases) family of cytoplasmic protein kinases [Narahzaki M. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 13130-13134, Nicholson, S.E. *et al.* (1999) *EMBO. J.* **18**, 375-385], CIS appears to act by competing with signaling molecules such as the STATs (Transducers and Activators of Transcription) family for binding to phosphorylated receptor cytoplasmic domains [Yoshimura, A. *et al.* (1995) *EMBO J.* **14**, 2816-2826; Matsumoto, A. *et al.* (1997) *Blood* **89**, 3148-3154].

A second class of SOCS box protein contains additionally WD-40 repeats which were initially identified in the mouse WSB-1 and -2 proteins. The functions of WD-40 proteins are not completely understood but seem to be rather divergent. In Cdc4p the WD-40 repeats probably are necessary for binding the substrate for Cdc34p [Mathias, N. *et al.* (1999) *Mol.*

Cell Biol. **19**, 1759-1767]. Cdc4p is a component of a ubiquitin ligase that tethers the ubiquitin-conjugating enzyme Cdc34p to its substrates. The posttranslational modification of a protein by ubiquitin usually results in rapid degradation of the ubiquitinated protein by the proteasome. The transfer of ubiquitin to substrate is a multistep process where WD-40 repeats might play an important function.

Other WD-40 containing proteins (e.g. the retino blastoma binding protein RbAp48) have been shown to bind metal ions (Zinc) and that this metal binding might mediate and/or regulate protein-protein interactions which are functionally important in chromatin metabolism [Kenzior, A.L. and Folk, W.R. (1998) *FEBS Lett.* **440**, 425-429]. These proteins are involved in the RAS-cAMP pathway that regulates cellular growth [Ach R.A. *et al.* (1997) *Plant Cell* **9**, 1595-1606].

The SPRY domain has been identified in pyrin or marenostrin, a protein which is mutated in patients with Mediterranean fever and which is similar to the butyrophilin family. While butyrophilins seem to be involved in the lactation process in mammals, the function pyrin is unknown. Three proteins (SSB-1 to -3) have been identified to contain both SPRY and SOCS box motifs. The function of these proteins is also not known.

Ankyrin repeat containing proteins share a 33-residue repeating motif, an L-shaped structure with protruding β-hairpin tips which mediate specific macromolecular interactions with cytoskeletal, membrane, and regulatory proteins. These proteins play fundamental roles in diverse biological activities including growth and development, intracellular protein trafficking, the establishment and maintenance of cellular polarity, cell adhesion signal transduction, and mRNA transcription. Three proteins that contain ankyrin repeats (ASB-1 to -3) have been identified to contain a C-terminal SOCS box additionally to the ankyrin repeats. The function of these proteins or the individual domains remains to be discovered [Hilton, D.J. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 114-119].

A few small GTPases (RAR and RAR like) do also contain a SOCS box. GTPases are involved in signal transduction during cellular communication. The function of the SOCS box in this type of proteins is currently unclear [Hilton, D.J. *et al.* (1998) *Proc. Natl. Acad. Sci. USA* **95**, 114-119].

<u>Ca^{2+} as second messenger</u>

The bivalent cation Ca^{2+} is, besides cAMP, one of the two major second messengers in eukaryotic cells. Its intracellular concentration is tightly regulated and usually kept very

low compared to the cell's environment. Ca^{2+} binding proteins and transporters (Gap junction, Voltage-gated, second messenger-gated) help to sequester huge amounts of the ion in various organelles from where Ca^{2+} can be released upon extracellular stimuli. E.g. the contraction of the muscle is dependent on the presence of Ca^{2+} ions which are readily transported back into the organelles in order for the muscle to relax. In signal transduction, Ca^{2+} functions as a second messenger that activates Ca^{2+} dependent processes through the activation of Ca^{2+}/calmodulin dependent protein kinases (CaM kinases) which are the major effector molecules of Ca^{2+}. In the signaling cascades, the CaM dependent kinases activate phospholipases (e.g. phospholipase C) that in return activate other protein kinases such as protein kinase C.

<u>cAMP</u>

The cyclic AMP is produced by the enzyme adenylate cyclase in response to extracellular signals. Certain G-proteins stimulate the activity of adenylate cyclase which converts ATP to cAMP and PPi. Two molecules of cAMP bind to each of two regulatory subunits of cAMP dependent protein kinase which in turn dissociate from the two catalytic subunits of the heterotetramer R_2C_2. Upon release of the C-subunits, they become active and phosphorylate substrate proteins at Ser and Thr residues. The process leading from binding of extracellular molecules to their receptors, the transmission of the stimuli into the cell, the activation of adenylate cyclase and the subsequent activation of cAMP dependent protein kinase is one of two major signal transduction pathways in eukaryotic cells. Since the phosphorylation of proteins is a posttranslational modification of proteins, the kinases are described in the class "signal transduction."

<u>SARA</u>

Members of the transforming growth factor ß (TGFß) superfamily signal through a family of cell-surface transmembrane serine/threonine kinases, known as type I and type II receptors (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). Ligand induces formation of heteromeric complexes of these receptors, and signaling is initiated when receptor I is phosphorylated and activated by the constitutively active kinase of receptor II (Wrana et al., 1994). The activated type I receptor kinase then propagates the signal to a family of intracellular signaling mediators known as Smads (contraction of the C.elegans Sma and Drosophila Mad genes which were the first identified members of this class of signaling effectors).

Three classes of Smads with distinct functions have been defined: the receptor-regulated Smads, which include Smad1, 2, 3, 5, and 8; the common mediator Smad, Smad4; and the antagonistic Smads, which include Smad6 and 7 (Heldin et al., 1997; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). Receptor-regulated Smads (R-Smads) act as direct substrates of specific type I receptors, and the proteins are phosphorylated on the last two serines at the carboxyl terminus within a highly conserved SSXS motif (Macías-Silva et al., 1996 ; Abdollah et al., 1997 ; Kretzschmar et al., 1997 ; Liu et al., 1997b ; Souchelnytskyi et al., 1997). Regulation of R-Smads by the receptor kinase provides an important level of specificity in this system. Thus, Smad2 and Smad3 are substrates of TGFß or activin receptors and mediate signaling by these ligands (Macías-Silva et al., 1996 ; Liu et al., 1997b ; Nakao et al., 1997), whereas Smad1, 5, and 8 are targets of BMP receptors and propagate BMP signals (Hoodless et al., 1996 ; Chen et al., 1997b ; Kretzschmar et al., 1997 ; Nishimura et al., 1998). Once phosphorylated, R-Smads associate with the common Smad, Smad4 (Lagna et al., 1996 ; Zhang et al., 1997), and mediate nuclear translocation of the heteromeric complex. In the nucleus, Smad complexes then activate specific genes through cooperative interactions with DNA and other DNA-binding proteins such as FAST1, FAST2, and Fos/Jun (Chen et al., 1996 , Chen et al., 1997a ; Liu et al., 1997a ; Labbé et al., 1998 ; Zhang et al., 1998 ; Zhou et al., 1998). In contrast to R-Smads and Smad4, the antagonistic Smads, Smad6 and 7, appear to function by blocking ligand-dependent signaling (reviewed in Heldin et al., 1997).

Phosphorylation of R-Smads by the type I receptor is essential for activating the TGFß signaling pathway (Heldin et al., 1997 ; Attisano and Wrana, 1998 ; Kretzschmar and Massagué, 1998). However, little is known of how Smad interaction with receptors is controlled. A novel Smad2/Smad3 interacting protein has been described (Tsukazaki T. et al., 1998) that contains a double zinc finger, or FYVE domain, and which has been called SARA (<u>S</u>mad <u>a</u>nchor for <u>r</u>eceptor <u>a</u>ctivation). The SARA motif recruits Smad2 into distinct subcellular domains and co-localizes and interacts with TGFß receptors. TGFß signaling induces dissociation of Smad2 from SARA with concomitant formation of Smad2/Smad4 complexes and nuclear translocation. Moreover, deletion of the FYVE domain in SARA causes mislocalization of Smad2 and inhibits TGFß-dependent transcriptional responses. Thus, SARA defines a component of TGFß signaling that functions to recruit Smad2 to the receptor by controlling the subcellular localization of Smad.

References: Abdollah et al. (1997) J. Biol. Chem. 272, 27678-27685; Attisano et al. (1998) Curr. Opin. Cell Biol. 10, 188-194; Chen et al. (1996) Nature 383, 691-696; Chen et al. (1997a) Nature 389, 85-89; Chen et al. (1997b) Proc. Natl. Acad. Sci. USA 94, 12938-12943; Heldin et al. (1997) Nature 390, 465-471; Hoodless et al. (1996) Cell 85, 489-500; Kretzschmar et al. (1998) Curr. Opin. Genet. Dev. 8, 103-111; Kretzschmar et al. (1997) Genes Dev. 11, 984-995; Labbé et al. (1998) Mol. Cell 2, 109-120; Lagna et al. (1996) Nature 383, 832-836; Liu et al. (1997a) Genes Dev. 11, 3157-3167; Liu et al. (1997b) Proc. Natl. Acad. Sci. USA 94, 10669-10764; Macías-Silva et al. (1996) Cell 87, 1215-1224; Nakao et al. (1997) EMBO J. 16, 5353-5362; Nishimura et al. (1998) J. Biol. Chem. 273, 1872-1879; Souchelnytskyi et al. (1997) J. Biol. Chem. 272, 28107-28115; Tsukazaki et al. (1998) Cell 95, 779-791; Wrana et al. (1994) Nature 370, 341-347; Zhang et al. (1997) Curr. Biol. 7, 270-276; Zhang et al. (1998) Nature 394, 909-913; Zhou et al. (1998) Mol. Cell 2, 121-127.

Calcium

The bivalent cation Ca^{2+} is, along with cAMP, one of the two major second messengers in eukaryotic cells. Its intracellular concentration is tightly regulated and usually kept very low compared to the cell's environment. Ca^{2+} binding proteins and transporters (Gap junction, Voltage-gated, second messenger-gated) help to sequester huge amounts of the ion in various organelles from where Ca^{2+} can be released upon extracellular stimuli. E.g. the contraction of the muscle is dependent on the presence of Ca^{2+} ions which are readily transported back into the organelles in order for the muscle to relax. In signal transduction, Ca^{2+} functions as a second messenger that activates Ca^{2+} dependent processes through the activation of Ca^{2+}/calmodulin dependent protein kinases (CaM kinases) which are the major effector molecules of Ca^{2+}. In the signaling cascades, the CaM dependent kinases activate phospholipases (e.g. phospholipase C) that in return activate other protein kinases such as protein kinase C.

Rab proteins

In eukaryotic cells the compartmentalization of processes is a prerequisite for a tight regulation of processes and activities. The cells contain a highly dynamic set of membrane compartments that are responsible for packaging, sorting, secreting, and recycling proteins and other molecules. Trafficking between organelles within the secretory pathway occurs as

vesicles derived from a donor compartment fuse with specific acceptor membranes, resulting in the directional transfer of cargo molecules. This process is tightly controlled by the Rab/Ypt family of proteins (reviewed by Novick and Zerial, 1997), a branch of the superfamily of small GTPases. Rab proteins regulate a variety of functions, including vesicle translocation and docking at specific fusion sites. Rabs may also play critical roles in higher order processes such as modulating the levels of neurotransmitter release in neurons, a likely mechanism in synaptic plasticity that underlies learning and memory (Geppert and Südhof, 1998).

Small GTPases share a common three-dimensional fold that, in the GTP bound state, can bind a variety of downstream effector proteins. GTP hydrolysis leads to a conformational change in the "switch" regions that renders the GTPase unrecognizable to its effectors. In this way, by localizing and activating a select set of effectors, a common structural motif is used to control a wide array of distinct cellular processes.

The final steps in membrane fusion are likely to be driven by a set of proteins known as SNAREs. After a vesicle becomes docked, the cytoplasmic domains of VAMP (also termed synaptobrevin) and syntaxin on opposing membranes, in combination with a SNAP-25 molecule, coalesce into an elongated -helical bundle (Poirier et al., 1998 ; Sutton et al., 1998), which may lead to fusion. Because numerous SNARE isoforms have been identified that localize to distinct membrane compartments, it was originally proposed that the specificity of interaction between the SNARE proteins accounted for the specificity in membrane trafficking. Recent results, however, suggest that SNAREs are not specific in their ability to form complexes in vitro, suggesting that trafficking specificity requires additional factors (Yang et al., 1999). In this regard, Rab proteins are strong candidates for governing the specificity of vesicle trafficking. Like the SNAREs, many isoforms (40) of the Rab family have been identified that localize to specific membrane compartments (reviewed by Novick and Zerial, 1997).

Concomitant with the SNARE cycle, Rab proteins undergo a intricate cycle of membrane and protein interactions. Rabs are posttranslationally modified at C-terminal cysteines by the addition of two geranylgeranyl groups, which mediate membrane association when the Rab is in the GTP-bound state. After guanine nucleotide hydrolysis occurs, the Rab is extracted from the membrane upon forming a complex with a cytosolic GDP-dissociation inhibitor (GDI). This cytosolic intermediate is then recycled onto a newly forming vesicle,

most likely through a secondary factor termed a GDI dissociation factor (GDF), which displaces GDI. After the Rab becomes membrane bound, a guanidine nucleotide exchange factor (GEF) promotes release of GDP and the subsequent loading of GTP. In its GTP-bound conformation, the Rab is then free to associate with its specific set of effectors, which can in turn trigger events leading to the eventual fusion of the vesicle with a target membrane. To complete the cycle, perhaps after or concurrent with membrane fusion, a GTPase activating protein (GAP) accelerates nucleotide hydrolysis, switching off the GTPase. The remaining GDP-bound Rab can then participate in a new round of fusion.

Rab interactions with effectors are likely to regulate vesicle targeting and membrane fusion in three ways. First, a Rab may specifically facilitate vectorial vesicle transport. Vesicles are transported from their site of origin to acceptor compartments likely through associations with cytoskeletal elements and transport motors. A protein has been identified with a domain structure that suggests a connection between the cytoskeleton and the Rabs. This protein, called Rabkinesin-6, contains a kinesin-like ATPase motor domain followed by a coiled-coil stalk region and a RBD that specifically binds Rab6 (Echard et al., 1998). An additional link with the cytoskeleton is provided by the Rab effector, Rabphilin-3A. Rabphilin-3A has been shown in vitro to interact with -actinin, an actin-bundling protein, but only when not bound to Rab3A (Kato et al., 1996). These results raise the intriguing possibility that Rab proteins regulate vesicle interactions with the cytoskeleton and thereby play an active role in targeting vesicles to their appropriate destinations.

Second, Rab proteins may regulate membrane trafficking at the vesicle docking step. A number of Rab effectors, including Rabaptin-5, EEA1, Rabphilin-3A, and Rim, may serve as molecular tethers. Each effector protein contains a RBD, followed by a linker region (some having the potential to form elongated coiled-coil structures), and a domain capable of interacting with a second Rab or the target membrane. Rabaptin-5, for example, contains two RBDs, one near the N terminus that specifically recognizes Rab4 and a second near the C terminus that binds Rab5 (Vitale et al., 1998). Both Rim, which is localized to the target membrane, and Rabphilin-3A, which is localized to the vesicle, contain N-terminal RBDs and C-terminal Ca2+-binding C2 domains, implicating these effectors in synaptic vesicle localization or docking in response to Ca2+ influx (Wang et al., 1997). Tethering effectors may also recognize protein complexes on the acceptor membrane. Sec4p, a yeast Rab3A homolog, interacts with the exocyst (Guo et al., 1999), a complex of seven or more subunits

that is assembled at sites of vesicle fusion along the plasma membrane. The exocyst complex may therefore function as a landmark for Rab/effector-mediated vesicle docking.

Third, once a vesicle has become tethered to its fusion site, Rab proteins may selectively activate the SNARE fusion machinery. The mechanism of this activation is unknown but may involve direct interactions of Rabs or, more likely, their effectors with SNAREs. For example, Hrs-2 is a protein that binds to SNAP-25 and contains a Zn2+-finger motif characteristic of Rab-binding proteins such as Rabphilin-3A, Rim, EEA1, and Noc2, suggesting that Hrs-2 may form a physical link between Rabs and SNAREs (Bean et al., 1997). In addition, certain mutations in the syntaxin-binding protein Sly1p, the Sec1p homolog utilized in ER to Golgi trafficking, eliminate the requirement for Ypt1p, a Rab protein that functions at this trafficking step (Dascher et al., 1991). Rabs may therefore regulate SNARE associations through Sec1 family members. In support of this idea, a Rab effector was recently found to interact with a vacuole Rab, a Sec1p homolog, and a SNARE protein (Peterson et al., 1999), which suggests that this effector serves to connect Rab and SNARE function. In this way, Rabs and their effectors may facilitate the correct pairing of SNAREs.

References: Dascher et al. (1991). Mol. Cell. Biol. 11, 872-885; Echard et al. (1998). Science. 279, 580-585; Geppert et al. (1998). Annu. Rev. Neurosci. 21, 75-95; Guoet al. (1999). EMBO J. 18, 1071-1080; Kato et al. (1996). J. Biol. Chem. 271, 31775-31778; Novick et al. (1997). Curr. Opin. Cell Biol. 9, 496-504; Peterson et al. (1999). Curr. Biol. 9, 159-162; Poirier et al. (1998). Nat. Struct. Biol. 5, 765-769; Vitale et al. (1998). EMBO J. 17, 1941-1951; Wang et al. (1997). Nature. 388, 593-598; Yang et al. (1999). J. Biol. Chem. 274, 5649-5653.

Kinases

Reversible posttranslational modifications of proteins are major means of regulating cellular activities. Among the various modifications that are carried out by the cells, the addition of phosphoryl groups to Ser/Thr or Tyr residues is the most important and widely used. The phosphorylation of proteins is accomplished by protein kinases, while the reverse reaction, the removal of phosphoryl groups, is carried out by phosphatases. Kinases / Phosphatases regulate key positions e.g. in the processes of cell proliferation, differentiation and communication/signaling. These processes must be tightly regulated in order to maintain a steady state level of cellular fate. Mis-regulation of kinase activities (or that of

phosphatases) is made responsible for a multitude of disease processes such as oncogenesis, inflammatory processes, arteriosclerosis, and psoriasis.

Protein kinases constitute the largest protein family that is currently known. Several hundred kinases have been identified already. Classically, kinases are subdivided into two classes based on the amino acid residues in their substrates that are phosphorylated by the particular enzymes. The kinases specifically add phosphoryl groups from adenosine triphosphate (ATP) or, less frequently, guanosine triphosphate (GTP), either to serine and/or threonine or to tyrosine residues of substrate proteins. An estimated 1,000 to 10,000 proteins present in a typical mammalian cell are believed to be regulated also by the action of protein kinases.

Protein kinases are frequently integral parts of signaling cascades that transmit extracellular stimuli (e.g. hormones, neurotransmitters, growth- or differentiation factors) into the cell and result in various responses by the cells. The kinases play key roles in these cascades as they constitute a sort of 'molecular switches' turning on or off the activities of other enzymes and proteins, e.g. metabolic, regulatory, channels and pumps, receptors, cytoskeletal, transcription factors.

The regulation of kinase activities is accomplished by various means:

The best characterized example for the regulation via regulatory subunits is the cAMP-dependent protein kinase (PKA) which is also a prototype for second messenger activated protein kinases. This enzyme consists of a heterotetramer of two catalytic (C) and two regulatory (R) subunits. Upon binding of two molecules of second messenger (cAMP) in each R subunit, the catalytic subunits are released and active. Both of the catalytic and the regulatory subunits several isoforms exist. The combination of catalytic and regulatory subunits determines the localization of the holoenzyme and also the substrate spectrum that is available for phosphorylation. The consensus pattern necessary to be present in the substrate for PKA action is RRXS/T where X can be any amino acid.

The casein kinase II comprises another examples for holoenzymes that consist of catalytic and regulatory subunits. Other kinases that are activated by second messengers are cGMP-dependent protein kinase and Protein kinase C (PKC) which is activated by diacylglycerol, which in turn is produced by phospholipases by cleavage of phosphatidylcholine.

Receptor kinases usually consists of an extracellular domain which can bind effector molecules (e.g. growth factors and hormones) and transfer the stimulus to the intracellular domain of these proteins which usually is a protein tyrosine kinase. Other tyrosine kinases lack an extracellular domain but are associated with receptors which transfer the signal after effector binding by activating the associated protein kinase enzyme (e.g. Src kinase family; Src, Blk, Fgr, Fyn, Lck Lyn, Yes and Janus kinase family; Jak1-3, Tyk2).

Dysfunction of kinases, e.g. caused by non-functioning regulation, can be the cause of inflammatory diseases and uncontrolled proliferation. v-Src which is a truncated version of the C-Src protooncogene tyrosine kinase is a classical example for this process as v-Src does not contain the regulatory domain of the cellular gene and is thus constitutively active.

Several categories of proteins are coded for by clones of the invention within the overall group of "Signal transduction"and include, among others, the following:

Neurocalcin (Recoverin): Neurocalcin is a Ca(2+)-binding protein with three putative Ca(2+)-binding domains (EF-hands). In cattle, 6 isoforms are differentially expressed in the central nervous system, retina and adrenal gland. Homology with recoverin indicates involvement in Ca2+ dependent activation of guanylate cyclase.. These proteins can find application in modulating/blocking the guanylate cyclase-pathway. Diseases associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with these proteins include as reported by OMIN 1) autosomal dominant cone dystrophy (OMIN *600364); 2) cone dystrophy 3 (OMIN *600364); 3) cancer associated retinopathy (OMIN *179618). Clones in this category include: fbr2_23b21.

Proteins with a WW Domain: Proteins that contain a WW domain which has been originally described as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes. Examples of proteins containing the WW domain are Dystrophin, Utrophin, vertebrate YAP protein (binds the SH3 domain of the Yes oncoprotein), murine NEDD-4 (embryonic development and differentiation of the central nervous system), IQGAP (human GTPase activating protein acting on ras). Therefore these proteins should be involved in intracellular signal transduction. Diseases associated (as

potentially diagnostic, therapeutic, causative, and/or related, etc...) with these proteins include as reported by OMIN 1) Muscular Dystrophy, Pseudohypertrophic Progressive Duchenne and Becker Types (OMIN *310200). Clones in this category include: fbr2_23n16.

Protein substrates for cAMP-dependent protein kinase: Acting as a choride channel or chloride channel inhibitor these proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by OMIN with Cystic Fibrosis (OMIN #219700). Clones in this category include fbr2_82i17.

Sphingosine kinase: Sphingosine kinase is a new type of lipid kinase, which is regulated by growth factors. The enzyme phosphorylates sphingosine, which subsequently exerts intracellular and extracellular actions. Intracellulary, sphingosine 1-phosphate (SPP) promotes proliferation and inhibits apoptosis. In yeast, survival of cells exposed to heat shock indicates is dependent on SPP. Extracellulary, SPP inhibits cell motility and influences cell morphology, effects that appear to be mediated by the G protein-coupled receptor EDG1. These proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) as reported by OMIN with Gaucher Disease, Type I (OMIN *230800). Clones in this category include fbr2_82m6.

Vanilloid Receptors: VR1 seems to play an important role in the activation and sensitization of nociceptors. It is the receptor for e.g. capsaicin, a selective activator of nociceptors, a natural product of capsicum peppers. Related can find application as a target for the development of new nociception-modulating drugs. Clones in this category include tes3_20k2.

RCC1 (Regulator of chromosome condensation): RCC1 (regulator of chromosome condensation) is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein. RCC1 promotes the exchange of bound GDP with GTP, acting as a guanine-nucleotide dissociation stimulator. These proteins can find application in the regulation of gene expression by activition of nuclear GTP-binding proteins. The X-linked retinitis pigmentosa is a result of a defect GTPase regulator, which contains a RCC1-type repeat. OMIN also reports that RCC1 has associations (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with retinitis pigmentosa (OMIN *312610). Clones in this category include tes3_21d4.

Ras inhibitor proteins: Ras is a signal transducting molecule involved in the receptor tyrosine kinase/RAS/Map kinase signalling cascade. Ras proteins bind GDP/GTP and show

intrinsic GTPase activity. Mutations in ras, which change aa 12, 13 or 61 activate the potential of ras to transform cultured cells and are implicated in a variety of human tumours. Ras inhibitor proteins have been associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with many disease processes as reported by OMIN including: 1) Tumors of the lung, breast, brain, pituitary, pancrase, bone, skin, bladder, kidney, ovary, prostate and lymphocyte, Melanoma (OMIN *600160); 2) X-linked non-specific mental retardation (OMIN *300104); 3)adenomatouspolyposis of the colon (OMIN *175100); 4) Beckwith-Wieddemann Syndrome (#130650); and 5) Major affective disorder 1 (OMIN *125480). Clones in this category include ute1_22g21.

Mammalian proteins cornicon involving the EGF-receptor: Cornicon proteins are part of a signal transduction pathway involving the EGF-receptor. The EGF-receptor has been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) Familial hypercholesterolemia (OMIN 143890); 2) Leprechaunism (OMIN #246200); 3) Hemophilia B (OMIN *306900); 4) Ectodermal dysplasia 1; 5) Kartagenerer syndrome (OMIN *244400) and 6) Glioma of the brain (OMIN *137800).). Clones in this category include ute1_22e12.

Transmembrane proteins

Membrane region prediction was effected using the ALOM2 software (Klein et al., 1985; version 2 by K. Nakai). Similar to many other methods, the Kyte & Doolitle (1982) amino acid hydrophobicity scale is used in ALOM2 as the primary variable for classifying sequences in terms of their localization. High prediction accuracy is achieved through the system of intelligent decision rules and the utilization of a carefully selected training data set. The method also generates reliability estimates which makes it possible to distinguish between membrane-spanning proteins (I, intrinsic) and globular proteins with regions of high hydrophobicity buried in the core.

For a protein of length L, the block of length l with maximum hydrophobicity is found:

$$\max H = \max_{k=1,\ldots,L-l+1} (1/l) \sum_{i=k}^{k+l-1} H_i$$

where H_i represents the hydrophobicity of an individual residue.

Let P(I/maxH) and P(E/maxH) be the conditional probabilities that a protein is integral or peripheral, respectively, given its value of maximal hydrophobicity maxH, and let P(I) and P(E) be the prior probabilities of intrinsic and extrinsic membrane proteins estimated from the training set. Then a sequence is assigned to E if

P(E/maxH) > P(I/maxH)

or, after applying the Bayes rule,

P(E)P(maxH/E) > P(I)P(maxH/I),

where the conditional probabilities P(maxH/E) and P(maxH/I) can be determined based on the estimates of probability distributions of maxH in both groups.

Discriminant analysis allows to simplify this task by calculating the odds P(E/MaxH):P(I/maxH) as e^b, where b is the left-hand side of a linear or quadratic inequality. For example, for the window of length 17, the protein is allocated to the peripheral category E based on the empirically derived quadratic inequality:

$1.05(\mathrm{maxH})^2+12.30\mathrm{maxH}+17.49 > 0,$

whereas the optimal inequality for assigning membrane proteins (category I) is linear:

$-9.02\mathrm{maxH} + 14.27 > 0$

The odds parameter can be made more or less stringent. For example, one can require odds at least 1:10 for a protein to be classified as integral. This leads to higher selectivity but less sensitivity.

The boundaries of membrane-spanning regions in putative membrane proteins are detected by means of an iterative procedure whereby the most hydrophobic region corresponding to the value maxH is considered to be membrane and removed from the sequence. The classification procedure is then repeated again for the remaining sequence, and, if such a protein is again classified as integral, the next most hydrophobic region is considered.

Reference: Klein, P., Kanehisa, M., DeLisi, C. (1985) The detection and classification of membrane-spanning proteins. *Biochem Biophys Acta* **815**: 468-476

Transcription factors

Purified eukaryotic RNA polymerase II is unable to initiate promoter-specific transcription. A family of factors that collectively confer RNAPII promoter specificity is known as the general transcription factors (GTFs). They include the TATA-binding Protein (TBP) TFIIB, TFIIE, TFIIF and TFI IH. These factors are conserved among all eukaryotes.

RNAPII complexes containing the entire set of GTFs or a subset of GTFs together with other proteins have been isolated from mammalian and yeast cells. Although purified RNAPII and GTFs are sufficient for promoter-specific initiation, this system fails to respond to activators. This is mediated by a further complex termed mediator complex which associates with the carboxy-terminal heptapeptide domain (CTD) of the largest subunit of RNAPII.

Purification of human RNAPII complexes resulted in two distinct forms of human RNAPII after analysis of functional properties. One complex contained chromatin remodeling activities but was devoid of GTFs. The other complex did not contain factors that modify chromatin but contained a subset of SRB/mediator subunits and GTFs and other polypeptides that mediate transcriptional activation, a scenario similar to that reported for yeast.

A complex designated NAT (~2O SU) for negative regulator of transcription contains RNAPII, Cdk8, homologs of the yeast mediator complex as well as Rgrl and Srb1O/11 known as negative regulators of transcription.

A complex with striking similar structural and functional properties to NAT has been identified designated SMCC (~15 SU) (SRB/mediator coactivator complex), that can also mediate transcriptional activation.

The SMCC complex includes all reported NAT subunits including subunits of the TRAP complex. TRAP is a coactivator complex isolated on the basis of its interaction with the thyroid hormone receptor. Another coactivator complex DRIP, isolated on the basis of its

ability to interact with the vitamin D3 receptor, contains novel subunits as well as subunits of NAT/SMCC and TRAP complexes.

The effects of each of these coactivator complexes is dependent on the TFIID complex. It is not known if the T AF subunits of TFIID are required. It is likely that new coactivator complexes will be uncovered containing both novel and previously defined components.

Beside the huge amount of transcription factors which can be part of the RNAIIP holoenzyme or the coactivator complexes there is an even larger quantity of specific transcription factors binding to promoter elements within the DNA sequences of a given gene leading to activation or repression of transcription. A broad range of cellular responses like differentiation, proliferation, cell death and others are elicited through activating or repressing the transcription of target genes.

There are at least five superclasses of transcription factors:

1. Superclass contains members with characteristic basic domains:

Members are:

Leucine zipper factors, where the basic domain is followed by a leucine zipper of repeated leucine residues at every seventh position. The zipper mediates protein dimerization as a prerequisite for DNA-binding.

Helix-loop-helix factors (bHLH) contain a DNA-binding basic region followed by a motif of two potential amphipathic alpha-helices connected by a loop of variable length also mediating dimerization.

Factors with a combination of Helix-loop-helix and leucine zipper.

Further members of this superclass are NF-l, RF-X, and bHSH like proteins.

2. Superclass comprises factors containing zinc-coordinating DNA-binding domains.

Members are:

Proteins with Cys4 zinc finger of nuclear receptor type, where two such motifs differing in size, composition and function are present in each receptor molecule. Each finger comprises 4 cysteine residues coordinating one zinc ion. The second half including the second cysteine pair has alpha-helix conformation and the helix of the first finger binds to the DNA through the major groove. The sequence between the first two cysteines of the second finger mediates dimerization upon DNA-binding. This class includes the steroid hormone receptors and the thyroid hormone receptor-like factors. Other diverse cys4 zinc fingers have a motif of GATA-type.

Proteins with Cys2His2 zinc finger domain(s). Each finger comprises 2 cysteine and 2 histidine residues coordinating one zinc ion, and in some cases one histidine is replaced by another cysteine. The zinc ion is essential for DNA-binding.

Proteins with Cys6 cysteine-zinc cluster(s). Six cysteine residues coordinate two zinc ions, i. e. two of the thiol groups are coordinating two zinc ions each. Present in many fungal regulators.

Zinc fingers of alternating composition.

3. Superclass contains factors of helix-turn-helix type.

Members are:

Proteins with homeo domains. Homeo domains are three consecutive alpha-helix structures. Helix 3 contacts mainly the major groove of the DNA, some contacts at the minor groove are observed as well. Helix 2 and 3 resemble the helix-turn-helix structure of prokaryotic regulators.

Proteins with Paired box domain(s). This is a DNA-binding domain of approximately 130 amino acid residues. Its N-terminal half is basic, its C-terminal half is highly charged in general. It probably comprises 3 alpha-helices.

Proteins with Fork head / winged helix domain(s). This domain was identified by homology between HNF-3A and fkh. The domain comprises approx. 110 AA. Analysis of the crystal structure has revealed a compact structure of three alpha-helices, the third alpha-helix

being exposed towards the major groove of the DNA. The domain also exerts minor groove contacts. Upon binding to DNA, it induces a bend of 13 degree.

Heat shock factors

Proteins with Tryptophan clusters. The tryptophan clusters comprise several tryptophan residues with a spacing of 12-21 amino acid residues; the subclass of myb-type DNA-binding domains typically exhibit a spacing of 19-21 amino acid residues.

Proteins with TEA domain(s). The TEA domain has been identified as a region which is conserved among the transcription factors TEF-l, TECl and abaA. This domain in TEF-l has been shown to interact with DNA, although two additional regions may also contribute to DNA-binding. It is predicted to fold into three alpha-helices, with a randomly coiled region of 16-18 amino acid residues between helices 1 and 2, and a short stretch between helices 2 and 3 of 3-8 residues.

4. Superclass contains beta-Scaffold Factors with Minor Groove Contacts

Members are:

Proteins with RHR (Rel homology) region.

The structure of the Rel-type DBD exhibits a bipartite subdomain structure, each subdomain comprising a beta-barrel with five loops that form an extensive contact surface to the major groove of the DNA. Particularly, the first loop of the N-terminal subdomain (the highly conserved recognition loop) performs contacts with the recognition element on the DNA, but other loops are involved. The fact that the main DNA-contacts are made through loops has been suggested to provide a high degree of flexibility in binding to a range of different target sequences. Augmenting interactions are achieved by two alpha-helices within the N-terminal Part that form strong minor groove contacts to the A/T-rich center of the B-element. In p65, the sequence between both alpha-helices is much shorter and even helix 2 is truncated. The second, C-terminal domain is necessary mainly for protein dimerization.

p53 proteins

MADS (MCMl-agamous-deficiens-SRF) box proteins. Proteins of this class comprise a region of homology. The DNA-binding domain also comprises the dimerization capability. In the DNA-bound dimer (shown for SRF), two antiparallel amphipathic alpha-helices (alpha-I), form a coiled coil and are oriented approximately parallel on the minor groove. These helices make minor and major groove contacts, the N-terminal extensions form minor groove contacts. The bound DNA is bent and wrapped around the protein. It exhibits a compressed minor groove in the center and widened minor groove in the flanks.

Beta-Barrel alpha-helix transcription factors.

TATA-binding proteins

HMG proteins

Proteins of this class comprise a region of homology with the chromosomal non-histone HMG proteins such as HMG1. This region comprises the DNA-binding domain which in some instances such as HMG1 mediates sequence-unspecific, in other cases such LEF-1 sequence-specific binding to DNA. This domain exhibits a typical L-shaped conformation made up of 3 alpha-helices and an extended N-terminal extension of the first helix. The latter together with helix 1, which contains a kink, form the long arm of the L, whereas helices 1 and 2 form the short arm. Binding to the minor groove induces a sharp bending of the DNA by more than 90 degree, away from the bound protein. The overall topology of the DNA-protein complexes resembles somewhat that of the TBP-TATA box complex.

Heteromeric CCAAT factors

Proteins with Grainyhead domain(s)

Cold-shock domain factors. Cold-shock domain proteins are characterized by a highly conserved region first found in prokaryotic cold-shock proteins. This domain is a single-stranded nucleic acid-binding structure interacting with DNA or RNA. It consists of an antiparallel five-stranded beta-barrel, the strands of which are connected by turns and loops. Within this structure, a three-stranded beta-strand contains a conserved RNA-binding motif, RNPl. Not all CSD proteins are transcription factors. Those which specifically bind to a

certain sequence are termed Y-box proteins. Proteins of this class were previously called protamine-like domain proteins because of having a highly positively charged domain with interspersed proline residues.

Proteins with Runt homology domain

The members of this transcription factor class have been identified on the basis of their homology to a defined region within the Drosophilia protein Runt. The runt domain is part of the DNA-binding domain of these factors. It consists mainly of beta-strands, does not contain alpha-helical regions and seems to be most similar to the palm domain found in DNA polymerase beta (rat).

5. Superclass contains other transcription factors like Copper fist proteins, HMGI(Y), STAT, Pocket domain proteins and Ap2/EREBP-related factors.

The classification of transcription factors originates from TRANSFAC database:

http: //transfac.gbf.de/TRANSFAC/

Reference: Heinemeyer

Several categories of proteins are coded for by clones of the invention within the overall group of "Transcription Factors".and include, among others, the following:

Dcoh: Dcoh is a bifunctional protein, complexed with biopterin. It serves as dimerization cofactor of hepatocyte nuclear factor-1 and catalyzes the dehydration of the biopterin cofactor of phenylalanine hydroxylase. The Dcoh protein has been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) hyperphenylalanemia (OMIN 126090, #264070). Clones in this category include fkd2_46k12.

Signal transducing proteins: Beta-transducin subunits of G-proteins contain WD-40 repeats. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. Due to the zinc finger the novel protein seems to be a new molecule involved in signal transduction and transcription. These proteins have been reported by OMIN to be associated (as potentially diagnostic, therapeutic, causative, and/or related, etc...) with the following diseases: 1) essential hypertension (OMIN *139130). Clones in this category include ute1_1i2.

* * *

The invention, therefore, specifically contemplates the following assemblages of materials, which track the above-identified fourteen functional groupings, that are useful in practicing the profiling aspects of the invention. One type of assemblage is nucleic acid-based and can include the following groupings of sequences and their derivatives: all sequences; human fetal brain sequences; brain derived sequences; human fetal kidney library sequences; kidney derived sequences; human mammary carcinoma library sequences; mammary carcinoma derived sequences; human testis library sequences; testes derived sequences; cell cycle genes; cell structure and motility genes; differentiation and development genes; intracellular transport and trafficking genes; metabolism genes; nucleic acid management genes; signal transduction genes; transmembrane protein genes; and transcription factor genes. Other assemblages contain proteins or their corresponding antibodies or antibody fragments, divided along the same groupings.

Database Applications

Because they are human genes and gene products, the inventive molecules are useful as members of a database. Such a database may be used, for example, in drug discovery and rationale drug design or in testing the novelty and non-obviousness of newly sequenced materials. In addition, they are particularly suited in designing variants for the profiling (and other) applications described herein. Hence, the following discussion of electronic embodiments applies equally to such variants, which, naturally, will be generated and stored using a computer using known methodologies.

Accordingly, one aspect of the invention contemplates a database of at least one of the inventive sequences stored on computer readable media. Again, the individual sequences may be grouped with regard to the individual functional and structural groups mentioned above. While the individual sequences of a database may exist in printed form, they are preferably in electronic form, as in an ascii or a text file. They may also exist as word processing files or they may be stored in database applications like DB2, Sybase, Oracle, GCG and GenBank. One skilled in the art will understand the range of applications suitable for using and storing the electronic embodiments of the invention.

"Computer readable media" refers to any medium which can be read and accessed by a computer. These include: magnetic storage media, like floppy discs, hard drives and magnetic tape; optical storage media, like CD-ROM; electrical storage media, like RAM

and ROM; and hybrids of these categories, like magnetic/optical storage media. One skilled in the art will readily understand the scope of computer readable media and how to implement them.

Biological Activities and Assays for Implementing Therapeutic and Diagnostic Applications

This section provides assays for biological activity that are useful in characterizing and quantifying the biological activity of the inventive molecules and their derivatives, which is relevant to the pharmacological effects of the inventive molecules. As used in this section, it will be understood that "protein" may also refer to the inventive antibodies (including fragments).

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M + (preB M +), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., I. Immunol. 149:3778-3783, 1992; Bowman et al., I. Immunol. 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A. M. and Shevach, E. M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human interleukin gamma , Schreiber, R. D. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L. S. and Lipsky, P. E. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-Nordan, R. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Aced. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, F., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9-Ciarletta, A., Giannotti, J., Clark, S. C. and Turner, K. J. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to modify immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the

tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-vital immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient.

The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient mounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I alpha chain protein and beta 2 microglobulin protein or an MHC class II alpha chain protein and an MHC class II beta chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., I. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J. J. and Brunswick, M. In Current Protocols in Immunology. J. E. e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of

Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M. G. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I. K. and Briddell, R. A. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R. E. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Long term culture initiating cell assay, Sutherland, H. J. In Culture of Hematopoietic Cells. R. I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the

treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and

cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, H. I. and Rovee, D. T., eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

<u>Activin/Inhibin Activity</u>

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle

stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin alpha family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- beta group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of

cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Marguiles, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25:1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153:1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such

receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J. E. Coligan, A. M. Kruisbeek, D. H. Margulies, E. M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation intimation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of

cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in

a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Particular Applications for Certain Clones

The following sets out a non-exclusive list of applications for certain embodiments of the invention. In the interest of economy, applications relevant to multiple embodiments are not duplicated in this list. Other embodiments described in below have similar characteristics, as described therein. The artisan is directed, therefore, to this section for similar descriptions of the functions of other embodiment.

Testes

htes3_15c24: The new protein can find application in modulation of 2-hydroxyacid dehydrogenases-dependent pathways and as a new enzyme for biotechnologic production processes.

htes3_15i5: The new protein can find application in modulating the structure of the human spermatozoa radia spoke head and modulation of sperm motility in men.

htes3_15k11: The novel protein contains a protein kinase ATP-binding region signature and a serine/threonine protein kinase active-site signature. The new protein can find application in modulation of intracellular signal pathways dependent on this kinase.

htes3_17n12: The new protein can find application in modulating/blocking the expression of SOX-controlled genes.

htes3_20k2: The new protein can find application as a target for the development of new nociception-modulating drugs.

htes3_20m18: The new protein can find application in modulation of mitochondrial DNA replication and maintenance.

htes3_20d4: The new protein can find application in the regulation of gene expression by activition of nuclear GTP-binding proteins. The X-linked retinitis pigmentosa is a result of a defect GTPase regulator, which contains a RCC1-type repeat.

htes3_21j15: NY-CO-33 is a protein recognised by autologous antibodies of human colon cancer patients. The novel protein contains 4 C2H2 Zinc fingers and is a new putativ transcription factor. The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

The new protein can find application in modulating chromosome transport in mitosis and meiosis and modulation of cell division.

htes3_26g22: The new protein can find application in modulating chromosome transport in mitosis and meiosis and modulation of cell division. The novel TBP-binding protein is considered to participate in transcription regulation through the interaction with TBP. The new protein can find application in modulation of gene transcription.

htes3_21l16: The new protein can find application in modulation of protein translocation into the endoplasmic reticulum.

htes3_27d1: The novel protein can find application in modulation of ubiquitin- and protein metabolism in cells.

htes3_2m18: The novel protein can find application as multifunctional nuclease / exoribonuclease.

htes3_35b4: The new protein can find application in modulation of the mitotic spindle.

htes3_35b5: The novel protein can find application in modulating the v-ATPase activity in endocytic and secretory organelles.

htes3_35e21: Due to the close relationship to human interleukin-7, the novel interleukin is expected to act as a new growth factor for human B lineage cells. Additionally, the protein should induce the gene rearrangement of the T-cell receptor repertoire, leading to thymocyte commitment, and subsequently induce both cytotoxic T-cell- and lymphocyte-activated killer cells. This new interleukin could find clinical application in a variety of conditions of hematolymphopoietic failure and different tumours, because of its recruitment of B cell lineage cells, cytotoxic T-cell- and lymphocyte-activated killer cells.

htes3_35k16: Therefore it is a new fatty acid-CoA synthetasese/ligase with unknown substrate. The new protein can find application in modulation of fatty acid metabolism and as a new enzyme for biotechnologic production processes.

htes3_35n12: The new protein can find application in modulation of ADP-transport and energy metabolism in cells/mitochondria.

htes3_35n9: The new protein can find application in modulation of carboxylester metabolism and as a new enzyme for biotechnologic production processes.

htes3_35p22: The novel protein is closely raleted to human tre-2 and other enzymes involved in the degradation of ubiquitinated proteins. The human tre-2 oncogene encodes a deubiquitinating enzyme, indicating a role for the ubiquitin system in mammalian growth control. The novel protein can find application in cancer diagnostics and treatment, and in regulating protein stability and growth control via regulation of ubiquitination.

htes3_4h6: The novel kinesin protein can find application in modulating the function of kinesin and modulating intracellular transport via/on microtubules.

htes3_72k15: FGD1-related F-actin-binding protein (Farbin/FGD1) is a novel F-actin-binding protein. The gene locus fgd1 seems to be responsible for faciogenital dysplasia or Aarskog-Scott syndrome. Frabin binds F-actin and shows F-actin-cross-linking activity. Overexpression of frabin in Swiss 3T3 cells and COS7 cells induces cell shape change and c-Jun N-terminal kinase activation, as described for FGD1. Because FGD1 has been shown to serve as a GDP/GTP exchange protein for Cdc42 small G protein, it is likely that frabin is a direct linker between Cdc42 and the actin cytoskeleton. Cdc42p is an esin yeast, Cdc42p transduces signals to the actin cytoskeleton to initiate and maintain polarized growth and to mitogen-activated protein morphogenesis. In mammalian cells, Cdc42p regulates a variety of actin-dependent events and induces the JNK/SAPK protein kinase cascade, which leads to the activation of transcription factors within the nucleus. The novel protein seems to be the human orthologue of rat frabin.

The new protein can find application in modulating of cell structure and motility as well as modulation of the JNK/SAPK pathway.

htes3_72p16: As Mem3, the novel protein is similar to yeast VPS (vacuolar protein sorting) 35. The null allele of VPS35 results in yeast in a differential defect in the sorting of vacuolar carboxypeptidase Y (CPY), proteinase A (PrA), proteinase B (PrB), and alkaline phosphatase (ALP). The new protein can find application in modulation the sorting of proteins into different compartments.

htes3_7b22: The novel protein is related to paramyosin, a major structural component of thick filaments and invertebrate muscle. Paramyosins are promising antigens for immunization against several parasites, such as Schistosoma mansoni. The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamic.

htes3_7j3: The new protein is closely related to C-Tak1 and therefore should be involved in cell-cycle regulation, too. The new protein can find application in modulating/blocking the cell cycle.

htes3_7p9: The nuclear domain (ND)10 also described as POD or Kr bodies is involved in the development of acute promyelocytic leukemia and virus-host interactions. The NDP52 protein is part of this complex structure. In vivo, NDP52 is transcribed in all human tissues, but is redistributed upon viral infection and interferon treatment. ND10 plays an important role in the viral life cycle. The novel protein is similar to NDP52. It contains three leucine zippers and a RGD cell attachment site. This protein seems to be a novel part of the ND819) complex. The new protein can find application in modulation of viral infections and tumour events.

htes3_8m10: The poly(A)-binding protein (PABP) binds to the messenger (mRNA) 3'-poly(A) tail found on most eukaryotic mRNAs and together with the poly(A) tail has been implicated in governing the stability and the translation of mRNA. The new protein can find application in modulation of mRNA translation and processing/stability.

<u>Kidney</u>

hfkd2_24b15: The new protein can find application in modulation of hexose metabolism pathways and as a new enzyme for biotechnologic production processes.

hfkd2_24n20: The new protein seems to be part of the signalling pathway between tyrosine kinases and the membrane/cyto skeleton. The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamics.

hfkd2_3o17: The new protein can find application in modulation of the respiratory electron transport chain pathways of mitochondria.

hfkd2_46j20: The new protein can find application in modulating the homoprotocatechuate degradative pathway and as a enzyme for biotechnologic production processes.

hfkd2_46k19: The new protein can find application in modulating/blocking the expression of genes controlled by the hepatocyte nuclear factor-1.

hfkd2_46m4: SAR1 proteins are involved in vesicular transport between the endoplasmic reticulum and the Golgi apparatus.

hfkd2_46k14: rab6 is a ubiquitous ras-like GTPase involved in intra-Golgi transport. The new protein can find application in modulating the transport of vesicles inside the Golgi apparatus.

<u>Uterus Associated:</u>

hutel_18i19: The SREBP-2 protein is embedded in the membranes of the nucleus and endoplasmic reticulum. In cholesterol-depleted cells the proteins are cleaved to release soluble NH2-terminal fragments that enter the nucleus and activate genes encoding the low density lipoprotein receptor and enzymes of cholesterol synthesis. The new protein is a putative transcription factor capable of protein-protein interaction via a lim domain and additionally shows similarity to the common sunflower transcription factor SF3.

hutel_18l1: The novel protein is similar to several 40S ribosomal proteins and therefore seems to part of the corresponding ribosome sub-unit.

hutel_19g22: The new protein can find application in modulation of tissue-calcification, especially the uterus.

hutel_19h17: The new protein can find application in modulating the response of cells to oxysterols.

hutel_20b19: The novel protein seems to be a novel enzyme with sarcosine oxidase activity. The new protein can find application in modulation of sarcosine metabolism and as a new enzyme for biotechnologic production processes.

hutel_20g21: The novel protein seems to be a new ras inhibitor protein. The new protein can find application in modulating/blocking ras dependent signal transduction pathways.

hutel_20h13: The novel protein is a new human alpha-adaptin. The new protein can find application in modulating endocytosis and vesicle trafficking in cells.

hutel_20m11: The new protein can find application in modulating/blocking the activity of protein phosphatase-1 and in modulating the cell cycle.

hutel_20m24: This protein is a putative mannosyl transferase that is involved in the assembly of the core oligosaccharide Glc3Man9GlcNAc2. The new protein can find application in modulation of glycosylation of proteins and as a new enzyme for biotechnologic production processes.

hutel_22e12: The new protein can find application in modulating the cornichon modulated signal transduction way and also the EGF receptor signaling processes.

hutel_23e13: The novel protein contains a serine protease of the subtilase family with an aspartic acid-containing active site. The new protein can find application in modulation of proteinase activity in cells and as a new enzyme for proteomics and biotechnologic production processes.

hutel_24j6: The new protein can find application in modulation of cell-cell-adhesion.

hutel_24h3: The new protein can find application as a useful marker for chondro-osteogenic cell differentiation and for the modulation of chondro-osteogenic cell differentiation.

Fetal Brain:

hfbr2_16c16: The new protein can find application in modulating/blocking of cyto skeleton-membrane protein interaction.

hfbr2_23b21: The new protein can find application in modulating/blocking the guanylate cyclase-pathway.

hfbr2_23b10: The new protein can find application in modulation of splicing.

hfbr2_2b5: The novel protein contains the typical (xxG)n repeat of collagen proteins and a Pfam von Willebrand factor type A domain. Therefore, the protein seems to be a new collagen alpha chain. The new protein can find application in modulation of connective tissue, bone and cartilage development and maintainance.

hfbr2_2c17: The new protein can find application in modulating/blocking G-protein-dependent pathways.

hfbr2_2d15: The new protein can find application in modulating early spermatogenesis.

hfbr2_2i17: The new protein can find clinical application in modulating the transport of glycoproteins inside cells, especially of the LDL receptor.

hfbr2_2k14: Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. In addition, the novel protein contains a RGD cell attachment site. Therefore the novel protein is a new putative tumour-suppressor gene.

hfbr_3c18: RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. The novel protein contains a DEAD-box and is a new member of this subgroup.

hfbr_3g8: The new protein can find application modulating NAT assembly and action and therefore be important in metabolism of drugs and environmental mutagens.

hfbr2_62b11: The rac small GTPase is associated with type-I phosphatidylinositol 4-phosphate 5-kinase and regulating the production of phosphatidylinositol 4,5-bisphosphate. The new protein is expected to activate p21rac-related small GTPases.

hfbr2_62o17: The new protein can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins.

hfbr_6b24: The new protein can find application in modulation of rhamnose metabolism and as a new enzyme for biotechnologic production processes.

hfbr_72b18: The new protein can find application in modulating DNA repair and mutagenesis.

hfbr_78c4: The new protein can find application in modulating/blocking the response of cells to interferons.

hfbr_78k24: These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquinated proteins. The new protein can find application in modulation of protein stability/degradation in cells.

hfbr_82e4: The new protein can find clinical application in modulating/blocking calmodulin-mediated pathways in human neuronal cells.

VARIANTS OF THE INVENTIVE DNA MOLECULES

Variants in General

"Variants," according to the invention, include DNA and/or protein molecules that resemble, structurally and/or functionally, those set forth in herein. Variants may be isolated from natural sources ("homologs"), may be entirely synthetic or may be based in part on both natural and synthetic approaches.

The section set forth below presents various structural and functional characteristics of molecules within the invention. Preferred molecules are characterized by a combination of one or more of these characteristics. For instance, some preferred molecules are described with reference to at least two structural characteristics, while others may be described with reference to at least one structural and at least one functional characteristic.

It will be recognized by the skilled artisan that structure ultimately defines function, *i.e.* the functions of the molecules described herein derives from the structures of those

molecules. Accordingly, the structural variants described below that bear the closest structural relationship (as variously defined below) to the inventive molecules are the variants that most likely will preserve biological function. This relationship between structure and function will guide the skilled artisan in identifying the preferred embodiments of the invention.

Splicing Variants

It is well-known that eukaryotic structural genes are comprised of both protein coding and non-coding portions. When the messenger RNA is transcribed from the DNA template, it contains introns, which are non-coding, and exons, which are coding. In order to form a translation competent mRNA, the introns must be "spliced" out of this initial pre mRNA.

Specific sequences within the pre mRNA represent "splice junctions" that direct the cellular splicing machinery to the appropriate position. The splice junctions are loosely conserved sequence regions of the pre mRNA, which almost invariably begin with GT and end with AG (DNA perspective). The 5' end of the splice junction typically contains about nine somewhat conserved residues, for example, C/AAGTA/GAGT. The 3' end usually contains a pyrimidine rich stretch of at least about 11 nucleotides, followed by NC/TAGG. Splicing occurs before the GT and after the AG. Mount, *Nucleic Acids Res.* 10:459-72 (1982).

Interestingly, exons often correspond to discrete functional domains of the protein product. The intron/exon arrangement thus creates a linear array of nucleotides which can be correlated to discrete, and often interchangeable, functional protein fragments. Go, *Nature* 291:90-92 (1981); Branden *et al.*, *EMBO J.* 3:1307-10 (1984). This linear arrangement creates the possibility of generating multiple different full length proteins by rearranging the order of the different functional portions in the array. For example, if a set of exons are arranged 1-2-3-4, where (-) represents the introns separating the exons, a splicing event need not simply produce 1234, but may produce 123, 134, 124 and so on. Production of different mRNA products in this way is commonly called "alternative splicing." Andreadis *et al.*, *Ann. Rev. Cell Biol.* 3:207-42 (1987).

Some of the present DNA molecules can be represented in modular fashion in terms of their coding regions. Essentially, these modules are exons (though each "exon" may in fact be made up of several exons), which may be combined in different ways to form a variety of

different DNA molecules, each encoding a different functional protein. Splicing variants are indicated below.

Degenerate Variants

One aspect of the present invention provides "degenerate variants" of the nucleic acid fragments of the present invention. A "degenerate variant" is a nucleotide fragment which differs from those of inventive molecules by nucleotide sequence, but due to the degeneracy of the genetic code, encodes an identical polypeptide sequence.

Given the known relationship between DNA sequences and the proteins they encode, degenerate variants typically are described by reference to this relationship. It is well known that the degeneracy of the genetic code results in many possible DNA sequences which encode a particular protein. Indeed, of the three bases which comprise an amino acid-encoding triplet, the third position, and often the second, almost always may vary. This fact alone allows for a class of variant DNA molecules which encode protein sequences identical to those disclosed herein, yet have about 30% sequence variation. In other words, the variant DNA molecules are about 70% identical to the inventive DNAs, having no additional or deleted sequences. Thus, one aspect of the invention provides degenerate variant DNA molecules encoding the inventive protein sequences.

In one embodiment, these variants have at least about 70% sequence identity with the DNA molecules described herein. In a preferred embodiment, these variants have at least about 80% sequence identity to the inventive molecules. In a more preferred embodiment these variants have at least about 90% sequence identity with the inventive molecules.

Conservative Amino Acid Variants

Variants according to the invention also may be made that conserve the overall molecular structure of the encoded proteins. Given the properties of the individual amino acids comprising the disclosed protein products, some rational substitutions will be recognized by the skilled worker. Amino acid substitutions, *i.e.* "conservative substitutions," may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved.

For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine;

(c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α-helices. Similarly, certain amino acids, such as alanine, cysteine, leucine, methionine, glutamic acid, glutamine, histidine and lysine are more commonly found in α-helices, while valine, isoleucine, phenylalanine, tyrosine, tryptophan and threonine are more commonly found in β-pleated sheets. Glycine, serine, aspartic acid, asparagine, and proline are commonly found in turns. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. "Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions.

Functionally Equivalent Variants

Yet another class of DNA variants within the scope of the invention may be described with reference to the product they encode. As shown below, some of the inventive DNA molecules encode a protein having a degree of homology with known proteins, or protein domains. It is expected, therefore, that they will have some or all of the requisite functional features of such molecules. These "functionally equivalent variants" products are characterized by the fact that they are functionally equivalent, with respect to biological activity, to certain known molecules.

The instant invention provides information on common structural motifs, including consensus sequences that will guide the artisan in constructing functionally equivalent variants. It will be understood that the motifs, identified for each inventive protein, may be modified within the identified consensus sequences. Thus, the invention contemplates the proteins disclosed herein that contain variability in the consensus sequences identified, and the invention further contemplates the full range of nucleic acids encoding them, and the complements of those nucleic acids.

Hybridizing Variants

DNA variants within the invention also may be described by reference to their physical properties in hybridization. One skilled in the field will recognize that DNA can be used to identify its complement and, since DNA is double stranded, its equivalent or homolog, using nucleic acid hybridization techniques. It will also be recognized that hybridization can occur with less than 100% complementarity. However, given appropriate choice of conditions, hybridization techniques can be used to differentiate among DNA sequences based on their structural relatedness to a particular probe. For guidance regarding such conditions see, for example, Sambrook *et al.*, 1989, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, N.Y.; and Ausubel *et al.*, 1989, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Green Publishing Associates and Wiley Interscience, N.Y.

Structural relatedness between two polynucleotide sequences can be expressed as a function of "stringency" of the conditions under which the two sequences will hybridize with one another. As used herein, the term "stringency" refers to the extent that the conditions disfavor hybridization. Stringent conditions strongly disfavor hybridization, and only the most structurally related molecules will hybridize to one another under such conditions. Conversely, non-stringent conditions favor hybridization of molecules displaying a lesser degree of structural relatedness. Hybridization stringency, therefore, directly correlates with the structural relationships of two nucleic acid sequences. The following relationships are useful in correlating hybridization and relatedness (where T_m is the melting temperature of a nucleic acid duplex):

a. $T_m = 69.3 + 0.41(G+C)\%$

b. The T_m of a duplex DNA decreases by 1°C with every increase of 1% in the number of mismatched base pairs.

c. $(T_m)_{\mu 2} - (T_m)_{\mu 1} = 18.5 \log_{10}\mu 2/\mu 1$
where $\mu 1$ and $\mu 2$ are the ionic strengths of two solutions.

Hybridization stringency is a function of many factors, including overall DNA concentration, ionic strength, temperature, probe size and the presence of agents which disrupt hydrogen bonding. Factors promoting hybridization include high DNA

concentrations, high ionic strengths, low temperatures, longer probe size and the absence of agents that disrupt hydrogen bonding.

Hybridization usually is done in two stages. First, in the "binding" stage, the probe is bound to the target under conditions favoring hybridization. Stringency is usually controlled at this stage by altering the temperature. For high stringency, the temperature is usually between 65°C and 70°C, unless short (<20 nt) oligonucleotide probes are used. A representative hybridization solution comprises 6X SSC, 0.5% SDS, 5X Denhardt's solution and 100μg of non-specific carrier DNA. See Ausubel *et al.*, *supra*, section 2.9, supplement 27 (1994). Of course many different, yet functionally equivalent, buffer conditions are known. Where the degree of relatedness is lower, a lower temperature may be chosen. Low stringency binding temperatures are between about 25°C and 40°C. Medium stringency is between at least about 40°C to less than about 65°C. High stringency is at least about 65°C.

Second, the excess probe is removed by washing. It is at this stage that more stringent conditions usually are applied. Hence, it is this "washing" stage that is most important in determining relatedness via hybridization. Washing solutions typically contain lower salt concentrations. One exemplary medium stringency solution contains 2X SSC and 0.1% SDS. A high stringency wash solution contains the equivalent (in ionic strength) of less than about 0.2X SSC, with a preferred stringent solution containing about 0.1X SSC. The temperatures associated with various stringencies are the same as discussed above for "binding." The washing solution also typically is replaced a number of times during washing. For example, typical high stringency washing conditions comprise washing twice for 30 minutes at 55° C. and three times for 15 minutes at 60° C.

The present invention includes nucleic acid molecules that hybridize to the inventive molecules under high stringency binding and washing conditions. More preferred molecules (from an mRNA perspective) are those that are at least 50 % of the length of any one of those depicted in below. Particularly preferred molecules are at least 75 % of the length of those molecules.

Substitutions, Insertions, Additions and Deletions

In a general sense, the preferred DNA variants of the invention are those that retain the closest relationship, as described by "sequence identity" to the inventive DNA molecules. According to another aspect of the invention, therefore, substitutions, insertions, additions and deletions of defined properties are contemplated. It will be recognized that sequence

identity between two polynucleotide sequences, as defined herein, generally is determined with reference to the protein coding region of the sequences. Thus, this definition does not at all limit the amount of DNA, such as vector DNA, that may be attached to the molecules described herein. Preferred DNA sequence variants include molecules encoding proteins sharing some or all of any relevant biological activity of the native molecule.

In creating these variants, the skilled worker will be guided by reference to the protein structure. First, insertions and deletions in any recognized functional domain, above, generally should be avoided, except as noted below in the section entitled "Proteins," where this domain is discussed in detail. Alterations in such domains usually will be limited to conservative amino acid substitutions. In addition, where insertions and deletions are desired, this may be accomplished at the N- and/or C-terminus of the protein molecule (or the corresponding coding regions of the DNA). If insertions or deletions are made within the protein, deletions of major structural features usually should be avoided. Thus, a preferred place to make insertion or deletion variants is in non-structural regions, such as linker regions between two alpha helices.

"Substitutions" generally refer to alterations in the DNA sequence which do not change its overall length, but only alter one or more nucleotide positions, substituting one for another in the common sense of the word. One class of preferred substitutions, "degenerate substitutions," are those that do not alter the encoded amino acid sequence. Some subsitutions retains 50%, 55%, 60% or 65% identity. Preferred substitutions retain at least about 70% identity, more preferably at least 70% or 75% identity, with the inventive DNAs. Some more preferred molecules have at least about 80% identity, more preferably at least 80% or 85% identity. Particularly preferred DNAs share at least about 90% identity, more preferably at least 90% or 95% identity.

"Insertions," unlike substitutions, alter the overall length of the DNA molecule, and thus sometimes the encoded protein. Insertions add extra nucleotides to the interior (not the 5' or 3' ends) of the subject DNAs. Preferred insertions are made with reference to the protein sequence encoded by the DNA. Thus, it is most preferred to provide an insertion in the DNA at a location that corresponds to an area of the encoded protein which lacks structure. For instance, it typically would not be beneficial, if the preservation of biological activity is desired, to provide an insertion within an alpha-helical region or a beta-pleated sheet. Accordingly, non-structural areas, such as those containing helix-breaking glycines

and proline residues, are most preferred sites of insertion. Other preferred sites of insertion are the splice sites, which are indicated above in the description of the inventive DNA molecules.

While the optimal size of insertions will vary depending upon the site of insertion and its effect on the overall conformation of the encoded protein, some general guides are useful. Generally, the total insertions (irrespective of their number) should not add more than about 30% (or preferably not more than 30%) to the overall size of the encoded protein. More preferably, the insertion adds less than about 10-20% (yet more preferably 10-20%) in size, with less than about 10% being most preferred. The number of insertions is limited only by the number of suitable insertions sites, and secondarily by the foregoing size preferences.

"Additions," like insertions, also add to the overall size of the DNA molecule, and usually the encoded protein. However, instead of being made within the molecule, they are made on the 5' or 3' end, usually corresponding to the N- or C- terminus of the encoded protein. Unlike deletions, additions are not very size-dependent. Indeed, additions may be of virtually any size. Preferred additions, however, do not exceed about 100% of the size of the native molecule. More preferably, they add less than about 60 to 30% to the overall size, with less than about 30% being most preferred.

"Deletions" diminish the overall size of the DNA and, therefore, also reduce the size of the protein encoded by that DNA. Deletions may be made from either end of the molecule or internal to it. Typical preferred deletions remove discrete structural features of the encoded protein. For example, some deletions will comprise the deletion of one or more exons which may define a structural feature. Preferred deletions remove less than about 30% of the size of the subject molecule. More preferred deletions remove less than about 20% and most preferred deletions remove less than about 10%.

Computer-Defined Variants and Definition of "Sequence Identity"

In general, both the DNA and protein molecules of the invention can be defined with reference to "sequence identity." As used herein, "sequence identity" refers to a comparison made between two molecules using, for example, the standard Smith-Waterman algorithm that is well known in the art.

Some molecules have at lease about 50%, 55% or 60% identity. Preferred molecules are those having at least about 65% sequence identity, more preferably at least 65% or 70% sequence identity. Other preferred molecules have at least about 80%, more preferably at

least 80% or 85%, sequence identity. Particularly preferred molecules have at least about 90% sequence identity, more preferably at least 90% sequence identity. Most preferred molecules have at least about 95%, more preferably at least 95%, sequence identity. As used herein, two nucleic acid molecules or proteins are said to "share significant sequence identity" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) identity.

"Sequence identity" is defined herein with reference the Blast 2 algorithm, which is available at the NCBI (http://www.ncbi.nlm.nih.gov/BLAST), using default parameters. References pertaining to this algorithm include: those found at http://www.ncbi.nlm.nih.gov/BLAST/blast_references.html; Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) “Basic local alignment search tool.” J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) “Identification of protein coding regions by database similarity search.” Nature Genet. 3:266-272; Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) “Applications of network BLAST server” Meth. Enzymol. 266:131-141; Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997) “Gapped BLAST and PSI-BLAST: a new generation of protein database search programs.” Nucleic Acids Res. 25:3389-3402; and Zhang, J. & Madden, T.L. (1997) “PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation.” Genome Res. 7:649-656.

METHODS OF MAKING VARIANTS

It will be recognized that variants of the inventive molecules can be constructed in several different ways. For example, they may be constructed as completely synthetic DNAs. Methods of efficiently synthesizing oligonucleotides in the range of 20 to about 150 nucleotides are widely available. See Ausubel *et al.*, *supra*, section 2.11, Supplement 21 (1993). Overlapping oligonucleotides may be synthesized and assembled in a fashion first reported by Khorana *et al.*, J. Mol. Biol. 72:209-217 (1971); see also Ausubel *et al*, Section 8.2. The synthetic DNAs are designed with convenient restriction sites engineered at the 5' and 3' ends of the gene to facilitate cloning into an appropriate vector.

An alternative method of generating variants is to start with one of the inventive DNAs and then to conduct site-directed mutagenesis. See Ausubel *et al.*, *supra*, chapter 8, Supplement 37 (1997). In a typical method, a target DNA is cloned into a single-stranded

DNA bacteriophage vehicle. Single-stranded DNA is isolated and hybridized with a oligonucleotide containing the desired nucleotide alteration(s). The complementary strand is synthesized and the double stranded phage is introduced into a host. Some of the resulting progeny will contain the desired mutant, which can be confirmed using DNA sequencing. In addition, various methods are available that increase the probability that the progeny phage will be the desired mutant. These methods are well known to those in the field and kits are commercially available for generating such mutants.

ISOLATING HOMOLOGS

Methods

By using the sequences disclosed herein as probes or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs. "Homologs" are essentially naturally-occurring variants and include allelic, species-specific and tissue-specific variants.

Region-specific primers or probes derived from the nucleotide sequence(s) provided can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog using known methods (Innis *et al., PCR Protocols,* Academic Press, San Diego, CA (1990)). Such an application is useful in diagnostic methods, as described in more detail below, as well as in preparing full-length DNAs from various sources. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. As a general guide, the formula $3(G+C) + 2(A+T) = {}^{\circ}C$, is useful.

When using primers derived from the inventive sequences, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C), only sequences with greater than 75% sequence identity to the primer will be amplified. By employing lower stringency conditions (e.g., annealing at 35-37°C), sequences which have greater than 40-50% sequence identity to the primer also will be amplified.

The PCR product may be subcloned and sequenced to confirm that it indeed displays the expected sequence identity. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled

and used to screen a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to screen a genomic library.

PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source. A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal transferase reaction, the hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see e.g., Sambrook et al., 1989, *supra*.

When using DNA probes derived from the inventive sequences for colony/plaque hybridization, one skilled in the art will recognize that by employing medium to high stringency conditions (e.g., hybridizing at 50-65°C in 5X SSPC and 50% formamide, and washing at 50-65°C in 0.5X SSPC), sequences having regions with greater than 90% sequence identity to the probe can be obtained, and that by employing lower stringency conditions (e.g., hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in SSPC), sequences having regions with greater than 35-45% sequence identity to the probe will be obtained.

Suitably, genomic or cDNA libraries can be constructed and screened in accord with the previous paragraph. The libraries should be derived from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. The clone containing the homolog may then be purified through methods routinely practiced in the art, and subjected to sequence analysis.

Additionally, an expression library can be constructed utilizing DNA isolated from or cDNA synthesized from a tissue or organism that is known to express the gene of interest, or that is suspected of expressing the gene. In this manner, clones may be induced and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal gene product, as described herein. (For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, ANTIBODIES: A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor Press.)

Human Homologs

Any organism or tissue can be used as the source for homologs of the present invention so long as the organism or tissue naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs is human.

PROTEINS OF THE INVENTION

One class of proteins included within the invention is encoded by the inventive DNA molecules presented. Other proteins according to the invention are those encoded by the DNA variants described above. As noted, these variants are designed with the encoded proteins in mind.

A preferred class of protein fragments includes those fragments which retain any biological activity. These molecules share functional features common the family of proteins, although these characteristics may vary in degree.

According to one aspect of the invention fragments of the inventive proteins are contemplated. Some preferred fragments are those which are capable of eliciting an immune response. Generally these "antigenic" fragments will be from about five amino acids in length to about fifty amino acids in length. Some preferred antigenic fragments are from five to about twenty amino acids long. "Antigenic" response may refer to a T cell response, a B cell response or a response by cells of the macrophage/monocyte lineages. In most cases, however, it will refer to the immune response involved in the generation of antibodies. In other words, the relevant immune response is that of helper T cells and/or B cells. These preferred molecules comprise one or more T cell and /or B cell epitopes.

ANTIBODIES OF THE INVENTION

Antibodies raised against the proteins and protein fragments of the invention also are contemplated by the invention. Described below are antibody products and methods for producing antibodies capable of specifically recognizing one or more epitopes of the presently described proteins and their derivatives.

Antibodies include, but are not limited to polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies including single chain Fv (scFv) fragments, Fab fragments, $F(ab')_2$ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, epitope-binding fragments, and humanized forms of any of the above.

As known to one in the art, these antibodies may be used, for example, in the detection of a target protein in a biological sample. They also may be utilized as part of treatment methods, and/or may be used as part of diagnostic techniques whereby patients may be tested for abnormal levels or for the presence of abnormal forms of the such proteins.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth et al., *J. Immunol. Methods* 35:1-21 (1980); Kohler and Milstein, *Nature* 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), pp. 77-96). Antibodies may also be generated by the known techniques of phage display and *in vitro* immunization.

Polyclonal Antibodies

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as an inventive protein or an antigenic derivative thereof.

Polyclonal antiserum, containing antibodies to heterogeneous epitopes of a single protein, can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified, as known in the art, to enhance immunogenicity. Immunization methods include subcutaneous or intraperitoneal injection of the polypeptide.

Effective polyclonal antibody production is affected by many factors related both to the antigen and to the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and/or adjuvant. In addition, host animal response may vary with site of inoculation. Both inadequate or excessive doses of antigen may result in low titer antisera. In general, however, small doses (high ng to low μg levels) of antigen administered at multiple intradermal sites appears to be most reliable. Host animals may include but are not limited to rabbits, mice, chickens and rats, to name but a few. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

The protein immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin β-galactosidase) or through the inclusion of an adjuvant during immunization. Adjuvants include Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum.*

Booster injections can be given at regular intervals, with at least one usually being required for optimal antibody production. The antiserum may be harvested when the antibody titer begins to fall. Titer may be determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen. See, for example, Ouchterlony *et al.,* Chap. 19 in: *Handbook of Experimental Immunology,* Wier, ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). The antiserum may be purified by affinity chromatography using the immobilized immunogen carried on a solid support. Such methods of affinity chromatography are well known in the art.

Affinity of the antisera for the antigen may be determined by preparing competitive binding curves, as described, for example, by Fisher, Chap. 42 in: *Manual of Clinical Immunology,* second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D.C. (1980).

In addition to using protein an the immunogen, DNA molecules may be used directly. In this manner, a DNA encoding the protein immunogen is administered. Boosting and harvesting is done in a manner analogous to that detailed above. Yet another method of producing antibodies entails immunizing chickens and harvesting the antibodies from their eggs.

Monoclonal Antibodies

Monoclonal antibodies (MAbs), are homogeneous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture or *in vivo.* MAbs may be produced

by making hybridomas which are immortalized cells capable of secreting a specific monoclonal antibody.

Monoclonal antibodies to any of the proteins, peptides and epitopes thereof described herein can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495-497 (1975) (and U.S. Patent No. 4,376,110) or modifications of the methods thereof, such as the human B-cell hybridoma technique (Kosbor *et al.*, 1983, *Immunology Today* 4:72; Cole *et al.*, 1983, *Proc. Natl. Acad. Sci.* USA 80: 2026-2030), and the EBV-hybridoma technique (Cole *et al.*, 1985, MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In one method a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen are isolated.

The spleen cells are fused, typically using polyethylene glycol, with mouse myeloma cells, such as SP2/0-Ag14 myeloma cells. The excess, unfused cells are destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted, and aliquots are plated to microliter plates where growth is continued.

Antibody-producing clones (hybridomas) are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures. These include ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419 (1980), western blot analysis, radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175:109-124 (1988)) and modified methods thereof.

Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* BASIC METHODS IN MOLECULAR BIOLOGY, Elsevier, New York. Section 21-2 (1989). The hybridoma clones may be cultivated *in vitro* or *in vivo*, for instance as ascites. Production of high titers of mAbs *in vivo* makes this the presently preferred method of production. Alternatively, hybridoma culture in hollow fiber bioreactors provides a continuous high yield source of monoclonal antibodies.

The antibody class and subclass may be determined using procedures known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

MAbs may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. Methods of purifying monoclonal antibodies are well known in the art.

Antibody Derivatives and Fragments

Fragments or derivatives of antibodies include any portion of the antibody which is capable of binding the target antigen, or a specific portion thereof. Antibody derivatives include poly-specific (*e.g.*, bi-specific) antibodies, which contain binding sites specific for two or more different epitopes. These epitopes may be from the same or different inventive molecules or one or more epitope may be from a molecule not specifically disclosed here.

Antibody fragments specifically include $F(ab')_2$, Fab, Fab' and Fv fragments. These can be generated from any class of antibody, but typically are made from IgG or IgM. They may be made by conventional recombinant DNA techniques or, using the classical method, by proteolytic digestion with papain or pepsin. See CURRENT PROTOCOLS IN IMMUNOLOGY, chapter 2, Coligan *et al.*, eds., (John Wiley & Sons 1991-92).

$F(ab')_2$ fragments are typically about 110 kDa (IgG) or about 150 kDa (IgM) and contain two antigen-binding regions, joined at the hinge by disulfide bond(s). Virtually all, if not all, of the Fc is absent in these fragments. Fab' fragments are typically about 55 kDa (IgG) or about 75 kDa (IgM) and can be formed, for example, by reducing the disulfide bond(s) of an $F(ab')_2$ fragment. The resulting free sulfhydryl group(s) may be used to conveniently conjugate Fab' fragments to other molecules, such as detection reagents (*e.g.*, enzymes).

Fab fragments are monovalent and usually are about 50 kDa (from any source). Fab fragments include the light (L) and heavy (H) chain, variable (V_L and V_H, respectively) and constant (C_L C_H, respectively) regions of the antigen-binding portion of the antibody. The H and L portions are linked by an intramolecular disulfide bridge.

Fv fragments are typically about 25 kDa (regardless of source) and contain the variable regions of both the light and heavy chains (V_L and V_H, respectively). Usually, the V_L and V_H chains are held together only by non-covalent interacts and, thus, they readily dissociate. They do, however, have the advantage of small size and they retain the same binding properties of the larger Fab fragments. Accordingly, methods have been developed to crosslink the V_L and V_H chains, using, for example, glutaraldehyde (or other chemical crosslinkers), intermolecular disulfide bonds (by incorporation of cysteines) and peptide linkers. The resulting Fv is now a single chain (*i.e.*, SCFv).

Other antibody derivatives include single chain antibodies (U.S. Patent 4,946,778; Bird, Science 242:423-426 (1988); Huston *et al.*, Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward *et al.*, Nature 334:544-546 (1989)). Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain FV (SCFv).

One preferred method involves the generation of scFvs by recombinant methods, which allows the generation of Fvs with new specificities by mixing and matching variable chains from different antibody sources. In a typical method, a recombinant vector would be provided which comprises the appropriate regulatory elements driving expression of a cassette region. The cassette region would contain a DNA encoding a peptide linker, with convenient sites at both the 5' and 3' ends of the linker for generating fusion proteins. The DNA encoding a variable region(s) of interest may be cloned in the vector to form fusion proteins with the linker, thus generating an scFv.

In an exemplary alternative approach, DNAs encoding two Fvs may be ligated to the DNA encoding the linker, and the resulting tripartite fusion may be ligated directly into a conventional expression vector. The scFv DNAs generated any of these methods may be expressed in prokaryotic or eukaryotic cells, depending on the vector chosen.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab)_2$ fragments. Alternatively, Fab expression libraries may be constructed (Huse et al., 1989, *Science*, 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Derivatives also include "chimeric antibodies" (Morrison *et al.*, *Proc. Natl. Acad. Sci.*, 81:6851-6855 (1984); Neuberger *et al.*, *Nature*, 312:604-608 (1984); Takeda *et al.*, *Nature*, 314:452-454 (1985)). These chimeras are made by splicing the DNA encoding a mouse antibody molecule of appropriate specificity with, for instance, DNA encoding a human antibody molecule of appropriate specificity. Thus, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. These are also known sometimes as "humanized" antibodies and they offer the added

advantage of at least partial shielding from the human immune system. They are, therefore, particularly useful in therapeutic *in vivo* applications.

Labeled Antibodies

The present invention further provides the above-described antibodies in detectably labeled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labeling are well-known in the art, for example see (Sternberger *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer *et al.*, *Meth. Enzym.* 62:308 (1979); Engval *et al.*, *Immunol.* 109:129 (1972); Goding, *J. Immunol. Meth.* 13:215 (1976)). The labeled antibodies of the present invention can be used for *in vitro, in vivo,* and *in situ* diagnostic assays.

Immobilized Antibodies

The foregoing antibodies also may be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "*Handbook of Experimental Immunology*" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby *et al., Meth. Enzym.* 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro, in vivo,* and *in situ* assays as well as for immunoaffinity purification of the proteins of the present invention.

THERAPEUTIC AND DIAGNOSTIC COMPOSITIONS

The proteins, antibodies and polynucleotides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences* (16th ed., Osol, A., Ed., Mack, Easton PA (1980)). In order to form a pharmaceutically acceptable composition suitable for effective administration,

such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvate may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (*e.g.*, pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (*e.g.*, lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (*e.g.*, magnesium stearate, talc or silica); disintegrants (*e.g.*, potato starch or sodium starch glycolate); or wetting agents (*e.g.*, sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they maybe presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (*e.g.*, sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (*e.g.*, lecithin or acacia); non-aqueous vehicles (*e.g.*, almond oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (*e.g.*, methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the composition may take the form of tablets or lozenges formulated in conventional manner.

For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, *e.g.*, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, *e.g.* gelatin for

use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, *e.g.*, by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, *e.g.*, in ampules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, *e.g.*, sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, *e.g.*, containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

RECOMBINANT CONSTRUCTS AND EXPRESSION

The present invention further provides recombinant DNA constructs comprising one or more of the nucleotide sequences of the present invention. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a DNA or DNA fragment, typically bearing an open reading frame, is inserted, in either orientation.

The gene products encoded by the subject DNAs may be produced by recombinant DNA technology using techniques well known in the art. See, for example, the techniques described in Sambrook et al., 1989, *supra*, and Ausubel et al., 1989, *supra*. Alternatively, the DNA sequences may be chemically synthesized using, for example, synthesizers. See, for

example, the techniques described in OLIGONUCLEOTIDE SYNTHESIS, 1984, Gait, ed., IRL Press, Oxford, which is incorporated by reference herein in its entirety. They may be assembled from fragments and short oligonucleotide linkers, or from a series of oligonucleotides. The are preferably made by RT-PCR methods. The resulting synthetic gene is capable of being expressed in a recombinant vector.

In some cases the recombinant constructs will be expression vectors, which are capable of expressing the RNA and/or protein products of the encoded DNA(s). Thus, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the open reading frame (ORF). The vector may further comprise a selectable marker sequence.

Specific initiation signals may also be required for efficient translation of inserted target gene coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where a target DNA includes its own initiation codon and adjacent sequences is inserted into the appropriate expression vector, no additional translation control signals may be needed. However, in cases where only a portion of an ORF is used, exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire target. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner *et al.*, *Methods in Enzymol.* 153:516-544 (1987)). Some appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al., in Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Patent No. 5,082,767.

The present invention further provides host cells containing at least one of the DNAs of the present invention. The host cell can be virtually any cell for which expression vectors are available. It may be, for example, a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a prokaryotic

cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis *et al.*, *Basic Methods in Molecular Biology* (1986)).

A wide variety of expression systems are available, such as: yeast (*e.g. Saccharomyces, Pichia*) transformed with recombinant yeast expression vectors containing the target DNA; insect cell systems infected with recombinant virus expression vectors (*e.g.*, baculovirus) containing the target DNA sequences; plant cell systems infected with recombinant virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (*e.g.* Ti plasmid) containing target DNA coding sequences; or mammalian cell systems (*e.g.* COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (*e.g.*, metallothionein promoter) or from mammalian viruses (*e.g.*, the adenovirus late promoter; the vaccinia virus 7.5K promoter).

Depending on the system chosen, the resulting product may differ. For example, proteins expressed in most bacterial cultures, *e.g.*, *E. coli,* will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

Vectors

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting selection of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), α-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequence, and in one aspect of the invention, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal or C-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Bacterial Expression

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, if desirable, to provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli, Bacillus subtilis, Salmonella typhimurium* and various species within the genera Pseudomonas, Streptomyces, and Staphylococcus, although others may, also be employed as a matter of choice.

Bacterial vectors may be, for example, bacteriophage-, plasmid- or cosmid-based. These vectors can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids typically containing elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, GEM 1 (Promega Biotec, Madison, WI, USA), pBs, phagescript, PsiX174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pKK232-8, pDR540, and pRIT5 (Pharmacia).

These "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed. Bacterial promoters include lac, T3, T7, lambda P_R or P_L, trp, and ara.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed/induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the protein being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of antibodies or to screen peptide libraries, for example, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, *EMBO J.* 2:1791), in which the coding sequence may be ligated into the vector in frame with the *lac Z* coding region so that a fusion protein is produced; pIN vectors (Inouye *et al.* 1985, *Nucleic Acids*

Res. 13:3101-3109; Van Heeke *et al.*, 1989, *J. Biol. Chem.* 264:5503-5509); pET vectors, Studier *et al.*, *Methods in Enzymology* 185: 60-89 (Academic Press 1990); and the like.

Moreover, pGEX vectors may be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and easily can be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene protein can be released from the GST moiety.

In a one embodiment, full length cDNA sequences are appended with in-frame *BamHI* sites at the amino terminus and *EcoRI* sites at the carboxyl terminus using standard PCR methodologies (Innis et al., 1990, *supra*) and ligated into the pGEX-2TK vector (Pharmacia, Uppsala, Sweden). The resulting cDNA construct contains a kinase recognition site at the amino terminus for radioactive labeling and glutathione S-transferase sequences at the carboxyl terminus for affinity purification (Nilsson, *et al.* 1985, *EMBO J.* 4: 1075; Zabeau and Stanley, 1982, *EMBO J.* 1:1217.

Eukaryotic Expression

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell 23*:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Mammalian promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Exemplary mammalian vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). Selectable markers include CAT (chloramphenicol transferase).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the coding sequence of interest

may be ligated to an adenovirus transcription/translation control complex, *e.g.*, the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (*e.g.*, region E1 or E3) will result in a recombinant virus that is viable and capable of expressing a target protein in infected hosts. (*E.g.*, See Logan *et al.*, 1984, *Proc. Natl. Acad. Sci.* USA 81:3655-3659).

In one embodiment, cDNA sequences encoding the full-length open reading frames are ligated into pCMVß replacing the ß-galactosidase gene such that cDNA expression is driven by the CMV promoter (Alam, 1990, *Anal. Biochem.* 188: 245-254; MacGregor *et al.*, 1989, *Nucl. Acids Res.* 17: 2365; Norton *et al.* 1985, *Mol. Cell. Biol.* 5: 281).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (*e.g.*, glycosylation) and processing (*e.g.*, cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins.

Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, etc.

For long-term, high-yield production of recombinant proteins in eukaryotic cells, stable expression is preferred. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (*e.g.*, promoter, enhancer, sequences, transcription terminators, polyadenylation sites, *etc.*), and a selectable marker.

Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the target protein. Such engineered cell lines may be

particularly useful in screening and evaluation of compounds that affect the endogenous activity of the protein.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, *et al.*, *Cell* 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase(Szybalska *et al.*, *Proc. Natl. Acad. Sci. USA* 48:2026 (1962)), and adenine phosphoribosyltransferase(Lowy, *et al.*, *Cell* 22:817 (1980)) genes can be employed in tk^-, $hgprt^-$ or $aprt^-$ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for dhfr, which confers resistance to methotrexate (Wigler, *et al.*, *Proc. Natl. Acad, Sci. USA* 77:3567 (1980)); O'Hare, *et al.*, 1981, *Proc. Natl. Acad. Sci. USA* 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, *et al.*, 1981, *J. Mol. Biol.* 150:1); and hydro, which confers resistance to hygromycin (Santerre, *et al.*, 1984, *Gene* 30:147) genes.

An alternative fusion protein system allows for the ready purificationof non-denatured fusion proteins expressed in human cell lines (Janknecht, *et al.*, *Proc. Natl. Acad. Sci. USA* 88: 8972-8976 (1991)). In this system, the gene of interest is subcloned into a vaccinia-based plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni^{2+} nitriloacetic acid-agarose columns and histidine-tagged proteins are selectively eluted with imidazole-containingbuffers.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera frugiperda* cells. The target coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of a target gene coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (*E.g.*, see Smith et al., 1983, *J. Virol.* 46: 584; Smith, U.S. Patent No. 4,215,051).

While the present proteins can be expressed in recombinant systems, as described above, cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention.

Purification of Recombinant Proteins

Recombinant proteins produced may be isolated by host cell lysis. This may be followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, like lysozyme and chelators.

If inclusion bodies are formed in bacterial systems, they may be extracted from cell pellets using, for example, detergents, reducing agents, salts, urea, guanidinium chloride and extremes of pH (*e.g.* <4 or >10). If denaturation occurs, protein refolding steps (*e.g.*, dialysis) can be used, as necessary, in completing configuration of the mature protein. If disulfide bridges are present in the native protein, they may be reoxidized using known methods.

By way of specific non-limiting example, the recombinant bacterial cells, for example *E. coli,* are grown in any of a number of suitable media, for example LB, and the expression of the recombinant protein induced by adding IPTG (*e.g.*, *lac* operator-promoter) to the media or switching incubation to a higher temperature (*e.g.*, λ cI^{857}). After culturing the bacteria for a further period of between 2 and 24 hours, the cells are collected by centrifugation and washed to remove residual media. The bacterial cells are then lysed, for example, by disruption in a cell homogenizer and centrifuged to separate the cell membranes from the soluble cell components. If the protein aggregates into inclusion bodies, this centrifugation can be performed under conditions whereby the dense inclusion bodies are selectively enriched by incorporation of sugars such as sucrose into the buffer and centrifugation at a selective speed. The inclusion bodies can then be washed in any of several solutions to remove some of the contaminating host proteins, then solubilized in solutions containing high concentrations of urea (*e.g.* 8M) or chaotropic agents such as guanidinium hydrochloride in the presence of reducing agents such as ß-mercaptoethanol or DTT (dithiothreitol).

At this stage it may be advantageous to incubate the protein for several hours under conditions suitable for the protein to undergo a refolding process into a conformation which

more closely resembles that of the native protein. Such conditions generally include low protein concentrations less than 500 μg/ml), low levels of reducing agent, concentrations of urea less than 2 M and often the presence of reagents such as a mixture of reduced and oxidized glutathione which facilitate the interchange of disulphide bonds within the protein molecule. The refolding process can be monitored, for example, by SDS-PAGE or with antibodies which are specific for the native molecule. Following refolding, the protein can then be purified further and separated from the refolding mixture by chromatography on any of several supports including ion exchange resins, gel permeation resins or on a variety of affinity columns.

Labeling Proteins

When used as a component in assay systems such as those described, below, the target protein may be labeled, either directly or indirectly, to facilitate detection of the present *res*-like molecules either *in vitro* or *in vivo*. Any of a variety of suitable labeling systems may be used including but not limited to radioisotopes such as ^{125}I; enzyme labeling systems that generate a detectable colorimetric signal or light when exposed to substrate; and fluorescent labels.

Where recombinant DNA technology is used for protein production the, it may be advantageous to engineer fusion proteins that can facilitate labeling, immobilization and/or detection. These fusion proteins may, for example, add amino acids which facilitate further chemical modification. They also may add a functional moiety, such as an enzyme, which directly facilitates detection.

TRANSGENIC ANIMALS

The invention further contemplates animal models for studying the function of the present molecules and for overproducing the protein products. The disclosed DNA sequences may be used in conjunction with techniques for producing transgenic animals that are well known to those of skill in the art.

To prepare transgenic animals, target gene sequences may for example be introduced into, and overexpressed in, the genome of the animal of interest, or, if endogenous target gene sequences are present, they may either be overexpressed or, alternatively, be disrupted in order to underexpress or inactivate target gene expression, such as described for the disruption of apoE in mice (Plum *et al.*, *Cell* 71: 343-353 (1992)).

In order to overexpress a target gene sequence, the coding portion of the target gene sequence may be ligated to a regulatory sequence which is capable of driving gene expression in the animal and cell type of interest. Such regulatory regions will be well known to those of skill in the art, and may be utilized in the absence of undue experimentation.

For underexpression of an endogenous target gene sequence, such a sequence may be isolated and engineered such that when reintroduced into the genome of the animal of interest, the endogenous target gene alleles will be inactivated. Preferably, the engineered target gene sequence is introduced via gene targeting such that the endogenous target sequence is disrupted upon integration of the engineered target gene sequence into the animal's genome.

Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, and non-human primates, *e.g.*, baboons, monkeys, and chimpanzees may be used to generate cardiovascular disease animal models. Goats, cows and sheep are particularly preferred for producing protein *in vivo*.

Any technique known in the art may be used to introduce a target gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe *et al.*, U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten *et al.*, *Proc. Natl. Acad. Sci., USA* 82:6148-6152 (1985)); gene targeting in embryonic stem cells (Thompson *et al.*, *Cell* 56:313-321 (1989)); electroporation of embryos (Lo, *Mol. Cell. Biol.* 3:1803-1814 (1983)); and sperm-mediated gene transfer (Lavitrano *et al.*, *Cell* 57:717-723 (1989)); *etc.* For a review of such techniques, see Gordon, Transgenic Animals, *Intl. Rev. Cytol.* 115:171-229 (1989).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.*, mosaic animals. The transgene may be integrated as a single transgene or in concatamers, *e.g.*, head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching

of Lasko et al. (Lasko *et al.*, *Proc. Natl. Acad. Sci.* USA 89:3232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the target gene be integrated into the chromosomal site of the endogenous target gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous target gene of interest are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous target gene.

The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene of interest in only that cell type, by following, for example, the teaching of Gu *et al. Science* 265: 103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant target gene and protein may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include but are not limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR. Samples of target gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the target gene transgene gene product of interest.

The transgenic animals that express target gene mRNA or target gene transgene peptide (detected immunocytochemically, using antibodies directed against the target gene product's epitopes) at easily detectable levels should then be further evaluated to identify those animals which display characteristic increased susceptibility to carcinogenesis. Additionally, specific cell types within the transgenic animals may be analyzed and assayed *in vitro* for cellular phenotypes characteristic of mutant phenotype.

Once target gene transgenic founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include but are not limited to: outbreeding of founder animals with more

than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound target gene transgenics that express the target gene transgene of interest at higher levels because of the effects of additive expression of each target gene transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order both to augment expression and eliminate the possible need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; breeding animals to different inbred genetic backgrounds so as to examine effects of modifying alleles on expression of the target gene transgene and the possible development of carcinogenesis. One such approach is to cross the target gene transgenic founder animals with a wild type strain to produce an F1 generation that exhibits increased susceptibility to carcinogenesis. The F1 generation may then be inbred in order to develop a homozygous line, if it is found that homozygous target gene transgenic animals are viable.

Methods of generating "knockout" mice using homologous recombination in embryonic stem cells are well known in the art. Suitable methods are described, for example, in Mansour *et al.*, *Nature*, 336:348 (1988); Zijlstra *et al.*, *Nature*, 342:435 (1989) and 344:742 (1990); and Hasty *et al.*, *Nature*, 350:243 (1991). This genomic DNA can be obtained by conventional methods using the cDNA sequence as a probe in a commercially-available genomic DNA library.

Briefly, a genomic fragment is cleaved with a restriction endonuclease and a heterologous cassette containing a neomycin-resistance gene is inserted at the cleavage site. A suitable cassette is the GTI-II *neo* cassette described by Lufkin *et al.*, *Cell* 66:1105 (1991). The modified genomic fragment is cloned into a suitable targeting vector that is introduced into murine embryonic stem cells by electroporation. Cells that have undergone homologous recombination (and hence disruption of the gene) are selected by resistance to G418, and used to generate chimeric mice using well known methods. See Lufkin *et al., supra*. Traditional breeding methods then can be used to generate mice that are homozygous for the disrupted gene.

The phenotype of mice that are homozygous for the mutation then can be studied to provide insights into the role of the protein in, for example, carcinogenesis. These mice also can be used as models for developing new treatments for cancers. If this mutation is lethal in

homozygous mice (for example during embryogenesis) heterozygous mice, which express only half the amount of the protein can also be studied.

GENE THERAPY APPLICATIONS

When mutations in the inventive protein, or in the elements controlling expression of that protein, are found to be associated with a malignant phenotype, control of cellular proliferation can be restored by gene therapy methods. For example, overexpression of the protein can be counteracted by concurrent expression of an antisense molecule that binds to and inhibits expression of the mRNA encoding the protein. Alternatively, overexpression can be inhibited in an analogous manner using a ribozyme that cleaves the mRNA. In another embodiment, where expression of a mutated protein induces the malignant phenotype, concomitant expression of the non-mutated molecule via introduction of an exogenous gene may be used. Methods of using antisense and ribozyme technology to control gene expression, or of gene therapy methods for expression of an exogenous gene in this manner are well known in the art.

Each of these methods requires a system for introducing a vector into the cells containing the mutated gene. The vector encodes either an antisense or ribozyme transcript of the inventive protein. The construction of a suitable vector can be achieved by any of the methods well-known in the art for the insertion of exogenous DNA into a vector. *See, e.g.*, Sambrook *et al.*, *Molecular Cloning* (Cold Spring Harbor Press 2d ed. 1989), which is incorporated herein by reference. In addition, the prior art teaches various methods of introducing exogenous genes into cells *in vivo*. *See* Rosenberg *et al.*, *Science 242*:1575-1578 (1988) and Wolff *et al.*, *PNAS* 86:9011-9014 (1989), which are incorporated herein by reference. The routes of delivery include systemic administration and administration *in situ*. Well-known techniques include systemic administration with cationic liposomes, and administration *in situ* with viral vectors. Any one of the gene delivery methodologies described in the prior art is suitable for the introduction of a recombinant vector containing an inventive gene according to the invention into a MTX-resistant, transport-deficient cancer cell. A listing of present-day vectors suitable for the purpose of this invention is set forth in Hodgson, *Bio/Technology 13*: 222 (1995), which is incorporated by reference.

For example, liposome-mediated gene transfer is a suitable method for the introduction of a recombinant vector containing an inventive gene according to the invention

into a MTX-resistant, transport-deficient cancer cell. The use of a cationic liposome, such as DC-Chol/DOPE liposome, has been widely documented as an appropriate vehicle to deliver DNA to a wide range of tissues through intravenous injection of DNA/cationic liposome complexes. *See* Caplen *et al.*, *Nature Med.* 1:39-46 (1995) and Zhu *et al.*, *Science 261*:209-211 (1993), which are herein incorporated by reference. Liposomes transfer genes to the target cells by fusing with the plasma membrane. The entry process is relatively efficient, but once inside the cell, the liposome-DNA complex has no inherent mechanism to deliver the DNA to the nucleus. As such, the most of the lipid and DNA gets shunted to cytoplasmic waste systems and destroyed. The obvious advantage of liposomes as a gene therapy vector is that liposomes contain no proteins, which thus minimizes the potential of host immune responses.

As another example, viral vector-mediated gene transfer is also a suitable method for the introduction of the vector into a target cell. Appropriate viral vectors include adenovirus vectors and adeno-associated virus vectors, retrovirus vectors and herpesvirus vectors.

Adenoviruses are linear, double stranded DNA viruses complexed with core proteins and surrounded by capsid proteins. The common serotypes 2 and 5, which are not associated with any human malignancies, are typically the base vectors. By deleting parts of the virus genome and inserting the desired gene under the control of a constitutive viral promoter, the virus becomes a replication deficient vector capable of transferring the exogenous DNA to differentiated, non-proliferating cells. To enter cells, the adenovirus fibre interacts with specific receptors on the cell surface, and the adenovirus surface proteins interact with the cell surface integrins. The virus penton-cell integrin interaction provides the signal that brings the exogenous gene-containing virus into a cytoplasmic endosome. The adenovirus breaks out of the endosome and moves to the nucleus, the viral capsid falls apart, and the exogenous DNA enters the cell nucleus where it functions, in an epichromosomal fashion, to express the exogenous gene. Detailed discussions of the use of adenoviral vectors for gene therapy can be found in Berkner, *Biotechniques 6*:616-629 (1988) and Trapnell, *Advanced Drug Delivery Rev. 12*:185-199 (1993), which are herein incorporated by reference. Adenovirus-derived vectors, particularly non-replicative adenovirus vectors, are characterized by their ability to accommodate exogenous DNA of 7.5 kB, relative stability, wide host range, low pathogenicity in man, and high titers (10^4 to 10^5 plaque forming units per cell). *See* Stratford-Perricaudet *et al.*, *PNAS 89*:2581 (1992).

Adeno-associated virus (AAV) vectors also can be used for the present invention. AAV is a linear single-stranded DNA parvovirus that is endogenous to many mammalian species. AAV has a broad host range despite the limitation that AAV is a defective parvovirus which is dependent totally on either adenovirus or herpesvirus for its reproduction *in vivo*. The use of AAV as a vector for the introduction into target cells of exogenous DNA is well-known in the art. *See, e.g.*, Lebkowski *et al.*, *Mole. & Cell. Biol.* 8:3988 (1988), which is incorporated herein by reference. In these vectors, the capsid gene of AAV is replaced by a desired DNA fragment, and transcomplementation of the deleted capsid function is used to create a recombinant virus stock. Upon infection the recombinant virus uncoats in the nucleus and integrates into the host genome.

Another suitable virus-based gene delivery mechanism is retroviral vector-mediated gene transfer. In general, retroviral vectors are well-known in the art. *See* Breakfield *et al.*, *Mole. Neuro. Biol. 1*:339 (1987) and Shih *et al.*, in *Vaccines* 85: 177 (Cold Spring Harbor Press 1985). A variety of retroviral vectors and retroviral vector-producing cell lines can be used for the present invention. Appropriate retroviral vectors include Moloney Murine Leukemia Virus, spleen necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus. These vectors include replication-competent and replication-defective retroviral vectors. In addition, amphotropic and xenotropic retroviral vectors can be used. In carrying out the invention, retroviral vectors can be introduced to a tumor directly or in the form of free retroviral vector producing-cell lines. Suitable producer cells include fibroblasts, neurons, glial cells, keratinocytes, hepatocytes, connective tissue cells, ependymal cells, chromaffin cells. *See* Wolff *et al.*, *PNAS 84*:3344 (1989).

Retroviral vectors generally are constructed such that the majority of its structural genes are deleted or replaced by exogenous DNA of interest, and such that the likelihood is reduced that viral proteins will be expressed. *See* Bender *et al.*, *J. Virol.* 61:1639 (1987) and Armento *et al.*, *J. Virol. 61*:1647 (1987), which are herein incorporated by reference. To facilitate expression of the antisense or ribozyme molecule, of the inventive protein, a retroviral vector employed in the present invention must integrate into the genome of the host cell genome, an event which occurs only in mitotically active cells. The necessity for host cell replication effectively limits retroviral gene expression to tumor cells, which are highly

replicative, and to a few normal tissues. The normal tissue cells theoretically most likely to be transduced by a retroviral vector, therefore, are the endothelial cells that line the blood vessels that supply blood to the tumor. In addition, it is also possible that a retroviral vector would integrate into white blood cells both in the tumor or in the blood circulating through the tumor.

The spread of retroviral vector to normal tissues, however, is limited. The local administration to a tumor of a retroviral vector or retroviral vector producing cells will restrict vector propagation to the local region of the tumor, minimizing transduction, integration, expression and subsequent cytotoxic effect on surrounding cells that are mitotically active.

Both replicatively deficient and replicatively competent retroviral vectors can be used in the invention, subject to their respective advantages and disadvantages. For instance, for tumors that have spread regionally, such as lung cancers, the direct injection of cell lines that produce replication-deficient vectors may not deliver the vector to a large enough area to completely eradicate the tumor, since the vector will be released only form the original producer cells and their progeny, and diffusion is limited. Similar constraints apply to the application of replication deficient vectors to tumors that grow slowly, such as human breast cancers which typically have doubling times of 30 days versus the 24 hours common among human gliomas. The much shortened survival-time of the producer cells, probably no more than 7-14 days in the absence of immunosuppression, limits to only a portion of their replicative cycle the exposure of the tumor cells to the retroviral vector.

The use of replication-defective retroviruses for treating tumors requires producer cells and is limited because each replication-defective retrovirus particle can enter only a single cell and cannot productively infect others thereafter. Because these replication-defective retroviruses cannot spread to other tumor cells, they would be unable to completely penetrate a deep, multilayered tumor *in vivo*. *See* Markert *et al.*, *Neurosurg.* *77*: 590 (1992). The injection of replication-competent retroviral vector particles or a cell line that produces a replication-competent retroviral vector virus may prove to be a more effective therapeutic because a replication competent retroviral vector will establish a productive infection that will transduce cells as long as it persists. Moreover, replicatively competent retroviral vectors may follow the tumor as it metastasizes, carried along and propagated by transduced tumor cells. The risks for complications are greater, with replicatively competent vectors, however.

Such vectors may pose a greater risk then replicatively deficient vectors of transducing normal tissues, for instance. The risks of undesired vector propagation for each type of cancer and affected body area can be weighed against the advantages in the situation of replicatively competent verses replicatively deficient retroviral vector to determine an optimum treatment.

Both amphotropic and xenotropic retroviral vectors may be used in the invention. Amphotropic viruses have a very broad host range that includes most or all mammalian cells, as is well known to the art. Xenotropic viruses can infect all mammalian cell cells except mouse cells. Thus, amphotropic and xenotropic retroviruses from many species, including cows, sheep, pigs, dogs, cats, rats, and mice, *inter alia* can be used to provide retroviral vectors in accordance with the invention, provided the vectors can transfer genes into proliferating human cells *in vivo.*

Clinical trials employing retroviral vector therapy treatment of cancer have been approved in the United States. *See* Culver, *Clin. Chem. 40*: 510 (1994). Retroviral vector-containing cells have been implanted into brain tumors growing in human patients. *See* Oldfield *et al., Hum. Gene Ther. 4*: 39 (1993). These retroviral vectors carried the HSV-1 thymidine kinase (HSV-tk) gene into the surrounding brain tumor cells, which conferred sensitivity of the tumor cells to the antiviral drug ganciclovir. Some of the limitations of current retroviral based cancer therapy, as described by Oldfield are: (1) the low titer of virus produced, (2) virus spread is limited to the region surrounding the producer cell implant, (3) possible immune response to the producer cell line, (4) possible insertional mutagenesis and transformation of retroviral infected cells, (5) only a single treatment regimen of pro-drug, ganciclovir, is possible because the "suicide" product kills retrovirally infected cells and producer cells and (6) the bystander effect is limited to cells in direct contact with retrovirally transformed cells. *See* Bi *et al., Human Gene Therapy 4*: 725 (1993).

Yet another suitable virus-based gene delivery mechanism is herpesvirus vector-mediated gene transfer. While much less is known about the use of herpesvirus vectors, replication-competent HSV-1 viral vectors have been described in the context of antitumor therapy. *See* Martuza *et al., Science 252*: 854 (1991), which is incorporated herein by reference.

DIAGNOSTIC METHODS

The present invention also contemplates, for certain molecules described below, methods for diagnosis of human disease. In particular, patients can be screened for the occurrence of cancers, or likelihood of occurrence of cancers, associated with mutations in the encoded protein. DNA from tumor tissue obtained from patients suffering from cancer can be isolated and the gene encoding the protein can be sequenced. By examining a number of patients in this manner, mutations in the gene that are associated with a malignant cellular phenotype can be identified. In addition, correlation of the nature of the observed mutations with subsequent observed clinical outcomes allows development of prognostic model for the predicted outcome in a particular patient.

Screening for mutations conveniently can be carried out at the DNA level by use of PCR, although the skilled artisan will be aware that many other well known methods are available for the screening. PCR primers can be selected that flank known mutation sites, and the PCR products can be sequenced to detect the occurrence of the mutation. Alternatively, the 3' residue of one PCR primer can be selected to be a match only for the residue found in the unmutated gene. If the gene is mutated, there will be a mismatch at the 3' end of the primer, and primer extension cannot occur, and no PCR product will be obtained. Alternatively, primer mixtures can be used where the 3' residue of one primer is any nucleotide other than the nonmutated residue. Observation of a PCR product then indicates that a mutation has occurred. Other methods of using, for example, oligonucleotide probes to screen for mutations are described, or example, in U.S. Patent No. 4,871,838, which is herein incorporated by reference in its entirety.

Alternatively, antibodies can be generated that selectively bind either mutated or non-mutated protein. The antibodies then can be used to screen tissue samples for occurrence of mutations in a manner analogous to the DNA-based methods described *supra*.

The diagnostic methods described above can be used not only for diagnosis and for prognosis of existing disease, but may also be used to predict the likelihood of the future occurrence of disease. For example, clinically healthy patients can be screened for mutations in the inventive molecule that correlate with later disease onset. Such mutations may be observed in the heterozygous state in healthy individuals. In such cases a single mutation event can effectively disable proper functioning of the gene and induce a transformed or malignant phenotype. This screening also may be carried out prenatally or neonatally.

DNA molecules according to the invention also are well suited for use in so-called "gene chip" diagnostic applications. Such applications have been developed by, *inter alia*, Synteni and Affymetrix. Briefly, all or part of the DNA molecules of the invention can be used either as a probe to screen a polynucleotide array on a "gene chip," or they may be immobilized on the chip itself and used to identify other polynucleotides via hybridization to the surface of the chip. In this manner, for example, related genes can be identified, or expression patterns of the gene in various tissues can be simultaneously studied. Such gene chips have particular application for diagnosis of disease, or in forensic analysis to detect the presence or absence of an analyte. Suitable chip technology is described for example, in Wodicka *et al.*, *Nature Biotechnology*, 15:1359 (1997) which is hereby incorporated by reference in its entirety, and references cited therein.

PROTEIN-PROTEIN INTERACTIONS

Due to their similarity to certain known proteins, it is anticipated that some of the inventive protein molecules will interact with another class of cellular proteins. This is particularly true of those molecule containing leucine zipper motifs.

Any method suitable for detecting protein-protein interactions can be employed for identifying interacting targets. Among the traditional methods which can be employed are co-immunoprecipitation, crosslinking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of GAP gene products. Once identified, a GAP protein can be used, in conjunction with standard techniques, to identify its corresponding pathway gene. For example, at least a portion of the amino acid sequence of the pathway gene product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, e.g., Creighton, 1983, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained can be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for pathway gene sequences. Screening can be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and for screening are well-known. (See *e.g.*, Ausubel, *supra*, and PCR PROTOCOLS: A GUIDE TO METHODS AND APPLICATIONS, 1990, Innis *et al.*, eds. Academic Press, Inc., New York).

Additionally, methods can be employed which result in the simultaneous identification of interacting target genes. One method which detects protein interactions *in vivo*, the two-hybrid system, is described in detail for illustration purposes only and not by way of limitation. One version of this system has been described (Chien *et al.*, *Proc. Natl. Acad. Sci. USA*, 88: 9578-9582 (1991)) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to a known protein, in this case an inventive protein, and the other contains the activator protein's activation domain fused to an unknown protein (a putative GAP, for instance) that is encoded by a cDNA which has been recombined into this plasmid as part of a cDNA library. The plasmids are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (*e.g.*, *lacZ*) whose regulatory region contains the transcription activator's binding sites. Either hybrid protein alone cannot activate transcription of the reporter gene, the DNA-binding domain hybrid cannot because it does not provide activation function, and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodology can be used to screen activation domain libraries for proteins that interact with a known "bait" gene product. By way of example, and not by way of limitation, gene products known to be involved in TH cell subpopulation-related disorders and/or differentiation, maintenance, and/or effector function of the subpopulations can be used as the bait gene products. Total genomic or cDNA sequences are fused to the DNA encoding on activation domain. This library and a plasmid encoding a hybrid of the bait gene product fused to the DNA-binding domain are cotransformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. For example, and not by way of limitation, the bait gene can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the library plasmids responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

The present invention, thus generally described, will be understood more readily by reference to the following examples, which are provided by way of illustration and are not intended to be limiting of the present invention.

The examples below are provided to illustrate the subject invention. These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

EXAMPLES

EXAMPLE I: cDNA Library Construction

cDNA library plates and clones originated from five cDNA libraries that were constructed by directional cloning. These are available through the Resource Center (http://www.rzpd.de) of the German Genome Project. In particular, the hfbr2 (human fetal brain; RZPD number DKFZp564) and hfkd2 (human fetal kidney; DKFZp566) libraries were generated using the Smart kit (Clontech), except that PCR was carried out with primers that contained uracil residues to permit directional cloning without restriction digestion and ligation, and were complementary with the pAMP1 (LifeTechnologies) cloning sites for directional cloning. The htes3 (human testes; DKFZp434), hute1 (human uterus; DKFZp586) and hmcf1 (human mammary carcinoma; DKFZp727) libraries are conventional (Gubler, U., Hoffman, B.J., (1983), A simple and very efficient method for generating cDNA libraries. Gene 25, 263-269), size-selected cDNA libraries. They are cloned into pSPORT1 (LifeTechnologies) via a NotI site which is introduced during reverse transcription downstream of the oligo dT primer and a SalI site that is introduced by the ligation of a adapters. The human mammary carcinoma library was constructed fgrom MCF7 cells.

The cDNA sequences of this application were first identified among the sequences comprising various libraries. Technology has advanced considerably since the first cDNA libraries were made. Many small variations in both chemicals and machinery have been instituted over time, and these have improved both the efficiency and safety of the process. Although the cDNAs could be obtained using an older procedure, the procedure presented in this application is exemplary of one currently being used by persons skilled in the art. For the

purpose of providing an exemplary method, the mRNA isolation and cDNA library construction described here is for the MCF-7 library (DKFZp727) from which the clones named DKFZphmcfl_xxyyxx were obtained.

The human cell line MCF-7 was grown in DMEM supplemented with 10% fetal calf serum until confluency. 3 X 10^8 cells were harvested with a cell scraper in PBS. Cells were lysed in buffer containing 0.5 % NP-40 to leave the nuclei intact. The debris was pelleted by centrifugation at 15 000 x g for 10 minutes at 4 degrees Celsius. Proteins in the supernatant were degraded in presence of SDS and Proteinase K (30 minutes at 56 degrees Celsius). Precipitation of proteins was done in a Phenol/Chloroform extraction, RNA was precipitated from the aqueous phase with Na-acetate and Ethanol. Polyadenylated messages were isolated using Qiagen Oligotex (QIAGEN, Hilden Germany).

First strand cDNA synthesis was accomplished using an oligo (dT) primer which also contained an NotI restriction site. Second strand synthesis was performed using a combination of DNA polymerase I, *E. coli* ligase and RNase H, followed by the addition of a SalI adaptor to the blunt ended cDNA. The SalI adapted, double-stranded cDNA was then digested with NotI restriction enzyme, and fractionated by size on an agarose gel. DNA of the appropriate size was cut from the gel and cast into a second gel in a 90° angle. After electrophoresis in the second dimension, cDNA of the appropriate size was cut from the gel. The agarose block was broken down with help of gelase. The cDNA was purified with help of two phenol extractions and an ethanol precipitation. The cDNA was ligated into SalI/NotI pre-digested pSport1 vector (LifeTechnologies) and transformed into DH10B bacteria.

The libraries were arrayed into 384-well microtiter plates and spotted on high density nylon membranes for hybridization analysis. Filters and clones are available through the Resource Center. Whole plates were distributed to the sequencing partners of the consortium for systematic sequencing.

EXAMPLE II: Sequencing of cDNA Clones

All clones in the 384-well microtiter plates were sequenced from the 5' end. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on

ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry.

The resulting expressed sequence tag (EST) sequences ("r1 ESTs" = sequenced from 5′-end) were analysed for:

a) the lack of identical matches with known genes.

For this, the EST-sequence was blasted against the cDNA consortiums own database and after that against public databases and (with BLASTn and BLASTx against EMBL/EMBLNEW and assembled ESTs, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings). ESTs which were identical to known genes in more than 100 bp, with less than 2 mismatches, were excluded from further analysis.

b) the presence of an open reading frame

Open reading frames (ORFs) were detected with an tool developed by Munich Information Center for Protein Sequences (MIPS) called ORF-map. ORF-map visualises potential start and stop-codons. If an ORF without a stop codon was detected in a r1-EST, the sequence was processed further.

c) the presence of GC rich sequences

A script developed by MIPS computed the GC-content of the r1-sequence, which should be >40%. Writing similar scripts is within the ordinary skill of one in bioinformatics.

d) the lack of repeat structures

Repeats such as Alu, Line or CA-repeats were detected by blasting (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings) against a repeat-database compiled by MIPS. If a repeat was present within the r1-sequence, the sequence were not processed further.

Novel clones that met all criteria were identified to the sequencers, who then performed 3'-end sequencing of these clones. The resulting 3' ESTs ("s1 ESTs" = sequenced from 3′-end) were checked for

a) the lack of matches with known genes in public databases, and sequences already generated by us.

This was done by blasting against EMBL/EMBLNEW and assembled EST (BLASTn and BLASTx, please refer to EXAMPLE III: Bioinformatics analysis of full length cDNAs, for description and parameter settings).

b) the presence of polyadenylation signals.

Again only clones matching the selection criteria were chosen to be sequenced completely by the sequencers. Clones were selected after the following criteria:

A very good ORF had at least one BLASTx match to other proteins. A "good ORF" should extend to the 3' end and be longer than ~40 codons. If the ORF started in the r1 sequence, in front of the potential start codon, there should not exist too many competing start codons in frame with the ORF start codon and the start should match the Kozak consensus ATG. If the EST sequence was to short to decide according to the potential ORF, and there were only a few or no start codons in the sequence the GC content of the Sequence should be greater than 40%. The r1 sequences needed not contain an polyA-tail at the 3' end. In addition, the results of the blasting against the assembled human ESTs could help in questionable cases to decide whether to stop or to continue. A hit against these ESTs was an indication to go further.

Clones passing the above-described screening were sequenced in full. Sequencing was done preferentially using dye terminator chemistry (ABD or Amersham) on ABI automated DNA sequencers (ABI 377, Applied Biosystems), one partner used EMBL prototype instruments (Arakis) mainly with dye primer chemistry. Primer walking (Strauss et al., 1986, Specific-primer-directed DNA sequencing. Anal Biochem. 154, 353-360) was the preferred sequencing strategy because of the lower redundancy possible compared to random shotgun (Messing, J., Crea, R., Seeburg, H.P. (1981) A system for shotgun DNA sequencing. Nucleic Acids Res. 9, 32-39) methods. Walking primers were generally designed using software (e.g. Haas, S., Vingron, M., Poustka, A., Wiemann, S. (1998) Primer design in large-scale sequencing. Nucleic Acids Res. 26, 3006-3012, Schwager, C., Wiemann, S., Ansorge, W. (1995) GeneSkipper: integrated software environment for DNA sequence assembly and

alignment. HUGO Genome Digest 2, 8-9) that permitted complete automation of this usually time consuming process and helped in the parallel processing of large numbers of clones.

EXAMPLE III: Bioinformatics analysis of full length cDNAs

Each sequence obtained was compared on nucleotide level in a stepwise manner to sequences in EMBL/EMBLNEW, EMBL-EST, EMBL-STS using the BLASTn algorithm. Basic Local Alignment Search Tool (BLAST, Altschul S. F. (1993) J Mol Evol 36:290-300; Altschul, S. F. et al (1990) J Mol Biol 215:403-10) is used to search for local sequence alignments. BLAST produces alignments of both nucleotide (BLASTn) and amino acid sequences (BLASTp or BLASTx) to determine sequence similarity. BLAST is especially useful in determining exact matches or in identifying homologs, because of the local nature of the alignments. While it is useful for matches which do not contain gaps, it is inappropriate for performing motif-style searching. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment BLAST approach is to look threshold or cut off score set by the user. BLAST looks for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output. Parameter settings for the BLAST-operations (BLASTN 2.0a19MP-WashU) described were: EMBL-EMBLNEW: H=0 V=5 B=5 -filter seg; EMBL-EST: H=0 E=1e-10 B=500 V=500 -filter seg; EMBL-STS: H=0 V=5 B=5.

Search against EMBL/EMBLNEW was done to determine whether the cDNAs are already known, and also to find out whether the cDNAs are encoded by genomic sequences already sequenced and published/submitted to these databases.

Search against EMBL-EST was performed to get a first impression how abundant a particular cDNA would be and to get information on tissue specificity (so-called "electronic Northern-Blot", e.g. some of the cDNAs derived of the testis library show only hits to ESTs also derived of testis libraries).

The cDNA-sequences were blasted against EMBL-STS to determine STS-sequence-match to the cDNA, thus providing a mapping information to the new cDNA.

The potential protein-sequences were generated automatically by a script searching for the longest open reading frame (ORF) in each of the three forward frames with a minimum length of 90 codons. Next, the automatically generated ORFs were translated into protein sequences. These protein sequences were searched against the non redundant protein data set of PIR/SwissProt/Trembel/Tremblnew (BLASTP 2.0a19MP-WashU, parameter setting: V=7 B=7 H=0 -filter seg). If the script generated more than one ORF, one ORF was chosen manually by the annotater according to the degree of similarity to known proteins, the location of the ORF in the cDNA, the length, the amino acid composition and the content of Prosite-Motifs.

Additionally there was a BLASTx (BLASTX 2.0a19MP-WashU against non redundant protein database comprising PIR/SWISSPROT/TREMBL/TREMBLNEW; parameter-settings were: matrix/home/data/blast/matrix/aa/BLOSUM62 H=0 V=5 B=5 -filter seg) search to find potential frame shift in the complementary cds of the cDNAs and to identify unspliced or partly spliced cDNAs. The protein sequence was then transferred to the PEDANT system, in order to generate additional information on the new proteins. PEDANT (Protein Extraction, Description, and ANalysis Tool, Frishman, D. & Mewes, H.-W. (1997) PEDANTic genome analysis. Trends in Genetics , 13, 415-416) is a platform developed at the Munich Information Center for Protein Sequences (MIPS, Munich, Germany), which incorporates practically all bioinformatics methods important for the functional and structural characterisation of protein sequences. Computational methods used by PEDANT are:

FASTA

Very sensitive protein sequence database searches with estimates of statistical significance. Pearson W.R. (1990) Rapid and sensitive sequence comparison with FASTP and FASTA. Methods Enzymol. 183, 63-98.

BLAST2

Very sensitive protein sequence database searches with estimates of statistical significance. Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. Basic local alignment search tool. Journal of Molecular Biology 215, 403-10.

PREDATOR

High-accuracy secondary structure prediction from single and multiple sequences. Frishman, D. and Argos, P. (1997) 75% accuracy in protein secondary structure prediction. Proteins, 27, 329-335. Frishman, D. and Argos, P.(1996) Incorporation of long-distance interactions in a secondary structure prediction algorithm. Prot. Eng. 9, 133-142.

STRIDE

Secondary structure assignment from atomic coordinates. Frishman, D. and Argos, P.(1995) Knowledge-based secondary structure assignment. Proteins 23, 566-579.

CLUSTALW

Multiple sequence alignment. Thompson, J.D., Higgins, D.G. and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, positions-specific gap penalties and weight matrix choice. Nucleic Acids Research, 22:4673-4680.

TMAP

Transmembrane region prediction from multiply aligned sequences. Persson, B. and Argos, P. (1994) Prediction of transmembrane segments in proteins utilising multiple sequence alignments. J. Mol. Biol. 237, 182-192.

ALOM2

Transmembrane region prediction from single sequences. Klein, P., Kanehisa, M., and DeLisi, C. Prediction of protein function from sequence properties: A discriminant analysis of a database. Biochim. Biophys. Acta 787, 221-226 (1984). Version 2 by Dr. K. Nakai.

SIGNALP

Signal peptide prediction Nielsen, H., Engelbrecht, J., Brunak, S., and von Heijne, G (1997). Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites. Protein Engineering 10, 1-6.

SEG

Detection of low complexity regions in protein sequences. Wootton, J.C., Federhen, S. (1993) Statistics of local complexity in amino acid sequences and sequence databases. Computers & Chemistry 17, 149-163.

COILS

Detection of coiled coils. Lupas, A., M. Van Dyke, and J. Stock, "Predicting Coiled Coils from Protein Sequences." Science (1991) 252, 1162-1164.

PROSEARCH

Detection of PROSITE protein sequence patterns. Kolakowski L.F. Jr., Leunissen J.A.M., Smith J.E. (1992) ProSearch: fast searching of protein sequences with regular expression patterns related to protein structure and function. Biotechniques 13, 919-921.

BLIMPS

Similarity searches against a database of ungapped blocks. J.C. Wallace and Henikoff S., (1992) PATMAT: a searching and extraction program for sequence, pattern and block queries and databases, CABIOS 8, 249-254. Written by Bill Alford.

HMMER

Hidden Markov model software . Sonnhammer E.L.L., Eddy S.R., Durbin R. (1997) Pfam: A Comprehensive Database of Protein Families Based on Seed Alignments. Proteins 28, 405-420.

pI

Perl script that returns the amino acid composition, molecular weight, theoretical pI, and expected extinction coefficient of an amino acid sequence. By Fred Lindberg. The parameter-settings were as follows: known3d: score > 100; BLAST: E-value < 10; SCOP: <= 50 Alignments, E-Value < 0.0001; signalp: Y=0.7; untersucht vom N-Terminus her: 50 aa; funcat: E-value < 0.001; BLOCKS: <= 10 hits; BLIMPS: threshold 1100.0; COILS: threshold 0.95; SEG: threshold 20.0; BLAST in report: E-value < 0.001; PIR-KW, superfamilies, EC-Nummern in report: E-value < 0.00001; known3d in report: score > 120

The results of PEDANT analysis, together with the results of the similarity searches, constitute the basis for the structural and functional annotation of the cDNAs and the encoded proteins, as specified below.

EXAMPLE III: CELLULAR LOCALIZATIONS OF GFP-FUSION PROTEINS

Plasmids of cDNA-GFP fusions were transfected into mammalian tissue culture cells and allowed to express the proteins for up to 48 hours. Live cells were imaged at 24 hours and 48 hours after transfection and the localisations recorded. The chart, below, depicts the apparent final cellular localisations of 107 cDNA-GFP fusions.

In order to minimize the possibility of the GFP interfering with protein function and/or localization, two separate populations of cDNAs were generated encoding N-terminal or C-terminal GFP fusions. Clearly this appears to be a crucial strategy, since overall only 56% of the proteins localised to a specific compartment irrespective of the position of the GFP. In the instances where only one fusion localized, the complementary fusion either gave no expression or a nuclear and cytosolic staining - characteristic for GFP alone expression.

Each cDNA in turn was subjected to bioinformatic analysis. Where possible, the potential subcellular localisations of the expressed proteins were determined. This

information was then compared to the actual localisations determined from expression of the GFP-fusion proteins in mammalian cells.

DKFZphfbr2_16c16
----

group: Cell structure and motility

DKFZphfbr2_16c16.3 encodes a novel 586 amino acid protein with,similarity to the human actin binding protein MAYVEN and Drosophila Kelch.

MAVEN is a novel actin binding protein predominantly expressed in brain. Drosophila kelch is involved in the maintenance of ring canal organization during oogenesis. The amino half of the protein including the BTB domain mediates dimerization, while the amino half might allow cross-linking of ring canal actin filaments, thus organising the inner rim cytoskeleton. The kelch repeat domain is necessary for ring canal localisation and believed to mediate an additional interaction, possibly with actin. The new protein shares the features of both proteins and therefore should be involved in the organisation of cyto skeleton binding to membrane proteins.

The new protein can find application in modulating/blocking of cyto skeleton-membrane protein interaction.

similarity to Drosophila kelch

complete cDNA, complete cds, EST hits
on genomic level partly encoded by AC005082 and AC006039

Sequenced by Qiagen

Locus: unknown

Insert length: 3028 bp
Poly A stretch at pos. 3004, polyadenylation signal at pos. 2984

```
   1 GGGGGCCCGG GGACGCAGCC CAGTTGGTAG CGTCGCTCCC TGAGCGTTTC
  51 TAAGGGGGCC GCCCGGCCCT GTCTTTCGGC AGTGGCCGAG CCACCGCCGC
 101 CTGCCGCGCG TTCCAGAGCT GGGCGCTGCA GCTGCACTGC CGATCGCCGT
 151 GTTTGGTCGA TAGAATCCCC AGTGTGCCCA GAGAGTGCGA CCCCTCGCCC
 201 GGCCCGGCGA GCCCCGGGCG TGAACCGAGC TGAGGGAGGA TGGCAGCCTC
 251 TGGGGTGGAG AAGAGCAGCA AGAAGAAGAC CGAGAAGAAA CTTGCTGCTC
 301 GGGAAGAAGC TAAATTGTTG GCGGGTTTCA TGGGCGTCAT GAATAACATG
 351 CGGAAACAGA AAACGTTGTG TGACGTGATC CTCATGGTCC AGGAAAGAAA
 401 GATACCTGCT CATCGTGTTG TTCTTGCTGC AGCCAGTCAT TTTTTTAACT
 451 TAATGTTCAC AACTAACATG CTTGAATCAA AGTCCTTTGA AGTAGAACTC
 501 AAAGATGCTG AACCTGATAT TATTGAACAA CTGGTGGAAT TTGCTTATAC
 551 TGCTAGAATT TCCGTGAATA GCAACAATGT TCAGTCTTTG TTGGATGCAG
 601 CAAACCAATA TCAGATTGAA CCTGTGAAGA AAATGTGTGT TGATTTTTTG
 651 AAAGAACAAG TTGATGCTTC AAATTGTCTT GGTATAAGTG TGCTAGCGGA
 701 GTGTCTAGAT TGTCCTGAAT TGAAAGCAAC TGCAGATGAC TTTATTCATC
 751 AGCACTTTAC TGAAGTTTAC AAAACTGATG AATTTCTTCA ACTTGATGTC
 801 AAGCGAGTAA CACATCTTCT CAACCAGGAC ACTCTGACTG TGAGAGCAGA
 851 GGATCAGGTT TATGATGCTG CAGTCAGGTG GTTGAAATAC GATGAGCCTA
 901 ATCGCCAGCC ATTTATGGTT GATATCCTTG CTAAAGTCAG GTTTCCTCTT
 951 ATATCAAAGA ATTTCTTAAG TAAAACGGTA CAAGCTGAAC CACTTATTCA
1001 AGACAATCCT GAATGCCTTA AGATGGTGAT AAGTGGAATG AGGTACCATC
1051 TACTGTCTCC AGAGGACCGA GAAGAACTTG TAGATGGCAC AAGACCTAGA
1101 AGAAAGAAAC ATGACTACCG CATAGCCCTA TTTGGAGGCT CTCAACCACA
1151 GTCTTGTAGA TATTTTAACC CAAAGGATTA TAGCTGGACA GACATCCGCT
1201 GCCCCTTTGA AAAACGAAGA GATGCAGCAT GCGTGTTTTG GGACAATGTA
1251 GTATACATTT TGGGAGGCTC TCAGCTTTTC CCAATAAAGC GAATGGACTG
1301 CTATAATGTA GTGAAGGATA GCTGGTATTC GAAACTGGGT CCTCCGACAC
1351 CTCGAGACAG CCTTGCTGCA TGTGCTGCAG AAGGCAAAAT TTATACATCT
1401 GGAGGTTCAG AAGTAGGAAA CTCAGCTCTG TATTTATTTG AGTGCTATGA
1451 TACGAGAACT GAAAGCTGGC ACACAAAGCC CAGCATGCTG ACCCAGCGCT
1501 GCAGCCATGG GATGGTGGAA GCCAATGGCC TAATCTATGT TTGTGGTGGA
1551 AGTTTAGGAA ACAATGTTTC AGGGAGAGTG CTTAATTCCT GTGAAGTTTA
1601 TGATCCTGCC ACAGAAACAT GGACTGAGCT GTGTCCAATG ATTGAAGCCA
1651 GGAAGAATCA TGGGCTGGTA TTTGTAAAAG ACAAGATATT TGCTGTGGGT
1701 GGTCAGAATG GTTTAGGTGG TCTGGACAAT GTGGAATATT ACGATATTAA
1751 GTTGAACGAA TGGAAGATGG TCTCACCAAT GCCATGGAAG GGTGTAACAG
1801 TGAAATGTGC AGCAGTTGGC TCTATAGTTT ATGTCTTGGC TGGTTTTCAG
```

```
2301 AGAAGATTGG CTCATCAGTG AAGCGCAGTA TCTTAGCTCT AGATTCTATT
2351 TTCATGCATC ACAGAAGTGC TATACGGTTA GGTCTGTTTG TGCTCAGTCA
2401 AGAACTAAGA AATAGTATGA ATTGTAAGTC AAGATGGGCA ACTCAGATGG
2451 AGCAGCTTAG TCTCACAGTT TGCTTGTCTA TTTATTTTAT TTAGTGCCAA
2501 ATGTATTCCA TTTTAAAAGT AAGCCAGAGT GAGTCAAGGC ATATACACAC
2551 TTTCTCACAA AACTTCCTAA ACAGATTTGG GGGTTTAATA TGTCCAACTC
2601 CTCATGAAAT ATATTCAATC CACTTAAATA TATTCCATCT TTTTAACATA
2651 AAATGTAAAG CTTAGCACCC ATCATTAATT TATGTCTCTG TTTTATCCAG
2701 TGGTTAAAAA AGGATTCTGC CTCTTTAGTC CTCACTGTTA AATAAAACCC
2751 AATCATAGTA AGTGATTAAC TAGCAAAAAG TAAAGCTATT TATAGCAAAT
2801 TTCTAGATCA TTAGAAAAGC ACTGGTAGTT GTACAATATC AGTGTTGACT
2851 TTGAACTTCT TTAACGAGAT CATGAATTCT TTTCCCTTAG CCAAAACATG
2901 AAATATTTAA CCTAGTTGTC TCTAAAAGTT TTGTAATCAT GAGTTAGATA
2951 TATGTCATCT CCTATTCATT GCTTTTATGT GATCAATAAA TCTTTTACAA
3001 ACCCAAAAGA AAAAAAAAAA AAAAAAA
```

BLAST Results

Entry AC005082 from database EMBL:
Homo sapiens clone RG271G13; HTGS phase 1, 7 unordered pieces.
Score = 6460, P = 0.0e+00, identities = 1292/1292
4 exons matching Bp 1180-3007

Entry AC006039 from database EMBL:
*** SEQUENCING IN PROGRESS *** Homo sapiens clone NH0319F03; HTGS phase 1, 3 unordered pieces.
Score = 1780, P = 2.0e-117, identities = 368/377
5 exons matching Bp 6-860

Entry HSG20603 from database EMBL:
human STS A005Y34.
Score = 670, P = 1.0e-23, identities = 134/134

Medline entries

93201592:
kelch encodes a component of intercellular bridges in Drosophila egg chambers.

97412177:
Drosophila kelch is an oligomeric ring canal actin organizer.

Peptide information for frame 3

ORF from 240 bp to 1997 bp; peptide length: 586
Category: strong similarity to known protein

```
  1 MAASGVEKSS KKKTEKKLAA REEAKLLAGF MGVMNNMRKQ KTLCDVILMV
 51 QERKIPAHRV VLAAASHFFN LMFTTNMLES KSFEVELKDA EPDIIEQLVE
101 FAYTARISVN SNNVQSLLDA ANQYQIEPVK KMCVDFLKEQ VDASNCLGIS
151 VLAECLDCPE LKATADDFIH QHFTEVYKTD EFLQLDVKRV THLLNQDTLT
201 VRAEDQVYDA AVRWLKYDEP NRQPFMVDIL AKVRFPLISK NFLSKTVQAE
251 PLIQDNPECL KMVISGMRYH LLSPEDREEL VDGTRPRRKK HDYRIALFGG
301 SQPQSCRYFN PKDYSWTDIR CPFEKRRDAA CVFWDNVVYI LGGSQLFPIK
351 RMDCYNVVKD SWYSKLGPPT PRDSLAACAA EGKIYTSGGS EVGNSALYLF
401 ECYDTRTESW HTKPSMLTQR CSHGMVEANG LIYVCGGSLG NNVSGRVLNS
451 CEVYDPATET WTELCPMIEA RKNHGLVFVK DKIFAVGGQN GLGGLDNVEY
501 YDIKLNEWKM VSPMPWKGVT VKCAAVGSIV YVLAGFQGVG RLGHILEYNT
551 ETDKWVANSK VRAFPVTSCL ICVVDTCGAN EETLET
```

BLASTP hits

Entry KELC_DROME from database SWISSPROT:
RING CANAL PROTEIN (KELCH PROTEIN).
Length = 689
Score = 816 (287.2 bits), Expect = 1.9e-81, P = 1.9e-81
Identities = 187/542 (34%), Positives = 290/542 (53%)

Entry AC004021_1 from database TREMBL:
WUGSC:H_DJ0186K10.1"; Human PAC clone DJ0186K10 from 5q31, complete sequence. Homo sapiens (human)
Length = 497

```
Score = 704 (247.8 bits), Expect = 1.4e-69, P = 1.4e-69
Identities = 163/483 (33%), Positives = 253/483 (52%)

Entry HSDKG12_1 from database TREMBL:
"KIAA0132"; Human mRNA for KIAA0132 gene, complete cds. Homo
sapiens (human)
Length = 624
Score = 692 (243.6 bits), Expect = 2.6e-68, P = 2.6e-68
Identities = 175/527 (33%), Positives = 272/527 (51%)

Entry A45773 from database PIR:
kelch protein, long form - fruit fly (Drosophila melanogaster)
Length = 1476
Score = 817 (287.6 bits), Expect = 1.7e-80, P = 1.7e-80
Identities = 189/549 (34%), Positives = 292/549 (53%)


            Alert BLASTP hits for DKFZphfbr2_16c16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_16c16, frame 3
------------------------------------------------

                     Report for DKFZphfbr2_16c16.3

[LENGTH]       586
[MW]           65992.06
[pI]           6.08
[HOMOL]        PIR:A45773 kelch protein, long form - fruit fly (Drosophila melanogaster) 5e-85

[BLOCKS]       BL00075D Dihydrofolate reductase proteins
[SCOP]         d1gog_3 2.46.1.1.1 (151-537) Galactose oxidase, central domai 6e-36
[PIRKW]        zinc finger 2e-11
[PIRKW]        DNA binding 9e-10
[PIRKW]        transcription factor 1e-06
[SUPFAM]       A55R protein middle region homology 1e-35
[SUPFAM]       POZ domain homology 1e-35
[SUPFAM]       vaccinia virus 59K HindIII-C protein 5e-15
[SUPFAM]       A55R protein 1e-35
[SUPFAM]       myxoma virus M9-R protein 2e-11
[SUPFAM]       A55R protein carboxyl-terminal homology 1e-35
[PROSITE]      CAMP_PHOSPHO_SITE     2
[PROSITE]      MYRISTYL       8
[PROSITE]      CK2_PHOSPHO_SITE      10
[PROSITE]      TYR_PHOSPHO_SITE      1
[PROSITE]      PKC_PHOSPHO_SITE      11
[PROSITE]      ASN_GLYCOSYLATION     1
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY     3.75 %

SEQ    MAASGVEKSSKKKTEKKLAAREEAKLLAGFMGVMNNMRKQKTLCDVILMVQERKIPAHRV
SEG    ......xxxxxxxxxxxxxxxxxxxxxx................................
PRD  . ccceeeecccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhheeeecccccchhhhhe

SEQ    VLAAASHFFNLMFTTNMLESKSFEVELKDAEPDIIEQLVEFAYTARISVNSNNVQSLLDA
SEG    ............................................................
PRD    eecccccccccccccccchhhhheeeecccccchhhhhhhhhhhhheeeeccchhhhhhhh

SEQ    ANQYQIEPVKKMCVDFLKEQVDASNCLGISVLAECLDCPELKATADDFIHQHFTEVYKTD
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ    EFLQLDVKRVTHLLNQDTLTVRAEDQVYDAAVRWLKYDEPNRQPFMVDILAKVRFPLISK
SEG    ............................................................
PRD    hhhchhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhccch

SEQ    NFLSKTVQAEPLIQDNPECLKMVISGMRYHLLSPEDREELVDGTRPRRKKHDYRIALFGG
SEG    ............................................................
PRD    hhhhhhhhhhcccccchhhhhhhhhhhhcccccccccccccccccccccceeeeeeeecc

SEQ    SQPQSCRYFNPKDYSWTDIRCPFEKRRDAACVFWDNVVYILGGSQLFPIKRMDCYNVVKD
SEG    ............................................................
PRD    ccccceeeccccccccccccccccceeeeeeeceeeeeeecccccccccceeeecccccc

SEQ    SWYSKLGPPTPRDSLAACAAEGKIYTSGGSEVGNSALYLFECYDTRTESWHTKPSMLTQR
SEG    ............................................................
PRD    cccccccccccccceeeeeccceeeeecccccccccccceeeeeecccccccccccccccc
```

```
SEQ     CSHGMVEANGLIYVCGGSLGNNVSGRVLNSCEVYDPATETWTELCPMIEARKNHGLVFVK
SEG     ............................................................
PRD     ccceeeecceeeeeeccccccccccccccceeeecccccccccccccccccccceeeeeec

SEQ     DKIFAVGGQNGLGGLDNVEYYDIKLNEWKMVSPMPWKGVTVKCAAVGSIVYVLAGFQGVG
SEG     ............................................................
PRD     ceeeecccccccccccceeeecccccceeeecccccccceeeeeeccceeeeeccccccc

SEQ     RLGHILEYNTETDKWVANSKVRAFPVTSCLICVVDTCGANEETLET
SEG     ..............................................
PRD     cccceeeccccccccccccccccccccceeeeeeeeccccccccccc
```

Prosite for DKFZphfbr2_16c16.3

PS00001	442->446	ASN_GLYCOSYLATION	PDOC00001
PS00004	11->15	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	188->192	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	9->12	PKC_PHOSPHO_SITE	PDOC00005
PS00005	10->13	PKC_PHOSPHO_SITE	PDOC00005
PS00005	14->17	PKC_PHOSPHO_SITE	PDOC00005
PS00005	104->107	PKC_PHOSPHO_SITE	PDOC00005
PS00005	200->203	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005
PS00005	370->373	PKC_PHOSPHO_SITE	PDOC00005
PS00005	418->421	PKC_PHOSPHO_SITE	PDOC00005
PS00005	444->447	PKC_PHOSPHO_SITE	PDOC00005
PS00005	520->523	PKC_PHOSPHO_SITE	PDOC00005
PS00005	552->555	PKC_PHOSPHO_SITE	PDOC00005
PS00006	4->8	CK2_PHOSPHO_SITE	PDOC00006
PS00006	42->46	CK2_PHOSPHO_SITE	PDOC00006
PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	315->319	CK2_PHOSPHO_SITE	PDOC00006
PS00006	370->374	CK2_PHOSPHO_SITE	PDOC00006
PS00006	405->409	CK2_PHOSPHO_SITE	PDOC00006
PS00006	460->464	CK2_PHOSPHO_SITE	PDOC00006
PS00006	550->554	CK2_PHOSPHO_SITE	PDOC00006
PS00007	202->209	TYR_PHOSPHO_SITE	PDOC00007
PS00008	5->11	MYRISTYL	PDOC00008
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	389->395	MYRISTYL	PDOC00008
PS00008	424->430	MYRISTYL	PDOC00008
PS00008	436->442	MYRISTYL	PDOC00008
PS00008	440->446	MYRISTYL	PDOC00008
PS00008	487->493	MYRISTYL	PDOC00008
PS00008	493->499	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16c16.3)

DKFZphfbr2_16f21
----

group: brain derived

DKFZphfbr2_16f21 encodes a novel 208 amino acid protein with strong similarity to human zinc finger protein 216.

The novel protein shows strong similarity to the human zinc finger protein 216, but has no Zn finger.

PROSITE: Contains no Zinc finger; No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to zinc finger protein 216

complete cDNA, complete cds, EST hits
start matches Kozak consensus ANNatgG,

Sequenced by Qiagen

Locus: unknown

Insert length: 1512 bp
Poly A stretch at pos. 1490, polyadenylation signal at pos. 1474

```
   1 GGGAGCAAGC AGGGGTTCGG CGGCATTACC TGTACCCATT CACCGGCGGC
  51 TACCGGCGGC GGCGCGTAGC GTGTCAGGCG GAGAGACCCG CCGCCAGGTG
 101 TGCAACTGAG GAACATGGCT CAAGAAACTA ATCACAGCCA AGTGCCTATG
 151 CTTTGTTCCA CTGGCTGTGG ATTTTATGGA AACCCTCGTA CAAATGGCAT
 201 GTGTTCAGTA TGCTATAAAG AACATCTTCA AAGACAGAAT AGTAGTAATG
 251 GTAGAATAAG CCCACCTGCA ACCTCTGTCA GTAGTCTGTC TGAATCTTTA
 301 CCAGTTCAAT GCACAGATGG CAGTGTGCCA GAAGCCCAGT CAGCATTAGA
 351 CTCTACATCT TCATCTATGC AGCCCAGCCC TGTATCAAAT CAGTCACTTT
 401 TATCAGAATC TGTAGCATCT TCTCAATTGG ACAGTACATC TGTGGACAAA
 451 GCAGTACCTG AAACAGAAGA TGTGCAGGCT TCAGTATCAG ACACAGCACA
 501 GCAGCCATCT GAAGAGCAAA GCAAGCCTCT TGAAAAACCG AAACAAAAAA
 551 AGAATCGCTG TTTCATGTGC AGGAAGAAAG TGGGACTTAC TGGGTTTGAA
 601 TGCCGGTGTG GAAATGTTTA CTGTGGTGTA CACCGTTACT CAGATGTACT
 651 CAATTGCTCT TACAATTACA AAGCCGATGC TGCTGAGAAA ATCAGAAAAG
 701 AAAATCCAGT AGTTGTTGGT GAAAAGATCC AAAAGATTTG AACTCCTGCT
 751 GGAATACAAA ATTCTTGAGC ATCTGCAAAC TAAAAATTGA CTTGAGGTTT
 801 TTTTTTTCCT AGTCATTGGG AATGTAGAGC AGTGTATCTT GCATGTCATC
 851 GGAAGAATAG ATTTTTGTTT TGGTTTTGTT TTGAAAATGA CTCTGAACAT
 901 TTATTTCCAT TGCAATTTCT GTGGCTGAGG AGACTTAAAC TTTACAAGTA
 951 TTATCCTTTT AAGATCATTT TAATTTTAGT TGAGTGCAGA GGGCTTTTAT
1001 AACAAACGTG CAGAAATTTT GGAGGGCTGT GATTTTTCCA GTATTAAACA
1051 TGCATGCATT AATCTTGCAG TTTATTTTCT CATTATGTAT GTATATATCG
1101 CTTTTCTCTG CAGCACGATT TCTCTTTTGA TAATGCCCTT TAGGGCACAA
1151 CTAGTTATCA GTAACTGAAT GTATCTTAAT CATTATGGCT GCTTCTGTTT
1201 TTTCATTAAC AAAGGTTATT CATATGTTAG CATATAGTTT CTTTGCACCC
1251 ACTATTTATG TCTGAATCAT TTGTCACAAG AGAGTGTGTG CTGATGAGAT
1301 TGTAAGTTTG TGTGTTTAAA CTTTTTTTTG AGCGAGGGAA GAAAAAGCTG
1351 TATGCATTTC ATTGCTGTCT ACAGGTTTCT TTCAGATTAT GTTCATGGGT
1401 TTGTGTGTAT ACAATATGAA GAATGATCTG AAGTAATTGT GCTGTATTTA
1451 TGTTTATTCA CCAGTCTTTG ATTAAATAAA AAGGAAAACC AGAAAAAAAA
1501 AAAAAAAAAA AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 115 bp to 738 bp; peptide length: 208
Category: strong similarity to known protein

```
  1 MAQETNHSQV PMLCSTGCGF YGNPRTNGMC SVCYKEHLQR QNSSNGRISP
 51 PATSVSSLSE SLPVQCTDGS VPEAQSALDS TSSSMQPSPV SNQSLLSESV
101 ASSQLDSTSV DKAVPETEDV QASVSDTAQQ PSEEQSKPLE KPKQKKNRCF
151 MCRKKVGLTG FECRCGNVYC GVHRYSDVLN CSYNYKADAA EKIRKENPVV
201 VGEKIQKI
```

BLASTP hits

Entry ATF7H19_1 from database TREMBLNEW:
gene: "F7H19.10"; product: "putative protein"; Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project) >TREMBL:ATT12H17_21
gene: "T12H17.210"; product: "predicted protein"; Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project)
Score = 206, P = 2.1e-24, identities = 51/146, positives = 77/146

Entry PVPVPR3A_1 from database TREMBL:
gene: "PVPR3"; P.vulgaris PVPR3 protein mRNA, complete cds.
Score = 237, P = 4.9e-20, identities = 50/136, positives = 73/136

Entry AF062072_1 from database TREMBL:
gene: "ZNF216"; product: "zinc finger protein 216"; Homo sapiens zinc finger protein 216 (ZNF216) gene, complete cds.
Score = 591, P = 1.6e-57, identities = 124/215, positives = 147/215

Alert BLASTP hits for DKFZphfbr2_16f21, frame 1

TREMBL:AF062071_1 product: "zinc finger protein ZNF216"; Mus musculus zinc finger protein ZNF216 mRNA, complete cds., N = 1, Score = 590, P = 2.1e-57

TREMBLNEW:AB001773_1 gene: "pem-6"; product: "PEM-6"; Ciona savignyi pem-6 (posterior end mark 6) mRNA, complete cds., N = 1, Score = 421, P = 1.7e-39

```
>TREMBL:AF062071_1 product: "zinc finger protein ZNF216"; Mus musculus zinc
     finger protein ZNF216 mRNA, complete cds.
            Length = 213

  HSPs:

 Score = 590 (88.5 bits), Expect = 2.1e-57, P = 2.1e-57
 Identities = 123/213 (57%), Positives = 146/213 (68%)

Query:     1 MAQETNHSQVPMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQNSSNGRISPPAT---SVSS 57
             MAQETN +  PMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQ +S GR+SP  T   S S
Sbjct:     1 MAQETNQTPGPMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQQNS-GRMSPMGTASGSNSP 59

Query:    58 LSESLPVQCTDGSVPEAQSALDSTSSSMQPSPVSNQSLLSE--SVASSQLDSTSVDKAVP 115
               S+S  VQ  D  +   + A  STS    + PV+   +  +   ++ S+ D  +  K
Sbjct:    60 TSDSASVQRADAGLNNCEGAAGSTSEKSRNVPVAALPVTQQMTEMSISREDKITTPKT-E 118

Query:   116 ETEDVQASVSDTAQQPSEEQS--KPLEKPKQKKNRCFMCRKKVGLTGFECRCGNVYCGVH 173
             +E V    S +  QPS  QS  K  E PK KKNRCFMCRKKVGLTGF+CRCGN++CG+H
Sbjct:   119 VSEPVVTQPSPSVSQPSSSQSEEKAPELPKPKKNRCFMCRKKVGLTGFDCRCGNLFCGLH 178

Query:   174 RYSDVLNCSYNYKADAAEKIRKENPVVVGEKIQKI 208
             RYSD  NC Y+YKA+AA KIRKENPVVV EKIQ+I
Sbjct:   179 RYSDKHNCPYDYKAEAAAKIRKENPVVVAEKIQRI 213
```

Pedant information for DKFZphfbr2_16f21, frame 1

Report for DKFZphfbr2_16f21.1

[LENGTH] 208
[MW] 22541.23
[pI] 6.80
[HOMOL] TREMBL:AF062072_1 gene: "ZNF216"; product: "zinc finger protein 216"; Homo sapiens zinc finger protein 216 (ZNF216) gene, complete cds. 9e-57
[PIRKW] zinc 8e-13
[PIRKW] zinc finger 8e-13

```
[PIRKW]         fusion protein 8e-13
[SUPFAM]        unassigned ubiquitin-related proteins 8e-13
[SUPFAM]        ubiquitin homology 8e-13
[PROSITE]       MYRISTYL        2
[PROSITE]       CK2_PHOSPHO_SITE        7
[PROSITE]       ASN_GLYCOSYLATION       4
[KW]            Irregular
[KW]            LOW_COMPLEXITY      7.21 %

SEQ   MAQETNHSQVPMLCSTGCGFYGNPRTNGMCSVCYKEHLQRQNSSNGRISPPATSVSSLSE
SEG   ............................................................
PRD   cccccccccccccccccccccccccccccccchhhhhhhhhccccccccccccccccccc

SEQ   SLPVQCTDGSVPEAQSALDSTSSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDV
SEG   ...................xxxxxxxxxxxxxxx..........................
PRD   cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ   QASVSDTAQQPSEEQSKPLEKPKQKKNRCFMCRKKVGLTGFECRCGNVYCGVHRYSDVLN
SEG   ............................................................
PRD   ccccccccccccccccccccccccccceeecccccccceeeccccccccccccccccccc

SEQ   CSYNYKADAAEKIRKENPVVVGEKIQKI
SEG   ............................
PRD   ccchhhhhhhhhhhhhcccccccccccc
```

Prosite for DKFZphfbr2_16f21.1

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	42->46	ASN_GLYCOSYLATION	PDOC00001
PS00001	92->96	ASN_GLYCOSYLATION	PDOC00001
PS00001	180->184	ASN_GLYCOSYLATION	PDOC00001
PS00006	57->61	CK2_PHOSPHO_SITE	PDOC00006
PS00006	70->74	CK2_PHOSPHO_SITE	PDOC00006
PS00006	76->80	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	123->127	CK2_PHOSPHO_SITE	PDOC00006
PS00006	159->163	CK2_PHOSPHO_SITE	PDOC00006
PS00008	22->28	MYRISTYL	PDOC00008
PS00008	166->172	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16f21.1)

DKFZphfbr2_16g18
----

group: cell cycle

DKFZphfbr2_16g18.3 encodes a novel 984 amino acid protein with similarity to centromeric proteins of yeasts.

The novel protein shows similarity to S. pombe SPAC17A5.07c and the S. cerevisiae Smt4p suppressor of MIF2 gene. MIF2 encodes a centromeric protein with homology to the mammalian centromeric protein CENP-C. Mutations in MIF2 stabilise dicentric minichromosomes and confer high instability to chromosomes that bear a cis-acting mutation in element I of the yeast centromeric DNA (CDEI). Therefore the new protein should be involved in centromer organisation, too.

The new protein can find application in modulating/blocking the cell cycle and influencing the behavior of chromosomes, both natural and artificial in eukaryotic cells.

similarity to KIAA0797 and yeast Smt4p

complete cDNA, complete cds, EST hits
the yeast Smt4 protein seems to be involved in centromer function
and microtuble organisation

Sequenced by Qiagen

Locus: unknown

Insert length: 4826 bp
Poly A stretch at pos. 4756, polyadenylation signal at pos. 4736

```
   1 GGGTCGAGGT CGACGGTATC GATAAGTTTT TTTTTTTTTT TTTTTTTTTT
  51 TTTTCCTTTC CCCTCCCCCT CCCTCTCCAA GCCGGAGGGG TCCTGAGGTG
 101 ACAGCGCCTG CAACTGAAAT TTCAGCAGCG GGAGAAGATG GACAAGAGAA
 151 AGCTCGGGCG ACGGCCATCT TCATCCGAAA TCATCACAGA AGGAAAAAGG
 201 AAAAAGTCAT CTTCTGATTT ATCGGAGATA AGAAAGATGT TAAATGCAAA
 251 ACCAGAGGAT GTCCATGTTC AATCACCACT GTCCAAATTC AGAAGCTCAG
 301 AACGCTGGAC TCTCCCTTTG CAGTGGGAAA GAAGCCTAAG GAATAAAGTC
 351 ATCTCTCTAG ACCATAAAAA TAAAAAACAT ATCCGAGGGT GTCCTGTTAC
 401 TTCCAGGTCA TCACCAGAAA GGATACCCAG AGTTATATTG ACGAATGTCC
 451 TGGGAACGGA GTTAGGAAGA AAATACATAA GGACCCCACC TGTAACTGAG
 501 GGAAGTTTGA GTGATACAGA CAACTTGCAA TCAGAGCAAC TTTCTTCATC
 551 ATCTGATGGC AGCCTAGAAT CTTATCAAAA TCTAAACCCT CACAAGAGCT
 601 GTTATTTATC TGAAAGGGGC TCACAACGAA GTAAGACAGT AGATGACAAT
 651 TCTGCAAAGC AGACTGCGCA CAATAAAGAA AAACGAAGAA AGGATGATGG
 701 CATTTCTCTT TTAATATCTG ATACTCAGCC TGAAGACCTT AACAGTGGAA
 751 GTAGAGGTTG TGATCATCTC GAACAGGAAA GCAGAAACAA GGATGTTAAA
 801 TATTCTGATT CAAAAGTGGA ACTCACTCTG ATTTCCAGGA AGACAAAGAG
 851 AAGGCTTAGA AATAATTTAC CTGATTCTCA ATATTGTACT TCTTTGGATA
 901 AGTCAACAGA ACAGACAAAA AAACAAGAAG ATGACTCAAC AATATCCACT
 951 GAGTTTGAAA GGCCAAGTGA AAACTATCAT CAGGATCCAA AACTGCCTGA
1001 AGAAATTACA ACTAAACCTA CAAAAAGTGA TTTTACTAAG CTATCCTCAC
1051 TTAACAGTCA GGAGTTGACT TTGAGTAATG CCACCAAAAG TGCCTCTGCC
1101 GGTTCAACCA CTGAAACCGT TGAGTACTCT AATTCCATTG ATATTGTGGG
1151 GATTTCTTCC CTGGTTGAGA AGGATGAGAA TGAGTTGAAT ACCATAGAAA
1201 AGCCTATTCT AAGAGGACAT AATGAAGGGA ACCAATCACT GATCTCAGCT
1251 GAACCAATTG TTGTTTCCAG TGATGAAGAA GGACCTGTTG AACATAAAAG
1301 TTCAGAAATT CTTAAGTTAC AATCTAAGCA AGACCGTGAG ACAACTAATG
1351 AAAATGAGAG TACTTCTGAA TCAGCATTGT TAGAACTACC ATTGATTACA
1401 TGTGAATCTG TACAGATGTC ATCTGAATTA TGCCCATATA ATCCTGTCAT
1451 GGAGAACATT TCCAGTATTA TGCCTAGTAA TGAGATGGAT CTACAACTGG
1501 ATTTTATATT TACTTCTGTT TATATTGGTA AAATAAAAGG AGCTTCTAAA
1551 GGTTGTGTTA CAATCACAAA AAAATATATT AAGATCCCAT TTCAAGTGTC
1601 CCTGAATGAG ATTTCATTGC TAGTGGATAC CACACATTTA AAGCGGTTTG
1651 GGTTATGGAA AAGTAAGGAT GATAATCACA GTAAAAGGAG TCATGCTATT
1701 CTTTTCTTCT GGGTCTCTTC AGATTATCTT CAAGAGATTC AGACCCAATT
1751 AGAACACTCT GTATTAAGCC AGCAATCAAA ATCTAGTGAA TTCATTTTCC
1801 TTGAACTACA CAATCCTGTT TCACAGAGAG AAGAATTGAA GCTGAAAGAT
1851 ATTATGACGG AAATAAGTAT AATCAGTGGA GAATTAGAGC TTTCTTACCC
1901 GTTGTCTTGG GTTCAGGCAT TTCCTTTGTT TCAGAACCTC TCTTCAAAAG
1951 AAAGTTCTTT TATTCATTAT TACTGTGTTT CAACTTGTTC TTTCCCTGCT
2001 GGTGTTGCTG TTGCTGAAGA AATGAAGCTG AAATCAGTAT CTCAGCCCTC
2051 AAACACAGAT GCGGCCAAGC CTACTTACAC CTTCCTGCAG AAGCAAAGTA
2101 GCGGTTGCTA CTCCCTTTCT ATTACATCTA ATCCAGATGA AGAATGGCGG
2151 GAAGTCAGGC ACACTGGACT TGTTCAGAAG TTGATTGTAT ATCCTCCACC
2201 ACCTACTAAG GGGGGATTGG GAGTAACTAA TGAAGATCTG GAGTGTTTAG
2251 AAGAAGGAGA GTTTCTTAAT GATGTAATCA TTGATTTTTA CCTTAAGTAT
2301 CTTATATTGG AGAAGGCATC AGATGAACTT GTTGAACGAA GTCACATTTT
```

```
2351 TAGTAGCTTT TTCTATAAAT GCTTGACAAG AAAGGAAAAT AATTTAACAG
2401 AAGATAATCC AAATCTTTCA ATGGCACAGA GAAGACATAA AAGAGTAAGA
2451 ACATGGACTC GTCACATAAA CATTTTTAAT AAAGATTACA TCTTTGTACC
2501 TGTAAATGAG TCGTCTCACT GGTATCTCGC AGTCATTTGT TTTCCATGGT
2551 TAGAAGAAGC TGTGTATGAA GATTTTCCAC AAACTGTATC CCAGCAGTCC
2601 CAGGCTCAGC AGTCCCAAAG TGACAACAAA ACAATAGATA ATGATCTACG
2651 TACTACTTCG ACACTGTCTT TGAGTGCAGA GGATTCCCAA AGTACCGAGT
2701 CGAATATGTC AGTACCAAAG AAAATGTGTA AAAGGCCATG TATTCTTATA
2751 CTAGACTCCT TGAAAGCTGC TTCTGTACGA AACACAGTTC AGAATTTACG
2801 AGAGTATTTA GAGGTAGAGT GGGAAGTTAA ACTAAAAACT CATCGTCAAT
2851 TCAGCAAAAC AAACATGGTG GATCTATGCC CTAAAGTTCC TAAACAGGAC
2901 AATAGCAGTG ATTGTGGAGT ATATTTATTG CAGTATGTGG AAAGCTTCTT
2951 CAAGGATCCT ATTGTTAACT TTGAACTTCC AATTCATTTG GAGAAGTGGT
3001 TTCCTCGTCA TGTAATAAAG ACCAAACGGG AAGATATTCG AGAGCTCATC
3051 TTGAAACTTC ATTTACAGCA ACAGAAGGGC AGCAGTAGCT AGTTAATCTG
3101 TACAAACATG ACACAGATGT TCTCTAAGAT TACTGGAAAG CCCCTTACCA
3151 GCATTTGTGT TAGCCAGCTC ACAGAGAAGA AAATAACTTG CAGTAGTTTT
3201 ATAATAAGTC ATTGGAACAT TATTTAAAAT ATGTAGGACA CATTATTAGA
3251 ATTGTTGGGA TCTCATAGAT GGAATGGGAA TGGGGGTGAT ATAGATAAAC
3301 TTACTAGATA TAAATTAAAA TTTTATAAAT ATTTCATATT TTTCTGAGTA
3351 AATATGATTG GATTATGCAA CAGCATATGT AATATGGGAA TGTTTTGTAG
3401 ATAATAAAAC TTACATGATC TGTACTTCCA CGTGACTGGG TGCTGAGGGG
3451 AGTTAAAGCC TCCCTGGTGC CAGCCCCAGT GCTTGTCAAA TTTGCTGACA
3501 GGTCACATCA TATTGTAATT CTATTCTTTG CAGCTCAAGC ATGCAGTATG
3551 AATACTGTGT ATTTTTTAAA AAAATAATTT AGTATCAAGG CTTCAGAAAA
3601 TGCCATTTAC GGCATCCCTT CTGTATGTAA CAAAAAGACA TTCATAATGT
3651 TAGGAAGATG ATAAAAATTC GCTCTTTTAA AGTGCAGCTT ATTATTCTCA
3701 ATTGCTAAAT ACGATTACTC TGCTTTTTTT TTTTCATTTC TTTTGATGTC
3751 ATATGTGAGT ATCTTATAAT TTAGTTCATT TGTTCAGGGT AAAATTTGAA
3801 ACAAAAAATT TTACCTGTGC AAAATAGTTT TTTAAAAATT ATACATGTAG
3851 CTCAACTTGA GGTACTGCTA TATAAATATT CACTCACATT ATCACGGAAT
3901 TTATGTATAG TTTCTCTAAT ATAGAAGATA AAATTGGTGT CCTCATAACT
3951 TTAACAAAGA AAACCCTCAG TCCTATTTAT TAATGGGTAG AATTAAATAT
4001 ATAATTTTAT AGCTCAGTTT ACCCAGTATT CATCTGCAAA GCCAGATTGC
4051 TCTCATTGCT TTTATATTTT TAAATTGTAG CTTTTAGAGA CCTATGATCC
4101 TCATGGAACT TAATTTTTTA TTAAATATTC AGGTAACAGT TCTGAATTCA
4151 TGTGATAATG GTGGCATTAT ATATGATTAA ACACTTCAGA ACTTTCTAAT
4201 GTTATCAGGA GTATTTTGAG GGAGATATGA TTATATTGTA TTTTCTCAGA
4251 TAAGAAAAAT GTTTTTTAAC AATATTATTT TAATCTGTTT TAAGCATCTC
4301 TTAGATTTAC ATTATAACTA CATAAAGCAG TGAAGCAAAG GCAAATTAAG
4351 ATAAAGCTAG AAAGTCTGAA CATTTTATTT CAAAATCATA CGAATCGGGG
4401 TCAGTTAAGC CTCAGTATTC TTAGCTTTTG TTGATTTTGG CACTATCTTT
4451 ATATTATTAA ATATATTTGT TGTTTGGATA TTTCATATAA AGATGGCTAT
4501 AATTACATAT TTCATTCCCA ATTTGTGTGT GTTGGGGGGT ACTTTTAAAG
4551 GTGACTATTG TTTTGTACAT CTAATTTTGG GAAACCAAGT CTATAAGACA
4601 TCTTGTGATT TCTTAATGTT TTTGTTTGTA TGTTTTTCAA AGATATCACT
4651 GTCCTTTATC ATGTTTTGAA GATTGTTTAA AATTCATTTT CCTAAATTAA
4701 TGTGCAAGTA ATGTTTTGAG GATATCGGTG TTTTATATTA AACATATTTC
4751 CAATTCAAAA AAAAAAAAAA AAAAACTTAT CGATACCGTC GACCTCGATG
4801 ATGATGATGA TGATGATGAT GTCGAC
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 138 bp to 3089 bp; peptide length: 984
Category: similarity to known protein

```
  1 MDKRKLGRRP SSSEIITEGK RKKSSSDLSE IRKMLNAKPE DVHVQSPLSK
 51 FRSSERWTLP LQWERSLRNK VISLDHKNKK HIRGCPVTSR SSPERIPRVI
101 LTNVLGTELG RKYIRTPPVT EGSLSDTDNL QSEQLSSSSD GSLESYQNLN
151 PHKSCYLSER GSQRSKTVDD NSAKQTAHNK EKRRKDDGIS LLISDTQPED
201 LNSGSRGCDH LEQESRNKDV KYSDSKVELT LISRKTKRRL RNNLPDSQYC
251 TSLDKSTEQT KKQEDDSTIS TEFERPSENY HQDPKLPEEI TTKPTKSDFT
301 KLSSLNSQEL TLSNATKSAS AGSTTETVEY SNSIDIVGIS SLVEKDENEL
351 NTIEKPILRG HNEGNQSLIS AEPIVVSSDE EGPVEHKSSE ILKLQSKQDR
401 ETTNENESTS ESALLELPLI TCESVQMSSE LCPYNPVMEN ISSIMPSNEM
451 DLQLDFIFTS VYIGKIKGAS KGCVTITKKY IKIPFQVSLN EISLLVDTTH
```

```
501 LKRFGLWKSK DDNHSKRSHA ILFFWVSSDY LQEIQTQLEH SVLSQQSKSS
551 EFIFLELHNP VSQREELKLK DIMTEISIIS GELELSYPLS WVQAFPLFQN
601 LSSKESSFIH YYCVSTCSFP AGVAVAEEMK LKSVSQPSNT DAAKPTYTFL
651 QKQSSGCYSL SITSNPDEEW REVRHTGLVQ KLIVYPPPPT KGGLGVTNED
701 LECLEEGEFL NDVIIDFYLK YLILEKASDE LVERSHIFSS FFYKCLTRKE
751 NNLTEDNPNL SMAQRRHKRV RTWTRHINIF NKDYIFVPVN ESSHWYLAVI
801 CFPWLEEAVY EDFPQTVSQQ SQAQQSQSDN KTIDNDLRTT STLSLSAEDS
851 QSTESNMSVP KKMCKRPCIL ILDSLKAASV RNTVQNLREY LEVEWEVKLK
901 THRQFSKTNM VDLCPKVPKQ DNSSDCGVYL LQYVESFFKD PIVNFELPIH
951 LEKWFPRHVI KTKREDIREL ILKLHLQQQK GSSS
```

BLASTP hits

Entry SPAC17A5_7 from database TREMBL:
"SPAC17A5.07c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c17A5. Schizosaccharomyces pombe (fission yeast)
Length = 652
Score = 275 (96.8 bits), Expect = 1.9e-29, Sum P(3) = 1.9e-29
Identities = 56/120 (46%), Positives = 78/120 (65%)

Entry S49947 from database PIR:
SMT4 protein - yeast (Saccharomyces cerevisiae)
Length = 1034
Score = 163 (57.4 bits), Expect = 4.6e-16, Sum P(3) = 4.6e-16
Identities = 46/159 (28%), Positives = 76/159 (47%)

Entry YQG6_CAEEL from database SWISSPROT:
HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME II.
Length = 342
Score = 162 (57.0 bits), Expect = 6.1e-13, Sum P(3) = 6.1e-13
Identities = 37/119 (31%), Positives = 62/119 (52%)

Entry AB018340_1 from database TREMBL:
gene: "KIAA0797"; product: "KIAA0797 protein"; Homo sapiens mRNA for KIAA0797 protein, partial cds.
Score = 540, P = 1.9e-50, identities = 120/243, positives = 155/243

Alert BLASTP hits for DKFZphfbr2_16g18, frame 3

TREMBL:ATT16L1_11 gene: "T16L1.110"; product: "putative protein"; Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project), N = 2, Score = 239, P = 2.1e-18

>TREMBL:ATT16L1_11 gene: "T16L1.110"; product: "putative protein";
Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)
Length = 710

HSPs:

Score = 239 (35.9 bits), Expect = 2.1e-18, Sum P(2) = 2.1e-18
Identities = 51/135 (37%), Positives = 78/135 (57%)

```
Query:   683 IVYPPPPTKGGLGVTNEDLECLEEGEFLNDVIIDFYLKYLILEKASDELVERSHIFSSFF 742
             +VYP        + V  +D+E L+    F+ND IIDFY+KYL    + S +    R H F+ FF
Sbjct:   176 LVYPQGEPDAVV-VRKQDIELLKPRRFINDTIIDFYIKYL-KNRISPKERGRFHFFNCFF 233

Query:   743 YKCLTRKENNLTEDNPNLSMAQRRHKRVRTWTRHINIFNKDYIFVPVNESSHWYLAVICF 802
             +     RK  NL +  P+     +  ++RV+ WT+++++F KDYIF+P+N S HW L +IC
Sbjct:   234 F----RKLANLDKGTPSTCGGREAYQRVQKWTKNVDLFEKDYIFIPINCSFHWSLVIICH 289

Query:   803 PWLEEAVYEDFPQTV 817
             P      + + PQ V
Sbjct:   290 PGELVPSHVENPQRV 304
```

Score = 70 (10.5 bits), Expect = 2.1e-18, Sum P(2) = 2.1e-18
Identities = 13/28 (46%), Positives = 15/28 (53%)

```
Query:   948 PIHLEKWFPRHVIKTKREDIRELILKLH 975
             P HL  WFP      KR +I EL+  LH
Sbjct:   403 PSHLRNWFPAKEASLKRRNILELLYNLH 430
```

Pedant information for DKFZphfbr2_16g18, frame 3

Report for DKFZphfbr2_16g18.3

```
[LENGTH]        984
[MW]            112265.80
[pI]            6.13
[HOMOL]         TREMBL:AB018340_1 gene: "KIAA0797"; product: "KIAA0797 protein"; Homo sapiens
mRNA for KIAA0797 protein, partial cds. 8e-53
[FUNCAT]        03.22 cell cycle control and mitosis [S. cerevisiae, YIL031w] 9e-17
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YPL020c] 4e-06
[BLOCKS]        BL00494C Bacterial luciferase subunits proteins
[PROSITE]       AMIDATION       3
[PROSITE]       MYRISTYL        9
[PROSITE]       CAMP_PHOSPHO_SITE       2
[PROSITE]       CK2_PHOSPHO_SITE        30
[PROSITE]       TYR_PHOSPHO_SITE        1
[PROSITE]       PKC_PHOSPHO_SITE        19
[PROSITE]       ASN_GLYCOSYLATION       12
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY     4.47 %

SEQ   MDKRKLGRRPSSSEIITEGKRKKSSSDLSEIRKMLNAKPEDVHVQSPLSKFRSSERWTLP
SEG   ............................................................
PRD   cccccceeeccccceeeeecccccccccchhhhhhhhhcccccccccccccccccccchh

SEQ   LQWERSLRNKVISLDHKNKKHIRGCPVTSRSSPERIPRVILTNVLGTELGRKYIRTPPVT
SEG   ............................................................
PRD   hhhhhhhhhheeeeccccceeeccccccccccccceeeeeeeeeecccceeeccceeecccc

SEQ   EGSLSDTDNLQSEQLSSSSDGSLESYQNLNPHKSCYLSERGSQRSKTVDDNSAKQTAHNK
SEG   .........xxxxxxxxxxxxxxx....................................
PRD   cccccccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhh

SEQ   EKRRKDDGISLLISDTQPEDLNSGSRGCDHLEQESRNKDVKYSDSKVELTLISRKTKRRL
SEG   ............................................................
PRD   hhhhcccceeeeecccccccccccccccccccccccccccccccccceeeeeehhhhhhh

SEQ   RNNLPDSQYCTSLDKSTEQTKKQEDDSTISTEFERPSENYHQDPKLPEEITTKPTKSDFT
SEG   ............................................................
PRD   hcccccccccccccccchhhhhcccccccccccccccccccccccccccccccccccccc

SEQ   KLSSLNSQELTLSNATKSASAGSTTETVEYSNSIDIVGISSLVEKDENELNTIEKPILRG
SEG   ............................................................
PRD   ccccccccceeehhhhhhhcccccceeeecccceeeceeecccchhhhhhhhhhccccccc

SEQ   HNEGNQSLISAEPIVVSSDEEGPVEHKSSEILKLQSKQDRETTNENESTSESALLELPLI
SEG   .......................................xxxxxxxxxxxxxxxxx...
PRD   cccccceeeecceeeeeeccccccccccchhhhhhhhhhhhhcccccccchhhhhccccce

SEQ   TCESVQMSSELCPYNPVMENISSIMPSNEMDLQLDFIFTSVYIGKIKGASKGCVTITKKY
SEG   ............................................................
PRD   eecccccccccccccccccccceeeccccchhhhhhheeeeeeeeeeeecccccceeeeeeee

SEQ   IKIPFQVSLNEISLLVDTTHLKRFGLWKSKDDNHSKRSHAILFFWVSSDYLQEIQTQLEH
SEG   ............................................................
PRD   eeeecccccceeeeeeeccccceeeeeeeecccccccccceeeeeeeeeccchhhhhhhhhh

SEQ   SVLSQQSKSSEFIFLELHNPVSQREELKLKDIMTEISIISGELELSYPLSWVQAFPLFQN
SEG   ............................................................
PRD   hhhhcccccceeeeeeeeccccccchhhhhhhhhheeeeeccceeeeeccceeeeeeceeec

SEQ   LSSKESSFIHYYCVSTCSFPAGVAVAEEMKLKSVSQPSNTDAAKPTYTFLQKQSSGCYSL
SEG   ............................................................
PRD   ccccccccceeeeeccccccchhhhhhhhhhccccccccccccccceeeecccccccccce

SEQ   SITSNPDEEWREVRHTGLVQKLIVYPPPPTKGGLGVTNEDLECLEEGEFLNDVIIDFYLK
SEG   ............................................................
PRD   eecccccccceeeeeecccceeeeeeeccccccccccccccchhhhhhhhccchhhhhhhhh

SEQ   YLILEKASDELVERSHIFSSFFYKCLTRKENNLTEDNPNLSMAQRRHKRVRTWTRHINIF
SEG   ............................................................
PRD   hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhhhhhhhhhhhhhhhhc

SEQ   NKDYIFVPVNESSHWYLAVICFPWLEEAVYEDFPQTVSQQSQAQQSQSDNKTIDNDLRTT
SEG   ...................................xxxxxxxxxxx............
PRD   cceeeeeccccccceeeeeeeccchhhhhhhccccchhhhhhhhhhcccccccccccccc

SEQ   STLSLSAEDSQSTESNMSVPKKMCKRPCILILDSLKAASVRNTVQNLREYLEVEWEVKLK
SEG   ............................................................
PRD   cceeeeecccccceeeccccccccccccceeeeeccccccccchhhhhhhhhhhhhhhhhh

SEQ   THRQFSKTNMVDLCPKVPKQDNSSDCGVYLLQYVESFFKDPIVNFELPIHLEKWFPRHVI
```

```
SEG     ...........................................................
PRD     hhhhhccccccccccccccccccccceeeeehhhhhhhccccceeeccccccccccccchhh

SEQ     KTKREDIRELILKLHLQQQKGSSS
SEG     ........................
PRD     hhhhhhhhhhhhhhhhhhhccccc
```

Prosite for DKFZphfbr2_16g18.3

PS00001	314->318	ASN_GLYCOSYLATION	PDOC00001
PS00001	365->369	ASN_GLYCOSYLATION	PDOC00001
PS00001	406->410	ASN_GLYCOSYLATION	PDOC00001
PS00001	440->444	ASN_GLYCOSYLATION	PDOC00001
PS00001	513->517	ASN_GLYCOSYLATION	PDOC00001
PS00001	600->604	ASN_GLYCOSYLATION	PDOC00001
PS00001	752->756	ASN_GLYCOSYLATION	PDOC00001
PS00001	759->763	ASN_GLYCOSYLATION	PDOC00001
PS00001	790->794	ASN_GLYCOSYLATION	PDOC00001
PS00001	830->834	ASN_GLYCOSYLATION	PDOC00001
PS00001	856->860	ASN_GLYCOSYLATION	PDOC00001
PS00001	922->926	ASN_GLYCOSYLATION	PDOC00001
PS00004	8->12	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	21->25	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	54->57	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00005	88->91	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	162->165	PKC_PHOSPHO_SITE	PDOC00005
PS00005	172->175	PKC_PHOSPHO_SITE	PDOC00005
PS00005	233->236	PKC_PHOSPHO_SITE	PDOC00005
PS00005	236->239	PKC_PHOSPHO_SITE	PDOC00005
PS00005	260->263	PKC_PHOSPHO_SITE	PDOC00005
PS00005	291->294	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	515->518	PKC_PHOSPHO_SITE	PDOC00005
PS00005	562->565	PKC_PHOSPHO_SITE	PDOC00005
PS00005	602->605	PKC_PHOSPHO_SITE	PDOC00005
PS00005	747->750	PKC_PHOSPHO_SITE	PDOC00005
PS00005	874->877	PKC_PHOSPHO_SITE	PDOC00005
PS00005	879->882	PKC_PHOSPHO_SITE	PDOC00005
PS00005	901->904	PKC_PHOSPHO_SITE	PDOC00005
PS00005	962->965	PKC_PHOSPHO_SITE	PDOC00005
PS00006	11->15	CK2_PHOSPHO_SITE	PDOC00006
PS00006	24->28	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	123->127	CK2_PHOSPHO_SITE	PDOC00006
PS00006	125->129	CK2_PHOSPHO_SITE	PDOC00006
PS00006	137->141	CK2_PHOSPHO_SITE	PDOC00006
PS00006	167->171	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00006	225->229	CK2_PHOSPHO_SITE	PDOC00006
PS00006	251->255	CK2_PHOSPHO_SITE	PDOC00006
PS00006	271->275	CK2_PHOSPHO_SITE	PDOC00006
PS00006	295->299	CK2_PHOSPHO_SITE	PDOC00006
PS00006	323->327	CK2_PHOSPHO_SITE	PDOC00006
PS00006	341->345	CK2_PHOSPHO_SITE	PDOC00006
PS00006	377->381	CK2_PHOSPHO_SITE	PDOC00006
PS00006	396->400	CK2_PHOSPHO_SITE	PDOC00006
PS00006	402->406	CK2_PHOSPHO_SITE	PDOC00006
PS00006	408->412	CK2_PHOSPHO_SITE	PDOC00006
PS00006	488->492	CK2_PHOSPHO_SITE	PDOC00006
PS00006	509->513	CK2_PHOSPHO_SITE	PDOC00006
PS00006	536->540	CK2_PHOSPHO_SITE	PDOC00006
PS00006	562->566	CK2_PHOSPHO_SITE	PDOC00006
PS00006	602->606	CK2_PHOSPHO_SITE	PDOC00006
PS00006	638->642	CK2_PHOSPHO_SITE	PDOC00006
PS00006	664->668	CK2_PHOSPHO_SITE	PDOC00006
PS00006	697->701	CK2_PHOSPHO_SITE	PDOC00006
PS00006	747->751	CK2_PHOSPHO_SITE	PDOC00006
PS00006	826->830	CK2_PHOSPHO_SITE	PDOC00006
PS00006	846->850	CK2_PHOSPHO_SITE	PDOC00006
PS00006	962->966	CK2_PHOSPHO_SITE	PDOC00006
PS00007	216->223	TYR_PHOSPHO_SITE	PDOC00007
PS00008	84->90	MYRISTYL	PDOC00008
PS00008	106->112	MYRISTYL	PDOC00008
PS00008	141->147	MYRISTYL	PDOC00008
PS00008	161->167	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	468->474	MYRISTYL	PDOC00008

PS00008	505->511	MYRISTYL	PDOC00008
PS00008	622->628	MYRISTYL	PDOC00008
PS00008	693->699	MYRISTYL	PDOC00008
PS00009	6->10	AMIDATION	PDOC00009
PS00009	18->22	AMIDATION	PDOC00009
PS00009	109->113	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_16g18.3)

DKFZphfbr2_16i12
----

group: transmembrane protein

DKFZphfbr2_16i12 encodes a novel 185 amino acid protein, with strong similarity to PUT2 protein of Fugu rubripes.

The novel protein contains 1 transmembrane region.
PUT 2 is a Fugu rupies protein similar to the neural cell adhesion molecule L1 (L1-CAM) a mitosis-specific chromosome segregation protein (SMC1) and the calcium channel alpha-1 subunit homolog (CCA1).
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

strong similarity to Fugu rubripes PUT2

complete cDNA, complete cds, EST hits,
TRANSMEMBRANE 1

Sequenced by LMU

Locus: /map="873.3/875.1 cR from top of Chr1 linkage group"

Insert length: 1552 bp
Poly A stretch at pos. 1528, polyadenylation signal at pos. 1506

```
   1 GGGGGGGGAC AACTGGGTCT TTTGCGGCTG CAGCGGGCTT GTAGGCGTCC
  51 GGCTTTGCTG GCCCAGCAAG CCTGATAAGC ATGAAGCTCT TATCTTTGGT
 101 GGCTGTGGTC GGGTGTTTGC TGGTGCCCCC AGCTGAAGCC AACAAGAGTT
 151 CTGAAGATAT CCGGTGCAAA TGCATCTGTC CACCTTATAG AAACATCAGT
 201 GGGCACATTT ACAACCAGAA TGTATCCCAG AAGGACTGTT GTAGCAACTG
 251 CCTGCACGTG GTGGAGCCCA TGCCAGTGCC TGGCCATGAC GTGGAGGCCT
 301 ACTGCCTGCT GTGCGAGTGC AGGTACGAGG AGCGCAGCAC CACCACCATC
 351 AAGGTCATCA TTGTCATCTA CCTGTCCGTG GTGGGTGCCC TGTTGCTCTA
 401 CATGGCCTTC CTGATGCTGG TGGACCCTCT GATCCGAAAG CCGGATGCAT
 451 ACACTGAGCA ACTGCACAAT GAGGAGGAGA ATGAGGATGC TCGCTCTATG
 501 GCAGCAGCTG CTGCATCCCT CGGGGGACCC CGAGCAAACA CAGTCCTGGA
 551 GCGTGTGGAA GGTGCCCAGC AGCGGTGGAA GCTGCAGGTG CAGGAGCAGC
 601 GGAAGACAGT CTTCGATCGG CACAAGATGC TCAGCTAGAT GGGCTGGTGT
 651 GGTTGGGTCA AGGCCCCAAC ACCATGGCTG CCAGCTTCCA GGCTGGACAA
 701 AGCAGGGGGC TACTTCTCCC TTCCCTCGGT TCCAGTCTTC CCTTTAAAAG
 751 CCTGTGGCAT TTTTCCTCCT TCTCCCTAAC TTTAGAAATG TTGTACTTGG
 801 CTATTTTGAT TAGGGAAGAG GGATGTGGTC TCTGATCTCT GTTGTCTTCT
 851 TGGGTCTTTG GGGTTGAAGG GAGGGGGAAG GCAGGCCAGA AGGGAATGGA
 901 GACATTCGAG GCGGCCTCAG GAGTGGATGC GATCTGTCTC TCCTGGCTCC
 951 ACTCTTGCCG CCTTCCAGCT CTGAGTCTTG GGAATGTTGT TACCCTTGGA
1001 AGATAAAGCT GGGTCTTCAG GAACTCAGTG TTTGGGAGGA AAGCATGGCC
1051 CAGCATTCAG CATGTGTTCC TTTCTGCAGT GGTTCTTATC ACCACCTCCC
1101 TCCCAGCCCC AGCGCCTCAG CCCCAGCCCC AGCTCCAGCC CTGAGGACAG
1151 CTCTGATGGG AGAGCTGGGC CCCCTGAGCC CACTGGGTCT TCAGGGTGCA
1201 CTGGAAGCTG GTGTTCGCTG TCCCCTGTGC ACTTCTCGCA CTGGGGCATG
1251 GAGTGCCCAT GCATACTCTG CTGCCGGTCC CCTCACCTGC ACTTGAGGGG
1301 TCTGGGCAGT CCCTCCTCTC CCCAGTGTCC ACAGTCACTG AGCCAGACGG
1351 TCGGTTGGAA CATGAGACTC GAGGCTGAGC GTGGATCTGA ACACCACAGC
1401 CCCTGTACTT GGGTTGCCTC TTGTCCCTGA ACTTCGTTGT ACCAGTGCAT
1451 GGAGAGAAAA TTTTGTCCTC TTGTCTTAGA GTTGTGTGTA AATCAAGGAA
1501 GCCATCATTA AATTGTTTTA TTTCTCTCAA AAAAAAAAAA AAAAAAAATA
1551 TC
```

BLAST Results

Entry HS808349 from database EMBL:
human STS WI-11986.
Score = 1716, P = 5.7e-73, identities = 364/378

Entry HS487355 from database EMBL:
human STS WI-13088.
Score = 1358, P = 1.3e-56, identities = 274/277

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 81 bp to 635 bp; peptide length: 185
Category: similarity to unknown protein

```
  1 MKLLSLVAVV GCLLVPPAEA NKSSEDIRCK CICPPYRNIS GHIYNQNVSQ
 51 KDCCSNCLHV VEPMPVPGHD VEAYCLLCEC RYEERSTTTI KVIIVIYLSV
101 VGALLLYMAF LMLVDPLIRK PDAYTEQLHN EEENEDARSM AAAAASLGGP
151 RANTVLERVE GAQQRWKLQV QEQRKTVFDR HKMLS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_16i12, frame 3

TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence., N = 1, Score = 655, P = 2.8e-64

TREMBL:CER12C12_5 gene: "R12C12.6"; Caenorhabditis elegans cosmid R12C12., N = 1, Score = 225, P = 1e-18

>TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete sequence.
Length = 187

HSPs:

Score = 655 (98.3 bits), Expect = 2.8e-64, P = 2.8e-64
Identities = 124/163 (76%), Positives = 140/163 (85%)

```
Query:    22 KSSEDIRCKCICPPYRNISGHIYNQNVSQKDCCSNCLHVVEPMPVPGHDVEAYCLLCECR 81
             KS +D+RCKCICPPYRNISGHIYN+N +QKDC  NCLHVV+PMPVPG+DVEAYCLLCEC+
Sbjct:    31 KSFDDVRCKCICPPYRNISGHIYNRNFTQKDC--NCLHVVDPMPVPGNDVEAYCLLCECK 88

Query:    82 YEERSTTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMA 141
             YEERST TI+V I+I+LSVVGALLLYM FL+LVDPLIRKPD    + LHNEE++ED +
Sbjct:    89 YEERSTNTIRVTIIIFLSVVGALLLYMLFLLLVDPLIRKPDPLAQTLHNEEDSEDIQPQM 148

Query:   142 AAAASLGGP-RANTVLERVEGAQQRWKLQVQEQRKTVFDRHKML 184
             +     G P R NTVLERVEGAQQRWK QVQEQRKTVFDRHKML
Sbjct:   149 S-----GDPARGNTVLERVEGAQQRWKKQVQEQRKTVFDRHKML 187
```

Pedant information for DKFZphfbr2_16i12, frame 3

Report for DKFZphfbr2_16i12.3

```
[LENGTH]      185
[MW]          20764.29
[pI]          6.21
[HOMOL]       TREMBL:AF026198_5 gene: "PUT2"; product: "putative protein 2"; Fugu rubripes
neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1
(PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1)
gene, complete cds; and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2
(PUT2) genes, partial cds, complete sequence. 3e-68
[PROSITE]     MYRISTYL    1
[PROSITE]     CK2_PHOSPHO_SITE     4
[PROSITE]     PKC_PHOSPHO_SITE     2
[PROSITE]     ASN_GLYCOSYLATION    3
[KW]          SIGNAL_PEPTIDE 21
```

```
[KW]        TRANSMEMBRANE  1
[KW]        LOW_COMPLEXITY      2.70 %

SEQ    MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCCSNCLHV
SEG    ............................................................
PRD    ccceeeeeeeeccccccccccccccccceeeeeecccccccccceeeccccccccccccceeee
MEM    ............................................................

SEQ    VEPMPVPGHDVEAYCLLCECRYEERSTTTIKVIIVIYLSVVGALLLYMAFLMLVDPLIRK
SEG    ............................................................
PRD    eeccccccccccchhhhhhhhhhhhcccccceeeeeeehhhhhhhhhhhhhhhhhhhccccc
MEM    ...........................MMMMMMMMMMMMMMMMMMMMMMMMMMMMM...

SEQ    PDAYTEQLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDR
SEG    ....................xxxxx...................................
PRD    ccchhhhhhhhhhccccchhhhhhhhhhhhccccccchhhhhhhchhhhhhhhhhhhhhhhhhh
MEM    ............................................................

SEQ    HKMLS
SEG    .....
PRD    hhccc
MEM    .....
```

Prosite for DKFZphfbr2_16i12.3

PS00001	21->25	ASN_GLYCOSYLATION	PDOC00001
PS00001	38->42	ASN_GLYCOSYLATION	PDOC00001
PS00001	47->51	ASN_GLYCOSYLATION	PDOC00001
PS00005	49->52	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00006	23->27	CK2_PHOSPHO_SITE	PDOC00006
PS00006	49->53	CK2_PHOSPHO_SITE	PDOC00006
PS00006	154->158	CK2_PHOSPHO_SITE	PDOC00006
PS00006	176->180	CK2_PHOSPHO_SITE	PDOC00006
PS00008	148->154	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16i12.3)

DKFZphfbr2_16k22
----

group: brain derived

DKFZphfbr2_16k22 encodes a novel 108 amino acid protein with very weak similarity to thioredoxin of Bacillus subtilis.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to thioredoxin

complete cDNA, complete cds, genomic DNA?
no EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 2088 bp
Poly A stretch at pos. 2065, no polyadenylation signal found

```
   1 AAAAGGAAGA AGGAAATAAG GATATTTCAA GGGTTACCAA AGTCGAGGAA
  51 AACTATTTTA AGAAGAAATC TGAATTATTT GTGCACATAG GTTGTAATAA
 101 TAGCATCTTG CATTAAATGG TGTTTTCTAG CTTACAAAGT GGATTCATAT
 151 ACACTATTGT AACTGACTCT CTACAAACTT GCAAGGTTAG CAAGACAAAT
 201 GGTATTTTAA GATAACAAAC TGAGACTCAA AAAAGGCAAG TAACTCGTTC
 251 TACTTCCCAA AGCCAGAAAG TGGCAAAATA GAAAATGGAT CCTGAATCTC
 301 CAACACCATG CAAACTAAGA GAGGGAATCC TCTGTAGAGG GAATGGAAGT
 351 AAAAAGGCAC AAGTGGTGAT GTCACCTTCT GAACAGAGAT GGAACTTTTC
 401 TTCCTCTGAG AAAAAAGAGA AAAGATAGTT TTAAGTGGCA AAAGAACATG
 451 AAGCAATGTG AGGTGAAGAA ACAGAAAAGA CTATGGATGG AATTCCTAGA
 501 TGTGAGATAC ACAAAGTTCC ATTTCAAAGA GAAATATCTA TAGATAGGCA
 551 TAAAGTTACA CACCTGAACT ACCAACTCTG AACCAGTAAC TCAAGAGATA
 601 TTTTGTGTGT CCCACAAGCC ATATGGCTCT GGGGACAAAT TATCTGAAAG
 651 TGCCCAATAA GAAAAATATT TGAGGAAGGG GAGTTGGTGA GTGAATGAAT
 701 TAAAGGACAT CAGAAAGATA CATTGACTGT TCTCCTTCCC AGGAAACAAA
 751 GTGGCTAAGT CAAAACAACG GGCAGCTGTG GGATAGCAAA GAAAAAAAAA
 801 CTTCCAGGCC CAGGTTCTAG TGAAAGCTAC TATGGAAGTT AGCCACTCAA
 851 CTTTAGAACC AGAGGCTTCT TTTCCTCCTC CCTTCTTATC TTTTCTAGTT
 901 TATAGCAAAT TTATATTGAG CCACTTATTC TTTCTGAATG CTAGTTCCCC
 951 TTTAGCATTT CTTTTTCTTC ATTCCCTTTG GACTGGCCCA ATGCTTTGGC
1001 CCCTTATCAA AGCATTTTCT AAGAAACAGT CTGACAGCTC TAATTTGCAT
1051 CTGGTTATGC AAGATGTGGT TAAGAACATG GACTCTGGAG GTAAATACAC
1101 CTTGATTCCA ATTCATTCTC TCATTTATTC ATTCAGCAAA TATTTAGTGA
1151 ACATCTAACA TGTGCTAGGC ACTGTTCTAG TTGCTGAGGA TACAGCTTCA
1201 AACAAAATAA GGTCTCTGCA AGGATGCCTT CTCTTACCAC TCCTATTCAG
1251 CGTAGTATTG GAAGTCCTGG CCAGGGCAAT CAGGCAAGAA AAAGAAATCA
1301 AGGTCATCCA AATAGGAAGA GAGGAAGTCA AACTATCCCT GTTTACAGAC
1351 AACATGATCC TACATCTAGA AAAAAACCCA TTGTCTTAGC CCAAAAGCTT
1401 CTTAGGCTGA TAAACAACTT CAGCAAAGTC TTAGGATACA AAATCCATGT
1451 GCAAAAAACA CTAGCATTCT TATACACCAA CAACAGTCAA GCCGAGATCC
1501 AAATCAGGAA CAAACTCCTA TTCACAATTG CCACAAAAAC AATAGAACAG
1551 GAAAACAGCT AACTAGGAAG GTGAAAGATC TCTACAAGGA GAACTACAAA
1601 CCACTGCTCA CAGAAATCAG AGATGACACA TATAAATGGA AAAACATTCC
1651 ATGATCATGG ATAGGAAGAA TGAATATTAC TGAAATGGCT ATACTGTCCA
1701 AAGCAATTTA TAGATTCAAT GCTATTCCTA GTAAACTACC ATTGAGATTT
1751 TTTACAGAAC TAGAAAAAAA AAAAACTATT TTAAGGCTGG GCGCAGTGGC
1801 TCTCACCTGT AATCCCAGCA CTTTGGGAGG CCGAGATGGG TGGATCACGA
1851 GGTCAGGAGA TGGAAAACAT CCTGGCTAAC ATGGTGAAAC CCCGTCTCTA
1901 CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGTGGGCGC CTGTAATCCC
1951 AGCTGCTCGG GAGGCTGAGG CAGGATAATG GTGTGAACCC GGGAGGCAGA
2001 GCTTGCAGTG AGCTGAGATT GCACCACTGC ACTCCAGCCT GAGGGACAGA
2051 GTGAGACTCC ATCTCAAAAA AAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 832 bp to 1155 bp; peptide length: 108
Category: putative protein

```
  1 MEVSHSTLEP EASFPPPFLS FLVYSKFILS HLFFLNASSP LAFLFLHSLW
 51 TGPMLWPLIK AFSKKQSDSS NLHLVMQDVV KNMDSGGKYT LIPIHSLIYS
101 FSKYLVNI
```

BLASTP hits

Entry B37192 from database PIR:
thioredoxin - Bacillus subtilis Score = 71 (25.0 bits), Expect = 0.040,
P = 0.039
Identities = 16/49 (32%), Positives = 30/49 (61%)

Alert BLASTP hits for DKFZphfbr2_16k22, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_16k22, frame 1

Report for DKFZphfbr2_16k22.1

[LENGTH]	108	
[MW]	12281.47	
[pI]	8.06	
[PROSITE]	MYRISTYL	1
[PROSITE]	CAMP_PHOSPHO_SITE	1
[PROSITE]	CK2_PHOSPHO_SITE	1
[PROSITE]	PKC_PHOSPHO_SITE	1
[PROSITE]	ASN_GLYCOSYLATION	1
[KW]	Alpha_Beta	

```
SEQ    MEVSHSTLEPEASFPPPFLSFLVYSKFILSHLFFLNASSPLAFLFLHSLWTGPMLWPLIK
PRD    cccccccccccccccccchhhhhhhhhhhhhhhhcccccchhhhhhhhcccccccchhhhh

SEQ    AFSKKQSDSSNLHLVMQDVVKNMDSGGKYTLIPIHSLIYSFSKYLVNI
PRD    hhhcccccccceeehhhhhhcccccccceeeeeccceeeeccccccccc
```

Prosite for DKFZphfbr2_16k22.1

PS00001	36->40	ASN_GLYCOSYLATION	PDOC00001
PS00004	64->68	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00006	6->10	CK2_PHOSPHO_SITE	PDOC00006
PS00008	86->92	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_16k22.1)

DKFZphfbr2_16112
----

group: transmembrane protein

DKFZphfbr2_16112 encodes a novel 267 amino acid protein with similarity to gallus gallus putative transmembrane protein E3-16

The novel protein contains one putative transmembrane domain. In chicken, E3-16 is expressed specifically in the inner ear.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neurons involved in perception of hearing.

similarity to gallus putative transmembrane protein E3-16

complete cDNA, complete cds, EST hits
potental start at Bp 73 matchs kozak consensus PyCCataG
TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 2042 bp
Poly A stretch at pos. 2024, polyadenylation signal at pos. 2003

```
   1 GGGGGCGGCG GAGGCAGAGA CCGAGGCTGC ACCGGCAGAG GCTGCGGGGC
  51 GGACGCGCGG GCCGGCGCAG CCATGGTGAA GATTAGCTTC CAGCCCGCCG
 101 TGGCTGGCAT CAAGGGCGAC AAGGCTGACA AGGCGTCGGC GTCGGCCCCT
 151 GCGCCGGCCT CGGCCACCGA GATCCTGCTG ACGCCGGCTA GGGAGGAGCA
 201 GCCCCCACAA CATCGATCCA AGAGGGGGGG CTCAGTGGGC GGCGTGTGCT
 251 ACCTGTCGAT GGGCATGGTC GTGCTGCTCA TGGGCCTCGT GTTCGCCTCT
 301 GTCTACATCT ACAGATACTT CTTCCTTGCG CAGCTGGCCC GAGATAACTT
 351 CTTCCGCTGT GGTGTGCTGT ATGAGGACTC CCTGTCCTCC CAGGTCCGGA
 401 CTCAGATGGA GCTGGAAGAG GATGTGAAAA TCTACCTCGA CGAGAACTAC
 451 GAGCGCATCA ACGTGCCTGT GCCCCAGTTT GGCGGCGGTG ACCCTGCAGA
 501 CATCATCCAT GACTTCCAGC GGGGTCTGAC TGCGTACCAT GATATCTCCC
 551 TGGACAAGTG CTATGTCATC GAACTCAACA CCACCATTGT GCTGCCCCCT
 601 CGCAACTTCT GGGAGCTCCT CATGAACGTG AAGAGGGGGA CCTACCTGCC
 651 GCAGACGTAC ATCATCCAGG AGGAGATGGT GGTCACGGAG CATGTCAGTG
 701 ACAAGGAGGC CCTGGGGTCC TTCATCTACC ACCTGTGCAA CGGGAAAGAC
 751 ACCTACCGGC TCCGGCGCCG GGCAACGCGG AGGCGGATCA ACAAGCGTGG
 801 GGCCAAGAAC TGCAATGCCA TCCGCCACTT CGAGAACACC TTCGTGGTGG
 851 AGACGCTCAT CTGCGGGGTG GTGTGAGGCC CTCCTCCCCC AGAACCCCCT
 901 GCCGTGTTCC TCTTTTCTTC TTTCCGGCTG CTCTCTGGCC CTCCTCCTTC
 951 CCCCTGCTTA GCTTGTACTT TGGACGCGTT TCTATAGAGG TGACATGTCT
1001 CTCCATTCCT CTCCAACCCT GCCCACCTCC CTGTACCAGA GCTGTGATCT
1051 CTCGGTGGGG GGCCCATCTC TGCTGACCTG GGTGTGGCGG AGGGAGAGGC
1101 GATGCTGCAA AGTGTTTTCT GTGTCCCACT GTCTTGAAGC TGGGCCTGCC
1151 AAAGCCTGGG CCCACAGCTG CACCGGCAGC CCAAGGGGAA GGACCGGTTG
1201 GGGGAGCCGG GCATGTGAGG CCCTGGGCAA GGGGATGGGG CTGTGGGGGC
1251 GGGGCGGCAT GGGCTTCAGA AGTATCTGCA CAATTAGAAA AGTCCTCAGA
1301 AGCTTTTTCT TGGAGGGTAC ACTTTCTTCA CTGTCCCTAT TCCTAGACCT
1351 GGGGCTTGAG CTGAGGATGG GACGATGTGC CCAGGGAGGG ACCCACCAGA
1401 GCACAAGAGA AGGTGGCTAC CTGGGGGTGT CCCAGGGACT CTGTCAGTGC
1451 CTTCAGCCCA CCAGCAGGAG CTTGGAGTTT GGGGAGTGGG GATGAGTCCG
1501 TCAAGCACAA CTGTTCTCTG AGTGGAACCA AAGAAGCAAG GAGCTAGGAC
1551 CCCCAGTCCT GCCCCCCAGG AGCACAAGCA GGGTCCCCTC AGTCAAGGCA
1601 GTGGGATGGG CGGCTGAGGA ACGGGGCAGG CAAGGTCACT GCTCAGTCAC
1651 GTCCACGGGG GACGAGCCGT GGGTTCTGCT GAGTAGGTGG AGCTCATTGC
1701 TTTCTCCAAG CTTGGAACTG TTTTGAAAGA TAACACAGAG GGAAAGGGAG
1751 AGCCACCTGG TACTTGTCCA CCCTGCCTCC TCTGTTCTGA AATTCCATCC
1801 CCCTCAGCTT AGGGGAATGC ACCTTTTTCC CTTTCCTTCT CACTTTTGCA
1851 TGTTTTTACT GATCATTCGA TATGCTAACC GTTCTCAGCC CTGAGCCTTG
1901 GAGAGGAGGG CTGTAACGCC TTCAGTCAGT CTCTGGGGAT GAAACTCTTA
1951 AATGCTTTGT ATATTTTCTC AATTAGATCT CTTTTCAGAA GTGTCTATAG
2001 AACAATAAAA ATCTTTTACT TCTGAAAAAA AAAAAAAAAA AA
```

BLAST Results

No BLAST result

Medline entries

96325063:
Isolation of markers for chondro-osteogenic differentiation using cDNA library subtraction. Molecular cloning and characterization of a gene belonging to a novel multigene family of integral membrane proteins.

Peptide information for frame 1

ORF from 73 bp to 873 bp; peptide length: 267
Category: similarity to known protein

```
  1 MVKISFQPAV AGIKGDKADK ASASAPAPAS ATEILLTPAR EEQPPQHRSK
 51 RGGSVGGVCY LSMGMVVLLM GLVFASVYIY RYFFLAQLAR DNFFRCGVLY
101 EDSLSSQVRT QMELEEDVKI YLDENYERIN VPVPQFGGGD PADIIHDFQR
151 GLTAYHDISL DKCYVIELNT TIVLPPRNFW ELLMNVKRGT YLPQTYIIQE
201 EMVVTEHVSD KEALGSFIYH LCNGKDTYRL RRRATRRRIN KRGAKNCNAI
251 RHFENTFVVE TLICGVV
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_16112, frame 1

SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16)., N = 1, Score = 573, P = 1.4e-55

SWISSNEW:ITMB_MOUSE INTEGRAL MEMBRANE PROTEIN 2B (E25B PROTEIN)., N = 1, Score = 559, P = 4.2e-54

SWISSNEW:ITMA_HUMAN INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN)., N = 1, Score = 452, P = 9.1e-43

```
>SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN
     E3-16).
            Length = 262

  HSPs:

 Score = 573 (86.0 bits), Expect = 1.4e-55, P = 1.4e-55
 Identities = 118/264 (44%), Positives = 175/264 (66%)

Query:     1 MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCY 60
             MVK+SF  A+A     + A+K   ++         ++L+ P  + + P+      G     C+
Sbjct:     1 MVKVSFNSALA--HKEAANKEEENS-------QVLILPP-DAKEPEDVVVPAGHKRAWCW 50

Query:    61 -LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSLS-----SQVRTQM- 112
              +  G+  +L G++    Y+Y+YF   Q        + CG+ Y ED LS        +Q+++
Sbjct:    51 CMCFGLAFMLAGVILGGAYLYKYFAFQQ---GGVYFCGIKYIEDGLSLPESGAQLKSARY 107

Query:   113 -ELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTT 171
              +E++++I  +E+  E I+VPVP+F    DPADI+HDF R LTAY D+SLDKCYVI LNT+
Sbjct:   108 HTIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTS 167

Query:   172 IVLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLR 231
             +V+PP+NF ELL+N+K GTYLPQ+Y+I E+M+VT+ + + + LG FIY LC GK+TY+L+
Sbjct:   168 VVMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVDQLGFFIYRLCRGKETYKLQ 227

Query:   232 RRATRRRINKRGAKNCNAIRHFENTFVVETLIC 264
             R+    + I KR A NC  IRHFEN F +ETLIC
Sbjct:   228 RKEAMKGIQKREAVNCRKIRHFENRFAMETLIC 260
```

Pedant information for DKFZphfbr2_16112, frame 1

Report for DKFZphfbr2_16112.1

```
[LENGTH]       267
[MW]           30223.94
```

```
[pI]            8.16
[HOMOL]         SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16).
1e-49
[PROSITE]       PRENYLATION    1
[PROSITE]       MYRISTYL       5
[PROSITE]       CAMP_PHOSPHO_SITE      2
[PROSITE]       CK2_PHOSPHO_SITE       3
[PROSITE]       TYR_PHOSPHO_SITE       1
[PROSITE]       PKC_PHOSPHO_SITE       4
[PROSITE]       ASN_GLYCOSYLATION      1
[KW]            TRANSMEMBRANE  1
[KW]            LOW_COMPLEXITY    15.36 %

SEQ     MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVGGVCY
SEG     ...............xxxxxxxxxxxxxxxx.............................
PRD     ccccccccchhhhhhhhhhhhhhhhccccccceeeccccccccccccccccccccccchh
MEM     ....................................................MMMMMMMM

SEQ     LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMELEEDVKI
SEG     ..xxxxxxxxxxx...............................................
PRD     hhhhhhhhhhhhhhhhhhcchhhhhhhhhhccceeeeeeecccccccchhhhhhhhhhhhh
MEM     MMMMMMMMMMMMMMMMMMM.........................................

SEQ     YLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTIVLPPRNFW
SEG     ............................................................
PRD     hhcccceeeeccccccccccccchhhhhhhhhhhhhhhcccceeeeeccceeeccccchhh
MEM     ............................................................

SEQ     ELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRRRATRRRIN
SEG     ................................................xxxxxxxxxxxx
PRD     hhhhhhcccccccceeeeehhhhhhhcccccchhhhhheeecccccchhhhhhhhhhhhhhh
MEM     ............................................................

SEQ     KRGAKNCNAIRHFENTFVVETLICGVV
SEG     xx.........................
PRD     hhhhccceeeecccchhhhhheeeccc
MEM     ...........................
```

Prosite for DKFZphfbr2_16112.1

PS00001	169->173	ASN_GLYCOSYLATION	PDOC00001
PS00004	187->191	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	232->236	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	49->52	PKC_PHOSPHO_SITE	PDOC00005
PS00005	209->212	PKC_PHOSPHO_SITE	PDOC00005
PS00005	227->230	PKC_PHOSPHO_SITE	PDOC00005
PS00005	235->238	PKC_PHOSPHO_SITE	PDOC00005
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006
PS00006	110->114	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00007	119->127	TYR_PHOSPHO_SITE	PDOC00007
PS00008	52->58	MYRISTYL	PDOC00008
PS00008	53->59	MYRISTYL	PDOC00008
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	138->144	MYRISTYL	PDOC00008
PS00008	243->249	MYRISTYL	PDOC00008
PS00294	264->268	PRENYLATION	PDOC00266

(No Pfam data available for DKFZphfbr2_16112.1)

DKFZphfbr2_22f21
----

group: brain derived

DKFZphfbr2_22f21 encodes a novel 567 amino acid protein with weak similarity to C. elegans cosmide C18C4.5

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to C.elegans C18C4.5

EST HSAA6531/HSAA5273/ defines splice variant, or unspliced cDNA additional ~180 Bp at position 250

Sequenced by AGOWA

Locus: /map="311.4 cR from top of Chr14 linkage group"

Insert length: 1910 bp
Poly A stretch at pos. 1887, polyadenylation signal at pos. 1867

```
   1 TGGGCCCTTA GCAACGGCCT GGCGACGGTT TCCTTGCTGC TGCAGCCCCC
  51 GTCGGCTCCT CTTTTCCAGT CCTCCACTGC CGGGGCTGGG CCCGGCCGCG
 101 GGAAGGACCG AAGGGGATAC AGCGTGTCCC TGCGGCGGCT GCAAGAGGAC
 151 TAAGCATGGA TGGCAGCCGG AGAGTCAGAG CAACCTCTGT CCTTCCCAGA
 201 TATGGTCCAC CGTGCCTATT TAAAGGACAC TTGAGCACCA AAAGTAATGC
 251 TGCAGTAGAC TGCTCGGTTC CAGTAAGCAT GAGTACCAGC ATAAAGTATG
 301 CAGACCAACA ACGAAGAGAG AAACTCAAAA AGGAATTAGC ACAATGTGAA
 351 AAAGAGTTCA AATTAACTAA AACTGCAATG CGAGCCAATT ATAAAAATAA
 401 TTCCAAGTCA CTTTTTAATA CCTTACAAGA GCCCTCAGGC GAACCGCAAA
 451 TTGAGGATGA CATGTTAAAA GAAGAAATGA ATGGATTTTC ATCCTTTGCA
 501 AGGTCACTAG TACCCTCTTC AGAGAGACTA CACCTAAGTC TACATAAATC
 551 CAGTAAAGTC ATCACAAATG GTCCTGAGAA GAACTCCAGT TCCTCCCCGT
 601 CCAGTGTGGA TTATGCAGCC TCCGGGCCCC GGAAACTGAG CTCTGGAGCC
 651 CTGTATGGCA GAAGGCCCAG AAGCACATTC CCAAATTCCC ACCGGTTTCA
 701 GTTAGTCATT TCGAAAGCAC CCAGTGGGGA TCTTTTGGAT AAACATTCTG
 751 AACTCTTTTC TAACAAACAA TTGCCATTCA CTCCTCGCAC TTTAAAAACA
 801 GAAGCAAAAT CTTTCCTGTC ACAGTATCGC TATTATACAC CTGCCAAAAG
 851 AAAAAAGGAT TTTACAGATC AACGGATAGA AGCTGAAACC CAGACTGAAT
 901 TAAGCTTTAA ATCTGAGTTG GGGACAGCTG AGACTAAAAA CATGACAGAT
 951 TCAGAAATGA ACATAAAGCA GGCATCTAAT TGTGTGACAT ATGATGCCAA
1001 AGAAAAAATA GCTCCTTTAC CTTTAGAAGG GCATGACTCA ACATGGGATG
1051 AGATTAAGGA TGATGCTCTT CAGCATTCCT CACCAAGGGC AATGTGTCAG
1101 TATTCCCTGA AGCCCCCTTC AACTCGTAAA ATCTACTCTG ATGAAGAAGA
1151 ACTGTTGTAT CTGAGTTTCA TTGAAGATGT AACAGATGAA ATTTTGAAAC
1201 TTGGTTTATT TTCAAACAGG TTTTTAGAAC GACTGTTCGA GCGACATATA
1251 AAACAAAATA AACATTTGGA GGGGGAAAAA ATGCGCCACC TGCTGCATGT
1301 CCTGAAAGTA GACTTAGGCT GCACATCGGA GGAAAACTCG GTAAAGCAAA
1351 ATGATGTTGA TATGTTGAAT GTATTTGATT TTGAAAAGGC TGGGAATTCA
1401 GAACCAAATA AATTAAAAAA TGAAAGTGAA GTAACAATTC AGCAGGAACG
1451 TCAACAATAC CAAAAGGCTT TGGATATGTT ATTGTCGGCA CCAAAGGATG
1501 AGAACGAGAT ATTCCCTTCA CCAACTGAAT TTTTCATGCC TATTTATAAA
1551 TCAAAGCATT CAGAAGGGGT TATAATTCAA CAGGTGAATG ATGAAACAAA
1601 TCTTGAAACT TCAACTTTGG ATGAAAATCA TCCAAGTATT TCAGACAGTT
1651 TAACAGATCG GGAAACTTCT GTGAATGTCA TTGAAGGTGA TAGTGACCCT
1701 GAAAAGGTTG AGATTTCAAA TGGATTATGT GGTCTTAACA CATCACCCTC
1751 CCAATCTGTT CAGTTCTCCA GTGTCAAAGG CGACAATAAT CATGACATGG
1801 AGTTATCAAC TCTTAAAATC ATGGAAATGA GCATTGAGGA CTGCCCTTTG
1851 GATGTTTAAT CTTCATTAAT AAATACCTCA AATGGCCAGT AAAAAAAAAA
1901 AAAAAAAAAA
```

BLAST Results

Entry HS477360 from database EMBL:
human STS WI-14643.
Length = 418
Minus Strand HSPs:
Score = 1850 (277.6 bits), Expect = 2.5e-77, P = 2.5e-77
Identities = 392/405 (96%), Positives = 392/405 (96%), Strand = Minus / Plus

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 156 bp to 1856 bp; peptide length: 567
Category: similarity to unknown protein

```
  1 MDGSRRVRAT SVLPRYGPPC LFKGHLSTKS NAAVDCSVPV SMSTSIKYAD
 51 QQRREKLKKE LAQCEKEFKL TKTAMRANYK NNSKSLFNTL QEPSGEPQIE
101 DDMLKEEMNG FSSFARSLVP SSERLHLSLH KSSKVITNGP EKNSSSSPSS
151 VDYAASGPRK LSSGALYGRR PRSTFPNSHR FQLVISKAPS GDLLDKHSEL
201 FSNKQLPFTP RTLKTEAKSF LSQYRYYTPA KRKKDFTDQR IEAETQTELS
251 FKSELGTAET KNMTDSEMNI KQASNCVTYD AKEKIAPLPL EGHDSTWDEI
301 KDDALQHSSP RAMCQYSLKP PSTRKIYSDE EELLYLSFIE DVTDEILKLG
351 LFSNRFLERL FERHIKQNKH LEGEKMRHLL HVLKVDLGCT SEENSVKQND
401 VDMLNVFDFE KAGNSEPNKL KNESEVTIQQ ERQQYQKALD MLLSAPKDEN
451 EIFPSPTEFF MPIYKSKHSE GVIIQQVNDE TNLETSTLDE NHPSISDSLT
501 DRETSVNVIE GDSDPEKVEI SNGLCGLNTS PSQSVQFSSV KGDNNHDMEL
551 STLKIMEMSI EDCPLDV
```

BLASTP hits

Entry CEC18C4_3 from database TREMBL:
"C18C4.5"; Caenorhabditis elegans cosmid C18C4.
Length = 1091
Score = 98 (34.5 bits), Expect = 0.29, P = 0.25
Identities = 105/470 (22%), Positives = 192/470 (40%)

Alert BLASTP hits for DKFZphfbr2_22f21, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_22f21, frame 3

Report for DKFZphfbr2_22f21.3

```
[LENGTH]     567
[MW]         64120.02
[pI]         5.68
[PROSITE]    AMIDATION          1
[PROSITE]    MYRISTYL           3
[PROSITE]    CAMP_PHOSPHO_SITE       1
[PROSITE]    CK2_PHOSPHO_SITE        16
[PROSITE]    PKC_PHOSPHO_SITE        18
[PROSITE]    ASN_GLYCOSYLATION       4
[KW]         All_Alpha
[KW]         LOW_COMPLEXITY     1.23 %
```

```
SEQ  MDGSRRVRATSVLPRYGPPCLFKGHLSTKSNAAVDCSVPVSMSTSIKYADQQRREKLKKE
SEG  ............................................................
PRD  cccccceeeeeecccccccccccccccccccceeeeccccccchhhhhhhhhhhhhhhh

SEQ  LAQCEKEFKLTKTAMRANYKNNSKSLFNTLQEPSGEPQIEDDMLKEEMNGFSSFARSLVP
SEG  ............................................................
PRD  hhhhhhhhhhhhhhhhhhhhccccccceeecccccccchhhhhhhhhhhcccccccceeecc

SEQ  SSERLHLSLHKSSKVITNGPEKNSSSSPSSVDYAASGPRKLSSGALYGRRPRSTFPNSHR
SEG  ......................xxxxxxx...............................
PRD  ccchhhhhhhhceeeecccccccccccccccccccccccccccccccccccccccccccc

SEQ  FQLVISKAPSGDLLDKHSELFSNKQLPFTPRTLKTEAKSFLSQYRYYTPAKRKKDFTDQR
SEG  ............................................................
PRD  cceeeeeccccccccccccccccccccccccchhhhhhhhhhhhcccccchhhhhhhh

SEQ  IEAETQTELSFKSELGTAETKNMTDSEMNIKQASNCVTYDAKEKIAPLPLEGHDSTWDEI
SEG  ............................................................
PRD  hhhhhhhhhhhhhhcccccccccccchhhhhhhccceeehhhhhhcccccccccccccccc
```

```
SEQ     KDDALQHSSPRAMCQYSLKPPSTRKIYSDEEELLYLSFIEDVTDEILKLGLFSNRFLERL
SEG     ............................................................
PRD     ccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhccchhhhhhhhh

SEQ     FERHIKQNKHLEGEKMRHLLHVLKVDLGCTSEENSVKQNDVDMLNVFDFEKAGNSEPNKL
SEG     ............................................................
PRD     hhhhhhhhhcccchhhhhhhhhcccccccccccccccccccceeeeccccccccccccc

SEQ     KNESEVTIQQERQQYQKALDMLLSAPKDENEIFPSPTEFFMPIYKSKHSEGVIIQQVNDE
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccceeeeecccc

SEQ     TNLETSTLDENHPSISDSLTDRETSVNVIEGDSDPEKVEISNGLCGLNTSPSQSVQFSSV
SEG     ............................................................
PRD     cccccccccccccccccccccccccccceeeccccccceeeeccccccccccccceeeeecc

SEQ     KGDNNHDMELSTLKIMEMSIEDCPLDV
SEG     ...........................
PRD     ccccccchhhhhhhhhhhhhccccccc
```

Prosite for DKFZphfbr2_22f21.3

PS00001	81->85	ASN_GLYCOSYLATION	PDOC00001
PS00001	143->147	ASN_GLYCOSYLATION	PDOC00001
PS00001	262->266	ASN_GLYCOSYLATION	PDOC00001
PS00001	422->426	ASN_GLYCOSYLATION	PDOC00001
PS00004	159->163	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	4->7	PKC_PHOSPHO_SITE	PDOC00005
PS00005	27->30	PKC_PHOSPHO_SITE	PDOC00005
PS00005	45->48	PKC_PHOSPHO_SITE	PDOC00005
PS00005	122->125	PKC_PHOSPHO_SITE	PDOC00005
PS00005	132->135	PKC_PHOSPHO_SITE	PDOC00005
PS00005	178->181	PKC_PHOSPHO_SITE	PDOC00005
PS00005	202->205	PKC_PHOSPHO_SITE	PDOC00005
PS00005	209->212	PKC_PHOSPHO_SITE	PDOC00005
PS00005	212->215	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	309->312	PKC_PHOSPHO_SITE	PDOC00005
PS00005	317->320	PKC_PHOSPHO_SITE	PDOC00005
PS00005	322->325	PKC_PHOSPHO_SITE	PDOC00005
PS00005	353->356	PKC_PHOSPHO_SITE	PDOC00005
PS00005	395->398	PKC_PHOSPHO_SITE	PDOC00005
PS00005	500->503	PKC_PHOSPHO_SITE	PDOC00005
PS00005	539->542	PKC_PHOSPHO_SITE	PDOC00005
PS00005	552->555	PKC_PHOSPHO_SITE	PDOC00005
PS00006	89->93	CK2_PHOSPHO_SITE	PDOC00006
PS00006	149->153	CK2_PHOSPHO_SITE	PDOC00006
PS00006	245->249	CK2_PHOSPHO_SITE	PDOC00006
PS00006	264->268	CK2_PHOSPHO_SITE	PDOC00006
PS00006	295->299	CK2_PHOSPHO_SITE	PDOC00006
PS00006	328->332	CK2_PHOSPHO_SITE	PDOC00006
PS00006	337->341	CK2_PHOSPHO_SITE	PDOC00006
PS00006	390->394	CK2_PHOSPHO_SITE	PDOC00006
PS00006	455->459	CK2_PHOSPHO_SITE	PDOC00006
PS00006	481->485	CK2_PHOSPHO_SITE	PDOC00006
PS00006	486->490	CK2_PHOSPHO_SITE	PDOC00006
PS00006	494->498	CK2_PHOSPHO_SITE	PDOC00006
PS00006	498->502	CK2_PHOSPHO_SITE	PDOC00006
PS00006	500->504	CK2_PHOSPHO_SITE	PDOC00006
PS00006	513->517	CK2_PHOSPHO_SITE	PDOC00006
PS00006	559->563	CK2_PHOSPHO_SITE	PDOC00006
PS00008	164->170	MYRISTYL	PDOC00008
PS00008	256->262	MYRISTYL	PDOC00008
PS00008	350->356	MYRISTYL	PDOC00008
PS00009	167->171	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_22f21.3)

DKFZphfbr2_22h13
----

group: transmembrane protein

DKFZphfbr2_22h13 encodes a novel 520 amino acid protein, with similarity to Drosophila melanogaster EG:39E1.3.

The protein contains an ATP/GTP A Prosite pattern (P-loop). This loop interacts with one of the phosphate groups of a A or G nucleotide. It is found in numerous ATP- or GTP-binding proteins, such as ATP synthase alpha and beta subunits, Myosin heavy chains, Kinesin heavy chains and kinesin-like proteins, Dynamins and dynamin-like proteins, several kinases, DNA and RNA helicases, GTP-binding elongation factors and the Ras family of GTP-binding proteins. Additionally, the novel protein contains one putative transmembran domain.

No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

AC004780_1, differences to predicted genmodel

membrane regions: 1

AC004780_1, differences to predicted genmodel

complete cDNA, complete cds, EST hits
on genomic level encoded by AC004780,
differences to predicted genmodel!
TRANSMEMBRANE 1

Sequenced by AGOWA

Locus: unknown

Insert length: 2292 bp
Poly A stretch at pos. 2272, polyadenylation signal at pos. 2255

```
   1 GGGGGAGGGA ACTGATCTCA GCTCGGGCCC GCGTTACATC CTCCTCCTCT
  51 TCTTCCTTCG GCCCAGCTTT CCTTAGGGGC TGCAACCCGG ACGCCGAGGC
 101 CGGTTTCGGA GTGGGGAGTG CCCATTTTCT CTCCTTCCCA CGTTCCTGGC
 151 CCCCAGACGC CATTTGCAGG CGGGTGGCTT GGGTCAGCCT CCCCGCCCCC
 201 ACCCGACTCC CGTCACGGGA GAGCGCACAC CGCGCCCCGA GAACCAATCA
 251 GCAGCCGCGT TAGGTAACCA TGTCTGAGTC TGGACACAGT CAGCCTGGAC
 301 TCTATGGGAT AGAGCGGCGG CGACGGTGGA AGGAGCCTGG CTCTGGTGGC
 351 CCCCAGAATC TCTCTGGGCC TGGTGGTCGG GAGAGGGACT ACATTGCACC
 401 ATGGGAAAGA GAGAGAAGGG ATGCCAGCGA AGAGACAAGC ACTTCCGTCA
 451 TGCAGAAAAC CCCCATCATC CTCTCAAAAC CTCCAGCAGA GCGGTCAAAA
 501 CAGCCACCAC CTCCAACAGC CCCTGCTGCC CCGCCTGCTC CAGCCCCTCT
 551 GGAGAAGCCC ATCGTTCTCA TGAAGCCACG GGAGGAGGGG AAGGGGCCTG
 601 TGGCCGTGAC AGGTGCCTCT ACCCCTGAGG GCACCGCCCC ACCACCCCCT
 651 GCAGCCCCTG CGCCACCCAA GGGGGAGAAG GAGGGGCAGA GACCCACACA
 701 GCCTGTGTAC CAGATCCAGA ACCGGGGCAT GGGCACTGCC GCACCAGCAG
 751 CCATGGACCC TGTCGTGGGT CAGGCCAAAC TACTGCCCCC AGAGCGCATG
 801 AAGCACAGCA TCAAGTTGGT GGATGACCAG ATGAATTGGT GTGACAGTGC
 851 CATCGAGTAC CTGTTGGATC AGACTGATGT GTTGGTGGTT GGTGTCCTGG
 901 GCCTCCAGGG GACAGGCAAG TCCATGGTCA TGTCATTGTT GTCAGCCAAC
 951 ACTCCAGAGG AGGACCAGAG GACTTATGTT TTCCGGGCCC AGAGCGCTGA
1001 AATGAAGGAA CGAGGGGGCA ACCAGACCAG TGGCATCGAC TTCTTTATTA
1051 CCCAAGAACG GATTGTTTTC CTGGACACAC AGCCCATCCT GAGCCCTTCT
1101 ATCCTAGACC ATCTCATCAA TAATGACCGC AAACTGCCTC CAGAGTACAA
1151 CCTTCCCCAC ACTTACGTTG AAATGCAGTC ACTCCAGATT GCTGCCTTCC
1201 TTTTCACGGT CTGCCATGTG GTGATTGTTG TCCAGGACTG GTTCACAGAC
1251 CTCAGTCTCT ACAGGTTCCT GCAGACAGCA GAGATGGTGA AGCCCTCCAC
1301 CCCATCCCCC AGCCACGAGT CCAGCAGCTC ATCGGGCTCC GATGAAGGCA
1351 CCGAGTACTA CCCCCACCTA GTCTTCTTGC AGAACAAAGC TCGCCGAGAG
1401 GACTTCTGTC CTCGGAAGCT GCGGCAGATG CACCTGATGA TTGACCAGCT
1451 CATGGCCCAC TCCCACCTGC GTTACAAGGG AACTCTGTCC ATGTTACAAT
1501 GCAATGTCTT CCCGGGGCTT CCACCTGACT TCCTGGACTC TGAGGTCAAC
1551 TTATTCCTGG TACCCTTCAT GGACAGTGAA GCAGAGAGTG AAAACCCACC
1601 AAGAGCAGGA CCTGGTTCCA GCCCACTCTT CTCCCTGCTG CCTGGGTATC
1651 GTGGCCACCC CAGTTTCCAG TCCTTGGTGA GCAAGCTCCG GAGCCAAGTG
1701 ATGTCCATGG CCCGGCCACA GCTGTCACAC ACGATCCTCA CCGAGAAGAA
1751 CTGGTTCCAC TACGCTGCCC GGATCTGGGA TGGGGTGAGA AAGTCCTCTG
1801 CTCTGGCAGA GTACAGCCGC CTGCTGGCCT GAGGCCAAGG AGAGGAATGT
1851 CATGCAGGGG ACCTCCTGGG TCCGCAGTGT ACTGCGAGGG AGCACAGATG
1901 TCCATCCCCC GCTGGGGTGG AGAGCGGCAG CAGGCCTGAT GGATGAGGGA
1951 TCGTGGCTTC CCGGCCCAGA GACATGAGGT GTCCAGGGCC AGGCCCCCCA
```

```
2001 CCCTCAGTTG GGGCTGTTCC GGGGGTGACT GTGAGCGATC CCACCCCAAA
2051 CCTGAGATGG GGTAGCCCGT CCTGTGTCCT CCACAGGGAC AAGCAGTGGG
2101 AGGAGTCTGA ATGGTCACCA GGAAGCCCGG GCTCCATCTT GACCTCCTTT
2151 TTCAGGGACA GGAGCAACAG GCCCCTCTTC CCTGACTCTA AGCCCTTCCC
2201 TGTAAGGTGA GGCAGGGTCT GGAGAGCTCT TTATTGGAAC AGATCTGGTG
2251 GTTCAAATAA ACACAGTCAT GCAAAAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry AC004780 from database EMBL:
Homo sapiens chromosome 19, cosmid F17127, complete sequence.
Score = 2616, P = 0.0e+00, identities = 524/525
15 exons Bp 8031-31789

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 270 bp to 1829 bp; peptide length: 520
Category: similarity to unknown protein
Prosite motifs: ATP_GTP_A (211-219)

```
  1 MSESGHSQPG LYGIERRRRW KEPGSGGPQN LSGPGGRERD YIAPWERERR
 51 DASEETSTSV MQKTPIILSK PPAERSKQPP PPTAPAAPPA PAPLEKPIVL
101 MKPREEGKGP VAVTGASTPE GTAPPPPAAP APPKGEKEGQ RPTQPVYQIQ
151 NRGMGTAAPA AMDPVVGQAK LLPPERMKHS IKLVDDQMNW CDSAIEYLLD
201 QTDVLVVGVL GLQGTGKSMV MSLLSANTPE EDQRTYVFRA QSAEMKERGG
251 NQTSGIDFFI TQERIVFLDT QPILSPSILD HLINNDRKLP PEYNLPHTYV
301 EMQSLQIAAF LFTVCHVVIV VQDWFTDLSL YRFLQTAEMV KPSTPSPSHE
351 SSSSSGSDEG TEYYPHLVFL QNKARREDFC PRKLRQMHLM IDQLMAHSHL
401 RYKGTLSMLQ CNVFPGLPPD FLDSEVNLFL VPFMDSEAES ENPPRAGPGS
451 SPLFSLLPGY RGHPSFQSLV SKLRSQVMSM ARPQLSHTIL TEKNWFHYAA
501 RIWDGVRKSS ALAEYSRLLA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_22h13, frame 3

TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19, cosmid F17127, complete sequence., N = 2, Score = 1264, P = 1.3e-231

TREMBL:CEY54E2A_1 gene: "Y54E2A.2"; Caenorhabditis elegans cosmid Y54E2A, N = 2, Score = 219, P = 1.4e-15

```
>TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19, cosmid
     F17127, complete sequence.
          Length = 528

 HSPs:

 Score = 1264 (189.6 bits), Expect = 1.3e-231, Sum P(2) = 1.3e-231
 Identities = 254/302 (84%), Positives = 264/302 (87%)

Query:    46 ERERRDASEETSTSVMQKTPIILSKPPAERSKQPPPPTAPAAPPAPAPLEKPIVLMKPRE 105
             E+ER D+  + S   +Q+T     +     R  + P        +  A APLEKPIVLMKPRE
Sbjct:    39 EKER-DSDSDFSP--LQQTEGCQRRDKHFRHAENPHHPLKTSSRA-APLEKPIVLMKPRE 94

Query:   106 EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAPAAMDPV 165
             EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAPAAMDPV
Sbjct:    95 EGKGPVAVTGASTPEGTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAPAAMDPV 154

Query:   166 VGQAKLLPPERMKHSIKLVDDQMNWCDSAIEYLLDQTDVLVVGVLGLQGTGKSMVMSLLS 225
             VGQAKLLPPERMKHSIKLVDDQMNWCDSAIEYLLDQTDVLVVGVLGLQGTGKSMVMSLLS
Sbjct:   155 VGQAKLLPPERMKHSIKLVDDQMNWCDSAIEYLLDQTDVLVVGVLGLQGTGKSMVMSLLS 214
```

```
Query:   226 ANTPEEDQRTYVFRAQSAEMKERGGNQTSGIDFFITQERIVFLDTQPILSPSILDHLINN 285
             ANTPEEDQRTYVFRAQSAEMKERGGNQTSGIDFFITQERIVFLDTQPILSPSILDHLINN
Sbjct:   215 ANTPEEDQRTYVFRAQSAEMKERGGNQTSGIDFFITQERIVFLDTQPILSPSILDHLINN 274

Query:   286 DRKLPPEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYRFLQTAEMVKPSTP 345
             DRKLPPEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYR        K ++
Sbjct:   275 DRKLPPEYNLPHTYVEMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYRLWDLGCKCKSNSH 334

Query:   346 SP 347
             SP
Sbjct:   335 SP 336

 Score = 993 (149.0 bits), Expect = 1.3e-231, Sum P(2) = 1.3e-231
 Identities = 189/189 (100%), Positives = 189/189 (100%)

Query:   332 RFLQTAEMVKPSTPSPSHESSSSSGSDEGTEYYPHLVFLQNKARREDFCPRKLRQMHLMI 391
             RFLQTAEMVKPSTPSPSHESSSSSGSDEGTEYYPHLVFLQNKARREDFCPRKLRQMHLMI
Sbjct:   340 RFLQTAEMVKPSTPSPSHESSSSSGSDEGTEYYPHLVFLQNKARREDFCPRKLRQMHLMI 399

Query:   392 DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNLFLVPFMDSEAESENPPRAGPGSS 451
             DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNLFLVPFMDSEAESENPPRAGPGSS
Sbjct:   400 DQLMAHSHLRYKGTLSMLQCNVFPGLPPDFLDSEVNLFLVPFMDSEAESENPPRAGPGSS 459

Query:   452 PLFSLLPGYRGHPSFQSLVSKLRSQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA 511
             PLFSLLPGYRGHPSFQSLVSKLRSQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA
Sbjct:   460 PLFSLLPGYRGHPSFQSLVSKLRSQVMSMARPQLSHTILTEKNWFHYAARIWDGVRKSSA 519

Query:   512 LAEYSRLLA 520
             LAEYSRLLA
Sbjct:   520 LAEYSRLLA 528
```

Pedant information for DKFZphfbr2_22h13, frame 3

Report for DKFZphfbr2_22h13.3

```
[LENGTH]        520
[MW]            57650.81
[pI]            6.52
[HOMOL]         TREMBL:AC004780_1 product: "F17127_1"; Homo sapiens chromosome 19, cosmid
F17127, complete sequence. 0.0
[PROSITE]       ATP_GTP_A       1
[PROSITE]       MYRISTYL        8
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        8
[PROSITE]       GLYCOSAMINOGLYCAN       1
[PROSITE]       PKC_PHOSPHO_SITE        3
[PROSITE]       ASN_GLYCOSYLATION       2
[KW]            TRANSMEMBRANE   1
[KW]            LOW_COMPLEXITY     11.73 %

SEQ     MSESGHSQPGLYGIERRRRWKEPGSGGPQNLSGPGGRERDYIAPWERERRDASEETSTSV
SEG     ............................................................
PRD     cccccccccccccccccccccccccccccccccccccceeeeehhhhhhhhcccccccee
MEM     ............................................................

SEQ     MQKTPIILSKPPAERSKQPPPPTAPAAPPAPAPLEKPIVLMKPREEGKGPVAVTGASTPE
SEG     ..................xxxxxxxxxxxxxxx...........................
PRD     eeccceeecccccccccccccccccccccccccccceeeeecccccccccceeeeecccccc
MEM     ............................................................

SEQ     GTAPPPPAAPAPPKGEKEGQRPTQPVYQIQNRGMGTAAPAAMDPVVGQAKLLPPERMKHS
SEG     ..xxxxxxxxxx................................................
PRD     cccccccccccccccccccccccceeeeeecccccccccccccccceeecceeeccccchhhhh
MEM     ............................................................

SEQ     IKLVDDQMNWCDSAIEYLLDQTDVLVVGVLGLQGTGKSMVMSLLSANTPEEDQRTYVFRA
SEG     .................xxxxxxxxxxxxxxxxxx.........................
PRD     hhhhccchhhhhhhhhhccccceeeeeeccccccccchhhhhhhhccccchhhhhheeee
MEM     ............................................................

SEQ     QSAEMKERGGNQTSGIDFFITQERIVFLDTQPILSPSILDHLINNDRKLPPEYNLPHTYV
SEG     ............................................................
PRD     hhhhhhhccccceeeeeeeecceeeeeecccccccccccccccccccccccccccchh
MEM     ............................................................

SEQ     EMQSLQIAAFLFTVCHVVIVVQDWFTDLSLYRFLQTAEMVKPSTPSPSHESSSSSGSDEG
SEG     .........................................xxxxxxxxxxxxxxxx...
```

```
PRD   hhhhhhhhhhhhhhhhheeeeeeecccchhhhhhhhhhhhhhhcccccccccccccccccc
MEM   MMMMMMMMMMMMMMMMMMMMMMMM....................................

SEQ   TEYYPHLVFLQNKARREDFCPRKLRQMHLMIDQLMAHSHLRYKGTLSMLQCNVFPGLPPD
SEG   ............................................................
PRD   cccccceeeehhhhhhhccccchhhhhhhhhhhhhhhhhhcccccccccccccccccc
MEM   ............................................................

SEQ   FLDSEVNLFLVPFMDSEAESENPPRAGPGSSPLFSLLPGYRGHPSFQSLVSKLRSQVMSM
SEG   ............................................................
PRD   chhhhhheeeeecccccccccccccccccccceeeccccccccchhhhhhhhhhhhhhh
MEM   ............................................................

SEQ   ARPQLSHTILTEKNWFHYAARIWDGVRKSSALAEYSRLLA
SEG   ........................................
PRD   hhhhhhhheeecccchhhhhhhhhhhhcchhhhhhhhhccc
MEM   ........................................
```

Prosite for DKFZphfbr2_22h13.3

PS00001	30->34	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00002	32->36	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	507->511	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00005	215->218	PKC_PHOSPHO_SITE	PDOC00005
PS00005	491->494	PKC_PHOSPHO_SITE	PDOC00005
PS00006	117->121	CK2_PHOSPHO_SITE	PDOC00006
PS00006	193->197	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00006	254->258	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	298->302	CK2_PHOSPHO_SITE	PDOC00006
PS00006	355->359	CK2_PHOSPHO_SITE	PDOC00006
PS00006	436->440	CK2_PHOSPHO_SITE	PDOC00006
PS00008	26->32	MYRISTYL	PDOC00008
PS00008	139->145	MYRISTYL	PDOC00008
PS00008	153->159	MYRISTYL	PDOC00008
PS00008	211->217	MYRISTYL	PDOC00008
PS00008	214->220	MYRISTYL	PDOC00008
PS00008	249->255	MYRISTYL	PDOC00008
PS00008	356->362	MYRISTYL	PDOC00008
PS00008	505->511	MYRISTYL	PDOC00008
PS00017	211->219	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphfbr2_22h13.3)

DKFZphfbr2_22i4
----

group: brain derived

DKFZphfbr2_22i4.1 encodes a novel 228 amino acid protein with similarity to the N-terminus of human p52rIPK.

No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to Human P52rIPK N-terminus

complete cDNA, complete cds, few EST hits
function of P52rIPK, repressor of p58IPK protein kinase inhibitor
upstream regulator of interferon induced proteins

Sequenced by AGOWA

Locus: unknown

Insert length: 4748 bp
Poly A stretch at pos. 4726, polyadenylation signal at pos. 4709

```
   1 TGGGTCCGGT CCTAGGGTCA CACCCACCGC AGGGTCTGGC TTGGTACAGT
  51 TGGGTGCATG CAGAAGTAGG TGGAGCTGCT GTTGCAGCCT TGAGAGAGTT
 101 TTATTGTAAA ACTCTTGTAA TTTATAGTAA TCGGAGGGGA AAACACCTCT
 151 TCCTTTTAAT TGCTCTGAGG ACCGCTGCCA AAGAAACGCA GTAGATCCGC
 201 TCCCTCTTGG GGGCGGGGAG AAAGAACGGG TTGTGTCCGC CATGTTGGTG
 251 AAGTCAAGCG AAGGCGACTA GAGCTCCAGG AGGGCCAGTT CTGTGGGCTC
 301 TAGTCGGCCA TATTAATAAA GAGAAAGGGA AGGCTGACCG TCCTTCGCCT
 351 CCGCCCCCAC ATACACACCC CTTCTTCCCA CTCCGCTCTC ACGACTAAGC
 401 TCTCACGATT AAGGCACGCC TGCCTCGATT GTCCAGCCTC TGCCAGAAGA
 451 AAGCTTAGCA GCCAGCGCCT CAGTAGAGAC CTAAGGGCGC TGAATGAGTG
 501 GGAAAGGGAA ATGCCGACCA ATTGCGCTGC GGCGGGCTGT GCCACTACCT
 551 ACAACAAGCA CATTAACATC AGCTTCCACA GGTTTCCTTT GGATCCTAAA
 601 AGAAGAAAAG AATGGGTTCG CCTGGTTAGG CGCAAAAATT TTGTGCCAGG
 651 AAAACACACT TTTCTTTGTT CAAAGCACTT TGAAGCCTCC TGTTTTGACC
 701 TAACAGGACA AACTCGACGA CTTAAAATGG ATGCTGTTCC AACCATTTTT
 751 GATTTTTGTA CCCATATAAA GTCTATGAAA CTCAAGTCAA GGAATCTTTT
 801 GAAGAAAAAC AACAGTTGTT CTCCAGCTGG ACCATCTAAT TTAAAATCAA
 851 ACATTAGTAG TCAGCAAGTA CTACTTGAAC ACAGCTATGC CTTTAGGAAT
 901 CCTATGGAGG CAAAAAAGAG GATCATTAAA CTGGAAAAAG AAATAGCAAG
 951 CTTAAGAAGA AAAATGAAAA CTTGCCTACA AAAGGAACGC AGAGCAACTC
1001 GAAGATGGAT CAAAGCCACG TGTTTGGTAA AGAATTTAGA AGCAAATAGT
1051 GTATTACCTA AAGGTACATC AGAACACATG TTACCAACTG CCTTAAGCAG
1101 TCTTCCCTTG GAAGATTTTA AGATCCTTGA ACAAGATCAA CAAGATAAAA
1151 CACTGCTAAG TCTAAATCTA AAACAGACCA AGAGTACCTT CATTTAAATT
1201 TAGCTTGCAC AGAGCTTGAT GCCTATCCTT CATTCTTTTC AGAAGTAAAG
1251 ATAATTATGG CACTTATGCC AAAATTCATT ATTTAATAAA GTTTTACTTG
1301 AAGTAACATT ACTGAATTTG TGAAGACTTG ATTACAAAAG AATAAAAAAC
1351 TTCATATGGA AATTTTATTT GAAAATGAGT GGAAGTGCCT TACATTAGAA
1401 TTACGGACTT AAAAATTTTG CTAATAAATT GTGTGTTTGA AAGGTGTTTT
1451 TTGTTTTTGT CTTTTTAAAC TACTGTTAAA AGAACAGCTT ATGATAAGTA
1501 ATATGTTTAA CTTAGAGAAG AATTTTTTCC TGTACCAAAG TTGGCATATT
1551 GCATTCTAAA TAAGATGCTA AATAAGAGTT AACCAACATT CAACATGACC
1601 TTAAAACTGC TGGGTTTTGT ATTAATTAAA TTATAATTGG CACTGTGATT
1651 TGAAAAATTT ATAGAAAAAA AGGTACAGGG CAAGTTTTTA AATTAAAACT
1701 TTCTATATTT TGTTTTACCA GTAAAAGTGA GCTTATCATG GCCTCTCTCA
1751 TAAGAATGAT TTTAAAATAG GTTGTAAAAT ATTTTGAAAA TATTTGAATG
1801 TGAAGTACCA TTGAGTCATC CAAACTAGGT AAGGCCTCAA GTACTTTAAA
1851 CTAGTAAAAT CTAGTAGCTG ATAATATTCA CCTAAGTAAG TGTTGTAAAA
1901 TAATTCAGAG TTCAGGACCT AGCTTAGATA AATGTATACT ACTCTTTTTC
1951 TCATAGTAAA AATCTTACAT TTCCAACTTC AAAATTGGTG CTTCCATATT
2001 TGTTGATAAC CAAAACTCCT AAGGTTTTTT GTTTTCTTTT TAACTACTTT
2051 CCAAATGCAT ACTATACCTC AGAAATAGTG TATCAATATA GTGGGCTTTT
2101 TTTTTCCTCT TCATAAACCC ACAGTAAAAT TTAATCACAG GAAACTACTT
2151 ATATCTTCAC ACTTTGTATT GATAACTTAA AATGGCATCA GTTTATCTTA
2201 GACATCAGCT TGCTTTTTAT CTCCTTTTTT AGTGAGTGAA ATAGAGCAAC
2251 TAGCATGCCT GTGTTCCCAG CTACTTGGGA GGCTAAGGTG GGAAGATCAA
2301 TTGAACCTAG GAGGTTGAGG CTATAGTGAG CTGTGATTGC ACGACTGCAC
2351 TCCAGCCTGG GCAATGGAGT GAGACTCCTG TCTCTAAAAC AGCAACAACA
2401 AAAATAAAGC AACCATAGTG CATAAGGGAA ATTAAATGTT CCCTATAGAA
2451 ATATGTGTAT GTCTGTGATA GTGGTATGCA AATGCTAATT ATTTTATAAA
2501 ATAAAAGTTC AGAACTATTC TTATCATTGC CACTTGAACA ATTAAAGGGT
2551 TTGCTTTATT TCACTAATGT TTAATAGGAA CCCTTTGCTT CAAACAGCTT
```

```
2601 TGTTGAAATC ATGTAAAAAT TTGTTAATAG AGAATCAAGT TATTTAACTC
2651 AACTTATTTA ATTCAAGCTT GTGATACTAA CATACAAAGG TAGCATAAAC
2701 CAAGTCATAA ATTGCTGTAA TCTTTCCTGT AGAGTAATAG CTACTTCATG
2751 ATTTTTTTAA AAATTTCATT TTTTTGCTAT TTAGGATTGC ATTTGCTTGG
2801 CTCCTAGTAA CAATTCTTTT ACAGTATTAG CACTCTCTTT ACTAAGGAAT
2851 GCCTCCCAAG GAAATGCAAA GGTAGGAAAA GTCTCTTAGA ATGCCCATGA
2901 GGTATTTAAA ACAGATATTT ATGAAAATCT TTTTGTGAAT GTTATAAATC
2951 TTGCTAGTTA TTTTATCTTT ATCTTAAGTA TTAGATGTAG TTCCTTGGAA
3001 TTGTCATTAC ATATTTATTT TTTTCTAGTG TGGTTTCAAA TAACTTTTTG
3051 CCAACATATA ATCATCATCA AACATTCACT GACCATATCT ATTTTATAAC
3101 TCAAAATAAG TTGGACAAAT AATCATTTTA ATAAAAACTA TTTTTTCCAA
3151 GTATAACCAC TGTCATGTGG TTCACCCTTC ACCCCAGATA CAAAACACTT
3201 ATTTGTGTAG CCCAGTTCCC ATCTACAGTA ATACCTTGAA ACCTTAATAA
3251 ATTTTAAAAA TCATAAAAAT AAAATATTGT AAAATACAAC AAATTTTGGA
3301 CAAGGTTACT TCATCTTCAT TCATTATTAC CTGACAGTAT TAAACTACTA
3351 CTCAATAATT TTAGAGTAAA CTTTTCTGTG TTTTCCCCGT GATTTTCATT
3401 GTGCTGTCCT GACAACATGC TCCAAACTCT TTGCATCAAA TTGTTTTATT
3451 AACATACATT TGTCTACCTT AAAACTAGCT TTATTCACAG AGAAAGACCT
3501 AAAAGGAGTC TATTAAAATG CTGCTTTCAG TTTGATAGTT TTTTTTTTAA
3551 TCACTCTGAC CATAAACTAA CTGAAATTAT AATGGATTTT TTTTCCTCTC
3601 CCGGTCACAA CACAGATCTT CTGTTCATTT GTTCTCTGTC TACTGGGCAC
3651 CAACCTCTAC AAAGAACCAG CCAAAGGCTA GGTACTTGAT ATAAAAAGGA
3701 ATATTACATT ATTTTCTGCC CTCAAGTTGC TCTATCTCCT GAAAGAAACA
3751 AGTAATATTT ATAATACAAT ATGATAAATG CTACAAAAGA AATAGCTGTA
3801 AAGTCCTTTG GTAAATGCTG TTGAATTGGA ATTCAGTAAG AACTATAAAC
3851 TGTAGACCTT TTTATAATCA AATGCTTTTG TCTTGAAACA AAACAGATTC
3901 CTCCTTATAT TGACTTAGCA AAGGAGGTAC AAGGACATTG GCATTTGACC
3951 TGAATTATGG TGTTTTATTG AATGAGCTAT AAGACAACAT TTTTACCCTT
4001 TAAAATGAAC ACTGAACAAA TGTGTTAATG GTATCTTTGT TAAAAGGAAA
4051 ACATAGCTAT AAATAAAATA CTACATCGAA ATCCAGCACT GGAGTTCATT
4101 TGAAATTTGA TATTTTGTGT AAAGTAACAA ACCTATTAAC ACAGATTTTT
4151 AAAATAACTC AGAATCGTAT AAAGCACTTT GGTACTTATT TGTTCTCTTT
4201 TCCCTTACAT TCTGTGTGGT AGGTGGTATT ATCTCTGATT TACACATGAA
4251 GACATCCTTG TTAATGCAAT TTATTTATTC ATTCGGGCAT TTACTGTGTG
4301 CCAACTTGCA AAAGGAATAG AAATGTCTGT GATCTAGATA GTTCTAGATT
4351 GAACATAGAT TTTCTGCCAA CAAATCCTCT CTGCTGTTCA CATTATCCTT
4401 TGTTTAACGT ATGAACCAGG TTACTAAAAT AGGATAAATC ATGTGTCTTA
4451 GAATATGAAA ATAGTAAGGT CTTTGAGGTC ACTTGATCTT CTCTAAGTAG
4501 ACTTTATAAT ATTGTGTTTT ATCTCATTTC TCAATATTAG AATACGGGTA
4551 GATTTTAATT TTGCTATAAT ATAGGAAATG GTTCATCTTT GTACCAAAAT
4601 ATTGCATTCT TCTGATATTT AGACAGTTGG AAACTTTCTA AAATTGAGGA
4651 TTTTGTAGTG TATACTAAAT AATTGCATAT TCAAAAAAAT GTATTCTGAG
4701 TATGGTGATA TTAAACATTT TTCCCCAAAA AAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

98107671:
Regulation of interferon-induced protein kinase PKR: modulation of P58IPK inhibitory function by a novel protein, P52rIPK

Peptide information for frame 1

ORF from 511 bp to 1194 bp; peptide length: 228
Category: similarity to known protein

```
  1 MPTNCAAAGC ATTYNKHINI SFHRFPLDPK RRKEWVRLVR RKNFVPGKHT
 51 FLCSKHFEAS CFDLTGQTRR LKMDAVPTIF DFCTHIKSMK LKSRNLLKKN
101 NSCSPAGPSN LKSNISSQQV LLEHSYAFRN PMEAKKRIIK LEKEIASLRR
151 KMKTCLQKER RATRRWIKAT CLVKNLEANS VLPKGTSEHM LPTALSSLPL
201 EDFKILEQDQ QDKTLLSLNL KQTKSTFI
```

BLASTP hits

Entry AF007393_1 from database TREMBL:
product: "P52rIPK"; Homo sapiens P52rIPK mRNA, complete cds.
Score = 166, P = 2.5e-11, identities = 40/106, positives = 56/106

Alert BLASTP hits for DKFZphfbr2_22i4, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_22i4, frame 1

Report for DKFZphfbr2_22i4.1

```
[LENGTH]        228
[MW]            26259.94
[pI]            10.17
[HOMOL]         TREMBL:AF007393_1 product: "P52rIPK"; Homo sapiens P52rIPK mRNA, complete cds.
1e-09
[PROSITE]       MYRISTYL        1
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        2
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       3
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY     7.02 %

SEQ     MPTNCAAAGCATTYNKHINISFHRFPLDPKRRKEWVRLVRRKNFVPGKHTFLCSKHFEAS
SEG     ............................................................
PRD     cccccccccccccccccccccceeeecccccchhhhhhhhhhhhccccccceeehhhhhhh

SEQ     CFDLTGQTRRLKMDAVPTIFDFCTHIKSMKLKSRNLLKKNNSCSPAGPSNLKSNISSQQV
SEG     ..........................xxxxxxxxxxxxxxxx..................
PRD     cccccccccccccccccccceeeecccccchhhhhhhhhhccccccccccccccccccchhh

SEQ     LLEHSYAFRNPMEAKKRIIKLEKEIASLRRKMKTCLQKERRATRRWIKATCLVKNLEANS
SEG     ............................................................
PRD     hhhhcccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhheeeecccccc

SEQ     VLPKGTSEHMLPTALSSLPLEDFKILEQDQQDKTLLSLNLKQTKSTFI
SEG     ................................................
PRD     cccccccccccccccccccccchhhhhhcccccccccccccccccccc
```

Prosite for DKFZphfbr2_22i4.1

PS00001	19->23	ASN_GLYCOSYLATION	PDOC00001
PS00001	100->104	ASN_GLYCOSYLATION	PDOC00001
PS00001	114->118	ASN_GLYCOSYLATION	PDOC00001
PS00004	160->164	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	68->71	PKC_PHOSPHO_SITE	PDOC00005
PS00005	88->91	PKC_PHOSPHO_SITE	PDOC00005
PS00005	147->150	PKC_PHOSPHO_SITE	PDOC00005
PS00005	163->166	PKC_PHOSPHO_SITE	PDOC00005
PS00006	60->64	CK2_PHOSPHO_SITE	PDOC00006
PS00006	78->82	CK2_PHOSPHO_SITE	PDOC00006
PS00008	9->15	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_22i4.1)

DKFZphfbr2_22k3
----

group: brain derived

DKFZphfbr2_22k3 encodes a novel 538 amino acid protein with weak similarity to extensins.

No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to extensins

complete cDNA, complete cds, few EST hits
CpG Island in 5' UTR complete cDNA

Sequenced by AGOWA

Locus: unknown

Insert length: 2775 bp
Poly A stretch at pos. 2755, polyadenylation signal at pos. 2718

```
   1 GGGGCTGCCC GCGCGCTCCA CGGTGCAGAG CTCTAAGCGC GCGGGCTGGC
  51 AGGCTGCGGC GCGTCAAGGT CAGCCTGGAG CTGGGTGGCG GCCTGCCTGG
 101 GGGCGGGGGA CCCTACTGGA GGCCCGGGCT GGGGCCTCCC AGCGCCTCGG
 151 CCATATTGAA TAGCTTCGAC TGGACCGTCT TTGTCTGCGA AGTCCTGTCC
 201 CAAGTTCCAG CCGCGTCCCT GGGGCCTGGG GCAGGAAGAG TCGCTGGCAG
 251 CCCGCGCGCC CCAACTTGGA GCTGGGACAC CACGTTTCCA GCTTGGAGTG
 301 GGCCTTGAGC CTTGGGACTG ACCTCGCCCC CGGCTCACGT AGGCATCCTG
 351 GAAATTGATT CCCCCAAGTC CTTGGTGGGG GAGCCGGACT TGGTCAAGAC
 401 TGTACTTGTT GCAGGCGAAG AGATTGGAGG CGTTTGGCTC GTCCCTGGCT
 451 AGGGAGGTGA GACTCTCCGG TCAGCGTTGC TGGAACTCCC CCCATCCAGT
 501 CCCTCCCTCA AGACTAAGGG CTACAGTAGT TTGTTGGGGC TCATTGCCCC
 551 CTCACCCCAG ATATCACCCT GGAGATCTTA AAGACTCTCG AGAAAAGCCA
 601 CGTGGGGGGC TGGTTCCCCT GGGGCTTCCT GCCGTCCCCC GACTGCCTCA
 651 TTCTTTGGAG CGTCCCCGAT GTCTGCAAAG ATGTGGATTT GGACGTCCTC
 701 GTGGAAGCCC TAAAGCCCGT GGGGACATTT AAGAAGATCG GCAAGGTGTT
 751 CCGCAAGGAG GAGGACTCCA CGGTGGGGAT GCTGCAGATC GGGGAGGACG
 801 TCGACTATTT GCTCATCCCC CGGGAGGTCA GGCTGGCTGG GGGCGTCTGG
 851 AGAGTCATCT CTAAGCCCGC CACCAAGGAA GCAGAATTTC GGGAGCGGCT
 901 GACCCAGTTC CTGGAAGAAG AGGGCCGCAC CCTGGAGGAC GTGGCCCGCA
 951 TCATGGAGAA GAGCACCCCG CACCCGCCCC AGCCCCCCAA AAAGCCCAAG
1001 GAGCCCCGAG TGAGGAGGAG AGTGCAGCAG ATGGTGACTC CTCCGCCCCG
1051 GCTGGTCGTG GGCACGTACG ACAGCAGCAA CGCCAGCGAC AGCGAGTTCA
1101 GCGACTTCGA GACCTCCAGA GACAAGAGCC GCCAGGGCCC GCGGCGGGGC
1151 AAGAAGGTGC GCAAAATGCC CGTCAGCTAC CTGGGCAGCA AGTTCCTGGG
1201 AAGCGACCTG GAGAGTGAGG ATGATGAGGA ACTGGTCGAG GCCTTCCTCC
1251 GGCGACAGGA GAAGCAGCCC AGCGCGCCGC CTGCCCGCCG CCGCGTCAAC
1301 CTGCCAGTGC CCATGTTTGA GGACAACCTG GGGCCTCAGC TGTCCAAAGC
1351 GGACAGGTGG CGGGAGTATG TCAGCCAGGT GTCCTGGGGG AAGCTGAAGC
1401 GGAGGGTGAA GGGTTGGGCG CCGAGGGCGG GCCCCGGGGT GGGCGAGGCC
1451 CGGCTGGCCT CCACCGCAGT GGAGAGCGCA GGGGTATCAT CGGCGCCAGA
1501 GGGCACCAGC CCGGGGGATC GCTTGGGAAA CGCGGGAGAT GTTTGTGTGC
1551 CCCAGGCTTC CCCTAGGCGA TGGAGGCCCA AGATCAACTG GGCCTCCTTT
1601 CGGCGCCGCA GGAAGGAGCA GACAGCACCC ACAGGTCAGG GGGCAGACAT
1651 CGAGGCTGAT CAGGGGGGAG AGGCTGCAGA TAGTCAAAGG GAAGAGGCCA
1701 TAGCTGACCA GCGGGAAGGG GCTGCAGGTA ATCAGAGGGC TGGGGCCCCA
1751 GCTGACCAGG GGGCAGAGGC TGCAGATAAT CAGAGGGAAG AGGCTGCAGA
1801 TAATCAGAGG GCAGGGGCCC CAGCTGAGGA GGGGGCAGAG GCTGCAGATA
1851 ACCAGAGGGA AGAGGCTGCA GATAATCAGA GGGCAGAGGC CCCAGCTGAC
1901 CAGAGGTCAC AGGGCACAGA TAACCACAGG GAAGAGGCTG CAGATAATCA
1951 GAGGGCGGAG GCCCCAGCTG ACCAGGGGTC AGAGGTTACA GATAATCAAA
2001 GGGAAGAGGC CGTACATGAC CAGAGGGAAA GGGCCCCAGC TGTCCAGGGT
2051 GCAGATAATC AGAGGGCACA GGCCCGGGCT GGCCAGAGGG CAGAGGCTGC
2101 ACATAATCAG AGGGCAGGGG CCCCAGGTAT CCAGGAAGCT GAAGTCTCAG
2151 CTGCCCAAGG GACCACAGGA ACAGCTCCAG GAGCCAGGGC CCGGAAACAG
2201 GTCAAGACAG TGAGGTTCCA GACCCCTGGA CGCTTTTCGT GGTTTTGCAA
2251 GCGCCGGAGA GCCTTCTGGC ACACTCCCCG GTTGCCAACC CTGCCCAAGA
2301 GAGTCCCCAG GGCAGGAGAG GTCAGGAACC TCAGGGTGCT GAGGGCCGAG
2351 GCCAGAGCAG AAGCTGAGCA GGGAGAGCAA GAAGACCAGC TGTGAGGTGA
2401 GGGCTAGAGA CAGCCCACGG GCCCTCCCTC CAAGTGTGGG AGGGAGAGAT
2451 GCTCTGCCTC TGAACTTCAA AGTGGAGGTG GAGTGCTGGC CACGTCTCCA
2501 CCTAACAACC CTCTTTATTC TCTTGTTAAA GTTTTGTTCA TGCTTTGATT
2551 TTTTTTTAAA TTTTTTAGAG ACAGGGTCTC ACTCTGTTGC CCAGGCTGGA
2601 GTGCAGTGGC ATGATCATAA CTCACTGCAG CCTCAAACTT CTGGCCTCAA
2651 GTGATCCTCC TGCCTCGGCC TCCCAAAATG CTGGGATTAC AGATGTGAGC
```

```
2701 CACCACACAC ACCATCTGAT TAAAAAAAAA AAATACTGAT TCCCTGTAGC
2751 AACCCAAAAA AAAAAAAAAA AAAAA
```

BLAST Results

Entry HS164A7F from database EMBL:
H.sapiens CpG island DNA genomic Msel fragment, clone 164a7, forward read cpg164a7.ft1a .
Score = 740, P = 3.0e-25, identities = 150/151

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 779 bp to 2392 bp; peptide length: 538
Category: similarity to known protein

```
  1 MLQIGEDVDY LLIPREVRLA GGVWRVISKP ATKEAEFRER LTQFLEEEGR
 51 TLEDVARIME KSTPHPPQPP KKPKEPRVRR RVQQMVTPPP RLVVGTYDSS
101 NASDSEFSDF ETSRDKSRQG PRRGKKVRKM PVSYLGSKFL GSDLESEDDE
151 ELVEAFLRRQ EKQPSAPPAR RRVNLPVPMF EDNLGPQLSK ADRWREYVSQ
201 VSWGKLKRRV KGWAPRAGPG VGEARLASTA VESAGVSSAP EGTSPGDRLG
251 NAGDVCVPQA SPRRWRPKIN WASFRRRRKE QTAPTGQGAD IEADQGGEAA
301 DSQREEAIAD QREGAAGNQR AGAPADQGAE AADNQREEAA DNQRAGAPAE
351 EGAEAADNQR EEAADNQRAE APADQRSQGT DNHREEAADN QRAEAPADQG
401 SEVTDNQREE AVHDQRERAP AVQGADNQRA QARAGQRAEA AHNQRAGAPG
451 IQEAEVSAAQ GTTGTAPGAR ARKQVKTVRF QTPGRFSWFC KRRRAFWHTP
501 RLPTLPKRVP RAGEVRNLRV LRAEARAEAE QGEQEDQL
```

BLASTP hits

Entry RNU67136_1 from database TREMBL:
"A-kinase anchoring protein AKAP150"; Rattus norvegicus
A-kinase anchoring protein AKAP150 mRNA, complete cds. Rattus norvegicus (Norway rat)
Length = 714
Score = 182 (64.1 bits), Expect = 1.2e-10, P = 1.2e-10
Identities = 73/257 (28%), Positives = 104/257 (40%)

Alert BLASTP hits for DKFZphfbr2_22k3, frame 2

TREMBL:PFSANTY_1 product: "S-antigen"; Plasmodium falciparum KF1916
S-antigen gene, complete cds., N = 1, Score = 178, P = 3.7e-11

>TREMBL:PFSANTY_1 product: "S-antigen"; Plasmodium falciparum KF1916
S-antigen gene, complete cds.
Length = 285

HSPs:

Score = 178 (26.7 bits), Expect = 3.7e-11, P = 3.7e-11
Identities = 60/217 (27%), Positives = 97/217 (44%)

```
Query:   269 INWASFRRRRKEQTAPTGQGA-DIEADQGGEAADSQRE-EAIADQ---REGAAGNQRAGA 323
             +N  + +   + E      G+G  D E      E +D+  E E I  Q      E A  N+ AG+
Sbjct:    47 LNGKNGKGNKYEDLQEEGEGENDDEEHSNSEESDNDEENEIIVGQDGSNEKAGSNEEAGS 106

Query:   324 PADQGAEAADNQREEAADNQRAGAPAEEGA--EAADNQR----EEAADNQRAEAPADQRS 377
                  G+         E+A  N++AG+  E G+  EA  N+      EEA  N++A +      S
Sbjct:   107 NEKAGSNEEAGSNEKAGSNEKAGSNEEAGSNEEAGSNEEAGSNEEAGSNEKAGSNEKAGS 166

Query:   378 QGTDNHREEAADNQRAEAPADQGSEVTDNQREEAVHDQRERAPAVQGADNQRAQAR--AG 435
                     EEA  N++A  +  + GS          E+A  +++  +    G+ N++A  +    AG
Sbjct:   167 NEKAGSNEEAGSNEKAGSNEEAGSNEKAGSNEKAGSNEKAGSNEEAGS-NEKAGSNEEAG 225

Query:   436 QRAEAAHNQRAGA---PGIQEAEVSAAQGTTGTA-PGA 469
```

```
              EA  N+ AG+    G  E    +  +G  GT  PG+
Sbjct:   226 SNEEAGSNEEAGSNEEAGSNEGSEAGTEGPKGTGGPGS 263

 Score = 173 (26.0 bits), Expect = 1.5e-10, P = 1.5e-10
 Identities = 51/190 (26%), Positives = 83/190 (43%)

Query:   279 KEQTAPTGQ-GADIEADQGGEAADSQREEAIADQREGAAGNQRAGAPADQGAEAADNQRE 337
             +E     GQ G++ +A    EA  +++     A    E A  N++AG+     G+       E
Sbjct:    83 EENEIIVGQDGSNEKAGSNEEAGSNEK----AGSNEEAGSNEKAGSNEKAGSNEEAGSNE 138

Query:   338 EAADNQRAGAPAEEGAEAADNQREEAADNQRAEAPADQRSQGTDNHREEAADNQRAEAPA 397
             EA  N+ AG+  E G+        E+A  N++A +  +   S         EEA  N++A +
Sbjct:   139 EAGSNEEAGSNEEAGSNEKAGSNEKAGSNEKAGSNEEAGSNEKAGSNEEAGSNEKAGSNE 198

Query:   398 DQGSEVTDNQREEAVHDQRERAPAVQGADNQRAQARAGQRAEAAHNQRAGAPGIQEAEVS 457
                GS        EEA   +++   +      G++ +       AG     EA  N+ AG+     EA
Sbjct:   199 KAGSNEKAGSNEEAGSNEKAGSNEEAGSNEE-----AGSNEEAGSNEEAGSNEGSEAGTE 253

Query:   458 AAQGTTGTAPG 468
              +GT G   G
Sbjct:   254 GPKGTGGPGSG 264

 Score = 147 (22.1 bits), Expect = 1.6e-07, P = 1.6e-07
 Identities = 40/168 (23%), Positives = 70/168 (41%)

Query:   288 GADIEADQGGEAADSQR--EEAIADQREGAAGNQRAGAPADQGAEAADNQREEAADNQRA 345
             G++ EA     +A  +++        A    E A  N+ AG+   + G+          E+A  N++A
Sbjct:   111 GSNEEAGSNEKAGSNEKAGSNEEAGSNEEAGSNEEAGSNEEAGSNEKAGSNEKAGSNEKA 170

Query:   346 GAPAEEGAEAADNQREEAADNQRAEAPADQRSQGTDNHREEAADNQRAEAPADQGSEVTD 405
             G+  E G+          EEA  N++A +     S         EEA  N++A +  + GS
Sbjct:   171 GSNEEAGSNEKAGSNEEAGSNEKAGSNEKAGSNEKAGSNEEAGSNEKAGSNEEAGSNEEA 230

Query:   406 NQREEAVHDQR--ERAPAVQGADNQRAQARAGQRAEAAHNQRAGAPGI 451
                EEA  ++          +  G +  +         G   E +HN++       I
Sbjct:   231 GSNEEAGSNEEAGSNEGSEAGTEGPKGTGGPGSGGEHSHNKKKSKKSI 278

 Score = 101 (15.2 bits), Expect = 2.5e-02, P = 2.4e-02
 Identities = 26/100 (26%), Positives = 47/100 (47%)

Query:   281 QTAPTGQGADIEADQGGEAADSQREEAIADQREGAAGNQRAGAPADQGAEAADNQREEAA 340
             + A + + A     + G            EEA ++++ G+  N++AG+      G+          E+A
Sbjct:   162 EKAGSNEKAGSNEEAGSNEKAGSNEEAGSNEKAGS--NEKAGSNEKAGSNEEAGSNEKAG 219

Query:   341 DNQRAGAPAEEGAEAADNQREEAADNQRAEAPADQRSQGT 380
             N+ AG+  E G+         EEA  N+ +EA    +  +GT
Sbjct:   220 SNEEAGSNEEAGSNEEAGSNEEAGSNEGSEA-GTEGPKGT 258
```

Pedant information for DKFZphfbr2_22k3, frame 2

Report for DKFZphfbr2_22k3.2

```
[LENGTH]       538
[MW]           59402.19
[pI]           8.72
[HOMOL]        TREMBL:AF037364_1 gene: "MA1"; product: "paraneoplastic neuronal antigen MA1";
Homo sapiens paraneoplastic neuronal antigen MA1 (MA1) mRNA, complete cds. 4e-10
[PROSITE]      AMIDATION       1
[PROSITE]      MYRISTYL        12
[PROSITE]      CK2_PHOSPHO_SITE        11
[PROSITE]      PKC_PHOSPHO_SITE        6
[PROSITE]      ASN_GLYCOSYLATION       1
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY    18.03 %

SEQ     MLQIGEDVDYLLIPREVRLAGGVWRVISKPATKEAEFRERLTQFLEEEGRTLEDVARIME
SEG     ............................................................
PRD     cccccccccccccccccccccceeeeeeeccccchhhhhhhhhhhhhhhcchhhhhhhhh

SEQ     KSTPHPPQPPKKPKEPRVRRRVQQMVTPPPRLVVGTYDSSNASDSEFSDFETSRDKSRQG
SEG     .....xxxxxxxxxxxxxxxxxx.....................................
PRD     hccccccccccccccccchhhhhhhhhccccceeeeeccccccccccccccccccccccc

SEQ     PRRGKKVRKMPVSYLGSKFLGSDLESEDDEELVEAFLRRQEKQPSAPPARRRVNLPVPMF
SEG     ....................xxxxxxxxxxx.............................
PRD     cccccccccceeecccccccccccccchhhhhhhhhhhhhhcccccchhhhhhccccccc
```

```
SEQ   EDNLGPQLSKADRWREYVSQVSWGKLKRRVKGWAPRAGPGVGEARLASTAVESAGVSSAP
SEG   ............................................................
PRD   cccccccchhhhhhhhheeeeccchhhhhhcccccccccccchhhhhhhhhhhccccccc

SEQ   EGTSPGDRLGNAGDVCVPQASPRRWRPKINWASFRRRRKEQTAPTGQGADIEADQGGEAA
SEG   ............................................................
PRD   ccccccccccccccceeeecccccccccccchhhhhhhhhhhhcccccchhhhhcccchhh

SEQ   DSQREEAIADQREGAAGNQRAGAPADQGAEAADNQREEAADNQRAGAPAEEGAEAADNQR
SEG   ....................xxxxxxxxxxxxx...........xxxxxxxxxxxx....
PRD   hhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhh

SEQ   EEAADNQRAEAPADQRSQGTDNHREEAADNQRAEAPADQGSEVTDNQREEAVHDQRERAP
SEG   ............................................................
PRD   hhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ   AVQGADNQRAQARAGQRAEAAHNQRAGAPGIQEAEVSAAQGTTGTAPGARARKQVKTVRF
SEG   .......xxxxxxxxxxxxxx................xxxxxxxxxxxxxx.........
PRD   hhccchhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhcccccccchhhhhhhhhhhh

SEQ   QTPGRFSWFCKRRRAFWHTPRLPTLPKRVPRAGEVRNLRVLRAEARAEAEQGEQEDQL
SEG   .........................................xxxxxxxxxxxxxx...
PRD   cccccceeehhhhhhhccccccccccccccccccchhhhhhhhhhhhhhhhhhhhccc
```

Prosite for DKFZphfbr2_22k3.2

PS00001	101->105	ASN_GLYCOSYLATION	PDOC00001
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	261->264	PKC_PHOSPHO_SITE	PDOC00005
PS00005	273->276	PKC_PHOSPHO_SITE	PDOC00005
PS00005	302->305	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	499->502	PKC_PHOSPHO_SITE	PDOC00005
PS00006	51->55	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	112->116	CK2_PHOSPHO_SITE	PDOC00006
PS00006	142->146	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	189->193	CK2_PHOSPHO_SITE	PDOC00006
PS00006	229->233	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	302->306	CK2_PHOSPHO_SITE	PDOC00006
PS00008	95->101	MYRISTYL	PDOC00008
PS00008	220->226	MYRISTYL	PDOC00008
PS00008	242->248	MYRISTYL	PDOC00008
PS00008	296->302	MYRISTYL	PDOC00008
PS00008	314->320	MYRISTYL	PDOC00008
PS00008	317->323	MYRISTYL	PDOC00008
PS00008	328->334	MYRISTYL	PDOC00008
PS00008	352->358	MYRISTYL	PDOC00008
PS00008	400->406	MYRISTYL	PDOC00008
PS00008	450->456	MYRISTYL	PDOC00008
PS00008	461->467	MYRISTYL	PDOC00008
PS00008	464->470	MYRISTYL	PDOC00008
PS00009	123->127	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_22k3.2)

DKFZphfbr2_22k8
----

group: brain derived

DKFZphfbr2_22k8 encodes a novel 172 amino acid protein without similarity to known proteins.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: /map="7"

Insert length: 2789 bp
Poly A stretch at pos. 2769, polyadenylation signal at pos. 2756

```
   1 GGGGGAGCCA TGAGGCGCCA GCCTGCGAAG GTGGCGGCGC TGCTGCTCGG
  51 GCTGCTCTTG GAGTGCACAG AAGCCAAAAA GCATTGCTGG TATTTCGAAG
 101 GACTCTATCC AACCTATTAT ATATGCCGCT CCTACGAGGA CTGCTGTGGC
 151 TCCAGGTGCT GTGTGCGGGC CCTCTCCATA CAGAGGCTGT GGTACTTCTG
 201 GTTCCTTCTG ATGATGGGCG TGCTTTTCTG CTGCGGAGCC GGCTTCTTCA
 251 TCCGGAGGCG CATGTACCCC CCGCCGCTGA TCGAGGAGCC AGCCTTCAAT
 301 GTGTCCTACA CCAGGCAGCC CCCAAATCCC GGCCCAGGAG CCCAGCAGCC
 351 GGGGCCGCCC TATTACACTG ACCCAGGAGG ACCGGGGATG AACCCTGTCG
 401 GGAATTCCAC GGCAATGGCT TTCCAGGTCC CACCCAACTC ACCCCAGGGG
 451 AGTGTGGCCT GCCCGCCCCC TCCAGCCTAC TGCAACACGC CTCCGCCCCC
 501 GTACGAACAG GTAGTGAAGG CCAAGTAGTG GGGTGCCCAC GTGCAAGAGG
 551 AGAGACAGGA GAGGGCCTTT CCCTGGCCTT TCTGTCTTCG TTGATGTTCA
 601 CTTCCAGGAA CGGTCTCGTG GGCTGCTAAG GGCAGTTCCT CTGATATCCT
 651 CACAGCAAGC ACAGCTCTCT TTCAGGCTTT CCATGGAGTA CAATATATGA
 701 ACTCACACTT TGTCTCCTCT GTTGCTTCTG TTTCTGACGC AGTCTGTGCT
 751 CTCACATGGT AGTGTGGTGA CAGTCCCCGA GGGCTGACGT CCTTACGGTG
 801 GCGTGACCAG ATCTACAGGA GAGAGACTGA GAGGAAGAAG GCAGTGCTGG
 851 AGGTGCAGGT GGCATGTAGA GGGGCCAGGC CGAGCATCCC AGGCAAGCAT
 901 CCTTCTGCCC GGGTATTAAT AGGAAGCCCC ATGCCGGGCG GCTCAGCCGA
 951 TGAAGCAGCA GCCGACTGAG CTGAGCCCAG CAGGTCATCT GCTCCAGCCT
1001 GTCCTCTCGT CAGCCTTCCT CTTCCAGAAG CTGTTGGAGA GACATTCAGG
1051 AGAGAGCAAG CCCCTTGTCA TGTTTCTGTC TCTGTTCATA TCCTAAAGAT
1101 AGACTTCTCC TGCACCGCCA GGGAAGGATA GCACGTGCAG CTCTCACCGC
1151 AGGATGGGGC CTAGAATCAG GCTTGCCTTG GAGGCCTGAC AGTGATCTGA
1201 CATCCACTAA GCAAATTTAT TTAAATTCAT GGGAAATCAC TTCCTGCCCC
1251 AAACTGAGAC ATTGCATTTT GTGAGCTCTT GGTCTGATTT GGAGAAAGGA
1301 CTGTTACCCA TTTTTTTGGT GTGTTTATGG AAGTGCATGT AGAGCGTCCT
1351 GCCCTTTGAA ATCAGACTGG GTGTGTGTCT TCCCTGGACA TCACTGCCTC
1401 TCCAGGGCAT TCTCAGGCCC GGGGGTCTCC TTCCCTCAGG CAGCTCCAGT
1451 GGTGGGTTCT GAAGGGTGCT TTCAAAACGG GGCACATCTG GCCGGGAAGT
1501 CACATGGACT CTTCCAGGGA GAGAGACCAG CTGAGGCGTC TCTCTCTGAG
1551 GTTGTGTTGG GTCTAAGCGG GTGTGTGCTG GGCTCCAAGG AGGAGGAGCT
1601 TGCTGGGAAA AGACAGGAGA AGTACTGACT CAACTGCACT GACCATGTTG
1651 TCATAATTAG AATAAAGAAG AAGTGGTCGG AAATGCACAT TCCTGGATAG
1701 GAATCACAGC TCACCCCAGG ATCTCACAGG TAGTCTCCTG AGTAGTTGAC
1751 GGCTAGCGGG GAGCTAGTTC CGCCGCATAG TTATAGTGTT GATGTGTGAA
1801 CGCTGACCTG TCCTGTGTGC TAAGAGCTAT GCAGCTTAGC TGAGGCGCCT
1851 AGATTACTAG ATGTGCTGTA TCACGGGGAA TGAGGTGGGG GTGCTTATTT
1901 TTTAATGAAC TAATCAGAGC CTCTTGAGAA ATTGTTACTC ATTGAACTGG
1951 AGCATCAAGA CATCTCATGG AAGTGGATAC GGAGTGATTT GGTGTCCATG
2001 CTTTTCACTC TGAGGACATT TAATCGGAGA ACCTCCTGGG GAATTTTGTG
2051 GGAGACACTT GGGAACAAAA CAGACACCCT GGGAATGCAG TTGCAAGCAC
2101 AGATGCTGCC ACCAGTGTCT CTGACCACCC TGGTGTGACT GCTGACTGCC
2151 AGCGTGGTAC CTCCCATGCT GCAGGCCTCC ATCTAAATGA GACAACAAAG
2201 CACAATGTTC ACTGTTTACA ACCAAGACAA CTGCGTGGGT CCAAACACTC
2251 CTCTTCCTCC AGGTCATTTG TTTTGCATTT TTAATGTCTT TATTTTTTGT
2301 AATGAAAAAG CACACTAAGC TGCCCCTGGA ATCGGGTGCA GCTGAATAGG
2351 CACCCAAAAG TCCGTGACTA AATTCCGTTT GTCTTTTTGA TAGCAAATTA
2401 TGTTAAGAGA CAGTGATGGC TAGGGCTCAA CAATTTTGTA TTCCCATGTT
2451 TGTGTGAGAC AGAGTTTGTT TTCCCTTGAA CTTGGTTAGA ATTGTGCTAC
2501 TGTGAACGCT GATCCTGCAT ATGGAAGTCC CACTTTGGTG ACATTTCCTG
2551 GCCATTCTTG TTTCCATTGT GTGGATGGTG GGTTGTGCCC ACTTCCTGGA
2601 GTGAGACAGC TCCTGGTGTG TAGAATTCCC GGAGCGTCCG TGGTTCAGAG
2651 TAAACTTGAA GCAGATCTGT GCATGCTTTT CCTCTGCAGC AATTGGCTCG
2701 TTTCTCTTTT TTGTTCTCTT TTGATAGGAT CCTGTTTCCT ATGTGTGCAA
```

```
2751 AATAAAAATA AATTTGGGCA AAAAAAAAAA AAAAAAAAA
```

BLAST Results

Entry HS671255 from database EMBL:
human STS SHGC-11828.
Length = 400
Minus Strand HSPs:
Score = 1822 (273.4 bits), Expect = 4.8e-76, P = 4.8e-76
Identities = 382/397 (96%), Positives = 382/397 (96%),

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 10 bp to 525 bp; peptide length: 172
Category: putative protein
Classification: unset

```
  1 MRRQPAKVAA LLLGLLLECT EAKKHCWYFE GLYPTYYICR SYEDCCGSRC
 51 CVRALSIQRL WYFWFLLMMG VLFCCGAGFF IRRRMYPPPL IEEPAFNVSY
101 TRQPPNPGPG AQQPGPPYYT DPGGPGMNPV GNSTAMAFQV PPNSPQGSVA
151 CPPPPAYCNT PPPPYEQVVK AK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_22k8, frame 1

PIR:S14970 extensin class I (clone w17-1) - tomato, N = 1, Score = 118,
P = 2.3e-07

>PIR:S14970 extensin class I (clone w17-1) - tomato
Length = 132

HSPs:

Score = 118 (17.7 bits), Expect = 2.3e-07, P = 2.3e-07
Identities = 30/82 (36%), Positives = 35/82 (42%)

```
Query:    87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
             PPP    P      Y + PP P P    P P YY  P  P  +P         +  P  SP
Sbjct:    32 PPPSPSPPP--PYYYKSPPPPSPSP--PPPYYYKSPPPPDPSPPPPYYYKSPPPPSPSPP 87

Query:   147 GSVACPPPPAYCNTPPPP--YEQV 168
                  PPPP Y + PPPP  YE +
Sbjct:    88 PPSPSPPPPTYSSPPPPPPFYENI 111
```

Score = 104 (15.6 bits), Expect = 6.9e-06, P = 6.9e-06
Identities = 28/78 (35%), Positives = 34/78 (43%)

```
Query:    87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
             PP     P +   Y + PP P P    P P YY  P  P  +P        ++ PP  P
Sbjct:     1 PPSPSPPPPY---YYKSPPPPSPSP--PPPYYYKSPPPPSPSP---PPPYYYKSPP-PPS 51

Query:   147 GSVACPPPPAYCNTPPPP 164
              S    PPPP Y  +PPPP
Sbjct:    52 PS---PPPPYYYKSPPPP 66
```

Score = 102 (15.3 bits), Expect = 1.1e-05, P = 1.1e-05
Identities = 30/78 (38%), Positives = 33/78 (42%)

```
Query:    87 PPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQ 146
             PPP    P      Y + PP P P    P P YY  P  P  +P  S +      PP  P
Sbjct:    48 PPPSPSPPP--PYYYKSPPPPDPSP--PPPYYYKSPPPPSPSPPPPSPS-----PP-PPT 97
```

```
Query:   147 GSVACPPPPAYCNTPPPP 164
             S    PPPP Y N P PP
Sbjct:    98 YSSPPPPPPFYENIPLPP 115

 Score = 95 (14.3 bits), Expect = 2.4e-04, P = 2.4e-04
 Identities = 24/61 (39%), Positives = 29/61 (47%)

Query:   104 PPNPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPNSPQGSVACPPPPAYCNTPPP 163
             PP+P P     P P YY  P  P  +P         ++ PP  P  S    PPPP Y  +PPP
Sbjct:     1 PPSPSP----PPPYYYKSPPPPSPSP---PPPYYYKSPP-PPSPS---PPPPYYYKSPPP 49

Query:   164 P 164
             P
Sbjct:    50 P 50

 Score = 68 (10.2 bits), Expect = 4.2e+00, P = 9.8e-01
 Identities = 24/69 (34%), Positives = 29/69 (42%)

Query:    87 PPPLIEEPAFNVSYTRQPP---NPGPGAQQPGPPYYTDPGGPGMNPVGNSTAMAFQVPPN 143
             PPP     P      Y   PP    +P P +  P PP Y+ P  P   P   +  +   PP
Sbjct:    63 PPPPDPSPPPPYYYKSPPPPSPSPPPPSPSPPPPTYSSPPPPP--PFYENIPL----PPV 116

Query:   144 SPQGSVACPPPP 155
                 S A PPPP
Sbjct:   117 IGV-SYASPPPP 127
```

Peptide information for frame 3

ORF from 0 bp to 368 bp; peptide length: 123
Category: questionable ORF
Classification: unset

```
    1 GSHEAPACEG GGAAARAALG VHRSQKALLV FRRTLSNLLY MPLLRGLLWL
   51 QVLCAGPLHT EAVVLLVPSD DGRAFLLRSR LLHPEAHVPP AADRGASLQC
  101 VLHQAAPKSR PRSPAAGAAL LH
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_22k8, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_22k8, frame 1

Report for DKFZphfbr2_22k8.1

```
[LENGTH]        172
[MW]            19194.47
[pI]            8.77
[KW]            SIGNAL_PEPTIDE 23
[KW]            TRANSMEMBRANE  1
[KW]            LOW_COMPLEXITY    27.33 %

SEQ     MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRL
SEG     ..........xxxxxxx...........................................
PRD     ccchhhhhhhhhhhhhhhhhhhhhhhcccccccccceeeeccccccccccchhhhhhhhh
MEM     ............................................................

SEQ     WYFWFLLMMGVLFCCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPPYYT
SEG     ...........................................xxxxxxxxxxxxxxxxx
PRD     hhhhhhhhhhhhhcccceeeeeccccccccccccccceeeecccccccccccccccccccc
MEM     ....MMMMMMMMMMMMMMMMM.......................................

SEQ     DPGGPGMNPVGNSTAMAFQVPPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK
SEG     xxxxxx.......................xxxxxxxxxxxxxxxx.......
PRD     cccccccccccccccceeecccccccccccccccccccccccccccccccccc
MEM     ....................................................
```

(No Prosite data available for DKFZphfbr2_22k8.1)

(No Pfam data available for DKFZphfbr2_22k8.1)

Pedant information for DKFZphfbr2_22k8, frame 3

Report for DKFZphfbr2_22k8.3

```
[LENGTH]        122
[MW]            12854.08
[pI]            10.27
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY     25.41 %

SEQ    GSHEAPACEGGGAAARAALGVHRSQKALLVFRRTLSNLLYMPLLRGLLWLQVLCAGPLHT
SEG    ....xxxxxxxxxxxxxxx.........................................
PRD    cccccccccchhhhhhhhcccchhhhhhhhhhhhhhhcccccchhhhhhhhcccccc

SEQ    EAVVLLVPSDDGRAFLLRSRLLHPEAHVPPAADRGASLQCVLHQAAPKSRPRSPAAGAAL
SEG    ............................................xxxxxxxxxxxxxxx.
PRD    cceeeeecccchhhhhhhhcccccccccccccchhhhhhhhhcccccccccchhhhhhc

SEQ    LH
SEG    ..
PRD    cc
```

(No Prosite data available for DKFZphfbr2_22k8.3)

(No Pfam data available for DKFZphfbr2_22k8.3)

DKFZphfbr2_23b10
----

group: nucleic acid managment

DKFZphfbr2_2b10 encodes a novel 580 amino acid protein with strong similarity to rat RNA helicase HEL117.

HEL117 is a DEAD/H box helicase, which co-localises with a splicing factor and thus seems to be involved in splicing.

The new protein can find application in modulation of splicing.

strong similarity to rat RNA helicase HEL117

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 2905 bp
Poly A stretch at pos. 2885, no polyadenylation signal found

```
   1 GGGGGCTCCG CTCCGCACCA CCAACCCCGG GCCGCAGTCC TGACGAGCGG
  51 GTCAGGGCTT GTCGGGCGGA AGCCTGGCCT GGAGCCTGGA AGGGGGAGAC
 101 GGCCCGAGCG GGAGCGGGAG CGGACGCGGC CTCAGTCCTG CGCGGAATAT
 151 TGAAGGATGT TTGTTCCAAG ATCTCTAAAA ATCAAGAGGA ATGCTAATGA
 201 TGATGGCAAA AGTTGTGTGG CTAAGATAAT TAAACCAGAC CCAGAAGACC
 251 TTCAGTTGGA CAAAAGCAGA GATGTTCCCG TTGATGCTGT AGCTACAGAA
 301 GCAGCCACAA TAGACAGGCA CATCAGCGAA TCATGCCCTT TCCCCAGCCC
 351 AGGTGGCCAG TTGGCAGAGG TTCATTCAGT AAGTCCCGAG CAGGGTGCGA
 401 AGGACAGCCA TCCTTCTGAA GAGCCCGTTA AGTCATTTTC CAAAACACAG
 451 CGCTGGGCAG AACCAGGGGA ACCCATCTGT GTTGTCTGTG GTCGTTATGG
 501 AGAGTATATC TGTGATAAGA CAGATGAAGA TGTGTGTAGT TTGGAGTGTA
 551 AAGCGAAACA TCTTCTACAA GTTAAGGAAA AGGAAGAGAA ATCAAAACTC
 601 AGCAATCCAC AGAAGGCTGA TTCTGAGCCA GAGTCTCCAC TGAATGCTTC
 651 CTATGTCTAC AAAGAGCACC CCTTTATTTT GAACCTTCAG GAAGACCAGA
 701 TTGAAAATCT TAAACAGCAG CTGGGAATTT TAGTTCAAGG GCAAGAAGTC
 751 ACCAGGCCCA TTATTGACTT TGAACATTGT AGTCTCCCTG AGGTCTTAAA
 801 TCACAACTTG AAGAAATCAG GCTATGAGGT GCCAACTCCC ATTCAAATGC
 851 AGATGATTCC TGTGGGACTT CTGGGAAGAG ACATTCTGGC CAGTGCAGAT
 901 ACTGGCTCAG GAAAAACAGC TGCTTTTCTT CTTCCTGTTA TCATGCGAGC
 951 TTTATTCGAG AGCAAAACTC CATCTGCGCT CATTCTTACA CCAACCAGAG
1001 AGTTAGCCAT TCAGATAGAG AGACAAGCTA AAGAATTGAT GAGTGGCCTG
1051 CCACGCATGA AAACTGTGCT TCTTGTAGGG GGCTTACCCT TACCCCCACA
1101 GCTTTATCGT CTGCAACAAC ATGTTAAGGT TATCATAGCA ACCCCTGGGC
1151 GACTTCTGGA TATAATAAAG CAGAGCTCTG TAGAACTCTG TGGTGTAAAG
1201 ATTGTGGTAG TAGATGAAGC TGATACCATG TTAAAGATGG GTTTTCAACA
1251 ACAAGTGCTT GACATTTTGG AAAACATTCC TAATGATTGT CAGACCATTT
1301 TGGTTTCAGC CACAATTCCA ACTAGCATAG AACAGCTAGC AAGCCAGCTT
1351 CTGCATAATC CTGTGAGAAT TATCACTGGA GAAAAGAACC TACCTTGTGC
1401 CAATGTACGT CAGATTATTT TGTGGGTAGA AGACCCAGCC AAAAAGAAAA
1451 AATTATTTGA AATTTTAAAT GATAAGAAAC TCTTTAAGCC TCCAGTGTTA
1501 GTATTTGTGG ACTGCAAACT AGGAGCAGAT CTTTTGAGTG AAGCCGTTCA
1551 GAAAATCACA GGGCTGAAAA GCATATCTAT ACATTCGGAG AAGTCGCAAA
1601 TAGAAAGGAA AAACATATTG AAGGGATTAC TTGAAGGAGA CTATGAAGTT
1651 GTAGTGAGCA CAGGAGTCTT GGGACGAGGC CTAGACTTGA TCAGTGTCAG
1701 GCTGGTTGTC AATTTTGATA TGCCTTCAAG TATGGATGAG TATGTCCATC
1751 AGGAAAATAC CTACAAGTCT ACTTGGAGGA ATCCCCAGCA TTTTCAACAG
1801 GATGTCAGAA TGACCTTGGG CTATGTTGGC AAAGCACAAT GGGAAGAAGA
1851 CAACCAATTG AAGGTCAAAC TAGGCCTTAA AAAAAATTGT TCTTCCTAAA
1901 TGAAACTTTA TGTAAGACCC AAGCTTCCTT TATGTAAAAA TAGGATACTC
1951 ACTAGGCTTT GGGGCTGACA ATGGTTTTTA AATCTTGCTA ATCTTCCCTG
2001 GAATGAAACC AGCATGACTC AAAGAGAAAA AGAGAGTCTA TAATATTTTC
2051 TAATCCCTGA GTTCTTTTCT TTATATATTA AAAAGGATTA TTAGGCTGGG
2101 TGTGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGGGGAGT
2151 GGATCACCTG AGTTCGAGAC CAGCCTAACC AACATGGAGA AACCCTGTCT
2201 CTACTAAAAA TACAAAATTA GCCAGGCGTG GTGGCGCATG CCTGTAATCC
2251 CAGCTACTCA GGAGGCTACA GCAGGAGAAT TGCTTGAACT CGGGAGGCAG
2301 AGCCAAGATC GCACCACTGC ACTCCAGCCT GGGCAACAAG AGTGAAACTC
2351 TGTCTCAAAA TAATATTAAT GATAATAATA ATAATAATAA TAGGGATTAC
2401 TTGCATAATT GTTCTTTTAA AATTATTGGC AGTATTGCTG AATGTATTTA
2451 GATTTTTTCA CCAAGTGACA ACAACTGAAT TCATAAAGAT TCATCAACAA
2501 GACCTGATAA AAAAAAATGT AAGCATATTA TAGTGGATAC TTCCAAGACT
2551 CTTGGTCTAA CATGTATTAG AAAGCAGAAG GAGCCCAGGC ACAGGGGCTC
2601 CCGCCGGTAA TCCCAAAGCT TTGGGAAGCC AAGGCAGGTG GATCGCTTGA
2651 GCTCAGGAGT TAGAGACCAG CCTGGGCAAC ATGGTGAAAT CCCGTCACCA
```

```
2701 CAAAAAAATG CAAAAATTAA CTGGGCGTGG TGGCATGCAC CTGTAGTCCC
2751 AGCTACTCTG GAGGCTGAGG TGAGGGGAAT CACCTGAGCC GGGGGAATCA
2801 CCTGAGCCCA GGGAAGTTGA GGCTGCTGTG AGCCATGGTC ATGACACTGC
2851 CCTCCAGCCT GGACAACAGA TTGAGACCCT GTCTCAAAAA AAAAAAAAAA
2901 AAAAA
```

BLAST Results

No BLAST result

Medline entries

Medline:
A putative mammalian RNA helicase with an arginine-serine-rich domain

Peptide information for frame 1

ORF from 157 bp to 1896 bp; peptide length: 580
Category: strong similarity to known protein
Prosite motifs: ATP_GTP_A (247-255)
LEUCINE_ZIPPER (298-320)

```
  1 MFVPRSLKIK RNANDDGKSC VAKIIKPDPE DLQLDKSRDV PVDAVATEAA
 51 TIDRHISESC PFPSPGGQLA EVHSVSPEQG AKDSHPSEEP VKSFSKTQRW
101 AEPGEPICVV CGRYGEYICD KTDEDVCSLE CKAKHLLQVK EKEEKSKLSN
151 PQKADSEPES PLNASYVYKE HPFILNLQED QIENLKQQLG ILVQGQEVTR
201 PIIDFEHCSL PEVLNHNLKK SGYEVPTPIQ MQMIPVGLLG RDILASADTG
251 SGKTAAFLLP VIMRALFESK TPSALILTPT RELAIQIERQ AKELMSGLPR
301 MKTVLLVGGL PLPPQLYRLQ QHVKVIIATP GRLLDIIKQS SVELCGVKIV
351 VVDEADTMLK MGFQQQVLDI LENIPNDCQT ILVSATIPTS IEQLASQLLH
401 NPVRIITGEK NLPCANVRQI ILWVEDPAKK KKLFEILNDK KLFKPPVLVF
451 VDCKLGADLL SEAVQKITGL KSISIHSEKS QIERKNILKG LLEGDYEVVV
501 STGVLGRGLD LISVRLVVNF DMPSSMDEYV HQENTYKSTW RNPQHFQQDV
551 RMTLGYVGKA QWEEDNQLKV KLGLKKNCSS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_23b10, frame 1

PIR:A57514 RNA helicase HEL117 - rat, N = 2, Score = 615, P = 1.6e-60

TREMBL:AB018344_1 gene: "KIAA0801"; product: "KIAA0801 protein"; Homo sapiens mRNA for KIAA0801 protein, complete cds., N = 1, Score = 615, P = 2.8e-59

TREMBL:CEF01F1_1 gene: "F01F1.7"; Caenorhabditis elegans cosmid F01F1., N = 2, Score = 365, P = 1.9e-58

TREMBL:AF083255_1 product: "RNA helicase-related protein"; Homo sapiens RNA helicase-related protein mRNA, complete cds., N = 2, Score = 556, P = 1.5e-57

PIR:S14048 RNA helicase dbp2 - fission yeast (Schizosaccharomyces pombe), N = 1, Score = 591, P = 1.6e-57

```
>PIR:A57514 RNA helicase HEL117 - rat
           Length = 1,032

  HSPs:

 Score = 615 (92.3 bits), Expect = 1.6e-60, Sum P(2) = 1.6e-60
 Identities = 140/394 (35%), Positives = 236/394 (59%)

Query:   144 EKSKLSNPQKADSEPESPLNASYVYKEHPFILNLQEDQIENLKQQL-GILVQGQEVTRPI 202
             ++ KL  P          P   ++ Y E P +  + ++++    + ++ GI V+G+   +PI
Sbjct:   313 KQRKLLEPVDHGKIEYEPFRKNF-YVEVPELAKMSQEEVNVFRLEMEGITVKGKGCPKPI 371

Query:   203 IDFEHCSLPEVLNHNLKKSGYEVPTPIQMQMIPVGLLGRDILASADTGSGKTAAFLLPV- 261
```

```
              +  C +    + ++LKK GYE PTPIQ Q IP  + GRD++  A TGSGKT AFLLP+
Sbjct:   372 KSWVQCGISMKILNSLKKHGYEKPTPIQTQAIPAIMSGRDLIGIAKTGSGKTIAFLLPMF 431

Query:   262 --IM--RALFESKTPSALILTPTRELAIQIERQAKELMSGLPRMKTVLLVGGLPLPPQLY 317
              IM  R+L E + P A+I+TPTRELA+QI ++ K+    L ++ V + GG  +  Q+
Sbjct:   432 RHIMDQRSLEEGEGPIAVIMTPTRELALQITKECKKFSKTLG-LRVVCVYGGTGISEQIA 490

Query:   318 RLQQHVKVIIATPGRLLDIIKQSS---VELCGVKIVVVDEADTMLKMGFQQQVLDILENI 374
              L++  ++I+ TPGR++D++  +S     L  V  VV+DEAD M  MGF+ QV+ I++N+
Sbjct:   491 ELKRGAEIIVCTPGRMIDMLAANSGRVTNLRRVTYVVLDEADRMFDMGFEPQVMRIVDNV 550

Query:   375 PNDCQTILVSATIPTSIEQLASQLLHNPVRIITGEKNLPCANVRQIILWVEDPAKKKKLF 434
              D QT++ SAT P ++E LA ++L  P+ +  G +++ C++V Q ++ +E+  K KL
Sbjct:   551 RPDRQTVMFSATFPRAMEALARRILSKPIEVQVGGRSVVCSDVEQQVIVIEEEKKFLKLL 610

Query:   435 EILNDKKLFKPPVLVFVDCKLGADLLSEAVQKITGLKSISIHSEKSQIERKNILKGLLEG 494
              E+L    +    V++FVD +  AD L + + + +    +S+H    Q +R +I+     G
Sbjct:   611 ELLGHYQE-SGSVIIFVDKQEHADGLLKDLMRAS-YPCMSLHGGIDQYDRDSIINDFKNG 668

Query:   495 DYEVVVSTGVLGRGLDLISVRLVVNFDMPSSMDEYVHQ 532
              +++V+T V  RGLD+  + LVVN+  P+  ++YVH+
Sbjct:   669 TCKLLVATSVAARGLDVKHLILVVNYSCPNHYEDYVHR 706

 Score = 37 (5.6 bits), Expect = 1.6e-60, Sum P(2) = 1.6e-60
 Identities = 13/36 (36%), Positives = 17/36 (47%)

Query:   132 KAKHLLQVKEKEE---KSKLSNPQKADSEPESPLNA 164
              KA++  + KEK E    SK    K D E E   +A
Sbjct:   113 KAENRSRSKEKAEGGDSSKEKKKDKDDKEDEKEKDA 148
```

Pedant information for DKFZphfbr2_23b10, frame 1

Report for DKFZphfbr2_23b10.1

```
[LENGTH]        580
[MW]            64572.24
[pI]            6.13
[HOMOL]         TREMBL:CEF01F1_1 gene: "F01F1.7"; Caenorhabditis elegans cosmid F01F1. 8e-61

[FUNCAT]        30.10 nuclear organization    [S. cerevisiae, YNL112w] 2e-53
[FUNCAT]        04.01.04 rrna processing      [S. cerevisiae, YNL112w] 2e-53
[FUNCAT]        04.05.03 mrna processing (splicing)  [S. cerevisiae, YPL119c] 5e-53
[FUNCAT]        30.03 organization of cytoplasm      [S. cerevisiae, YOR204w] 2e-49
[FUNCAT]        05.04 translation (initiation, elongation and termination)  [S. cerevisiae,
YOR204w] 2e-49
[FUNCAT]        j mrna translation and ribosome biogenesis   [H. influenzae, HI0231 RNA] 2e-46
[FUNCAT]        06.10 assembly of protein complexes   [S. cerevisiae, YLL008w] 3e-43
[FUNCAT]        04.99 other transcription activities  [S. cerevisiae, YDL160c] 4e-39
[FUNCAT]        1 genome replication, transcription, recombination and repair      [H.
influenzae, HI0892] 3e-35
[FUNCAT]        04.05.01.07 chromatin modification    [S. cerevisiae, YMR290c] 6e-34
[FUNCAT]        98 classification not yet clear-cut   [S. cerevisiae, YOR046c] 3e-32
[FUNCAT]        09.01 biogenesis of cell wall         [S. cerevisiae, YJL033w] 8e-30
[FUNCAT]        30.16 mitochondrial organization      [S. cerevisiae, YDR194c] 5e-23
[FUNCAT]        99 unclassified proteins     [S. cerevisiae, YGL064c] 1e-16
[FUNCAT]        r general function prediction        [M. jannaschii, MJ1401] 5e-11
[FUNCAT]        11.10 cell death        [S. cerevisiae, YMR190c] 1e-06
[FUNCAT]        03.19 recombination and dna repair   [S. cerevisiae, YMR190c] 1e-06
[BLOCKS]        BL00115B Eukaryotic RNA polymerase II heptapeptide repeat proteins
[BLOCKS]        BL00039D DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039C DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039B DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039A DEAD-box subfamily ATP-dependent helicases proteins
[PIRKW]         nucleus 6e-53
[PIRKW]         RNA binding 9e-52
[PIRKW]         DEAD box 2e-43
[PIRKW]         transmembrane protein 1e-21
[PIRKW]         DNA binding 5e-48
[PIRKW]         ATP 4e-57
[PIRKW]         purine nucleotide binding 2e-43
[PIRKW]         P-loop 4e-57
[PIRKW]         hydrolase 6e-42
[PIRKW]         protein biosynthesis 2e-43
[PIRKW]         ATP binding 2e-50
[SUPFAM]        WW repeat homology 1e-49
[SUPFAM]        translation initiation factor eIF-4A 2e-43
[SUPFAM]        DEAD/H box helicase homology 4e-57
[SUPFAM]        recQ helicase homology 8e-06
```

```
[SUPFAM]        unassigned DEAD/H box helicases 4e-57
[SUPFAM]        ATP-dependent RNA helicase DBP1 2e-53
[SUPFAM]        ATP-dependent RNA helicase DHH1 6e-40
[SUPFAM]        tobacco ATP-dependent RNA helicase DB10 1e-49
[SUPFAM]        Bloom's syndrome helicase 8e-06
[PROSITE]       ATP_GTP_A       1
[PROSITE]       LEUCINE_ZIPPER 1
[PROSITE]       MYRISTYL        6
[PROSITE]       CK2_PHOSPHO_SITE        8
[PROSITE]       TYR_PHOSPHO_SITE        1
[PROSITE]       PKC_PHOSPHO_SITE        7
[PROSITE]       ASN_GLYCOSYLATION       1
[PFAM]          Helicases conserved C-terminal domain
[PFAM]          DEAD and DEAH box helicases
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY      3.10 %

SEQ     MFVPRSLKIKRNANDDGKSCVAKIIKPDPEDLQLDKSRDVPVDAVATEAATIDRHISESC
SEG     ............................................................
PRD     cccccee eecccccccccceeeeeeeeecccccee ecccccccccchhhhhhhhhhhcccc

SEQ     PFPSPGGQLAEVHSVSPEQGAKDSHPSEEPVKSFSKTQRWAEPGEPICVVCGRYGEYICD
SEG     ............................................................
PRD     cccccccceeeeccccccccccccccccccccccccccccccccccceeeeccccceeec

SEQ     KTDEDVCSLECKAKHLLQVKEKEEKSKLSNPQKADSEPESPLNASYVYKEHPFILNLQED
SEG     ............................................................
PRD     ccccccchhhhhhhhhhhhhhccccccccccccccccccccccceeeccccccccccchhh

SEQ     QIENLKQQLGILVQGQEVTRPIIDFEHCSLPEVLNHNLKKSGYEVPTPIQMQMIPVGLLG
SEG     ............................................................
PRD     hhhhhhhheeeecccccccccccccccchhhhhhhhhhhhcccccccccccccceeeecc

SEQ     RDILASADTGSGKTAAFLLPVIMRALFESKTPSALILTPTRELAIQIERQAKELMSGLPR
SEG     ............................................................
PRD     cceeeeecccccccceeeehhhhhhhhcccccceeeeecchhhhhhhhhhhhhhhhccccc

SEQ     MKTVLLVGGLPLPPQLYRLQQHVKVIIATPGRLLDIIKQSSVELCGVKIVVVDEADTMLK
SEG     ...xxxxxxxxxxxxxxxxx........................................
PRD     eeeeeeeccccccchhhhhhhhheeeeeecccccchhhhhhheeeeeeeeeeeeeehhhhhhh

SEQ     MGFQQQVLDILENIPNDCQTILVSATIPTSIEQLASQLLHNPVRIITGEKNLPCANVRQI
SEG     ............................................................
PRD     cccchhhhhhhhhcccccceeeeeecccchhhhhhhhhhhhhceeeeeeeecccccccccce

SEQ     ILWVEDPAKKKKLFEILNDKKLFKPPVLVFVDCKLGADLLSEAVQKITGLKSISIHSEKS
SEG     ............................................................
PRD     eeecccccchhhhhhhhhhhhhhcccccceeeeeeeecccchhhhhhhhhhhhhccceeeccccch

SEQ     QIERKNILKGLLEGDYEVVVSTGVLGRGLDLISVRLVVNFDMPSSMDEYVHQENTYKSTW
SEG     ............................................................
PRD     hhhhhhhhhhhcccccceeeeehhhhhhccccceeeeeeeeeeeecccccccccceeeecccccccc

SEQ     RNPQHFQQDVRMTLGYVGKAQWEEDNQLKVKLGLKKNCSS
SEG     ........................................
PRD     ccccccchhhhhhcccccchhhhhhhhhhhhhhhhcccccc
```

Prosite for DKFZphfbr2_23b10.1

PS00001	163->167	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	97->100	PKC_PHOSPHO_SITE	PDOC00005
PS00005	251->254	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	513->516	PKC_PHOSPHO_SITE	PDOC00005
PS00005	535->538	PKC_PHOSPHO_SITE	PDOC00005
PS00005	539->542	PKC_PHOSPHO_SITE	PDOC00005
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00006	221->225	CK2_PHOSPHO_SITE	PDOC00006
PS00006	340->344	CK2_PHOSPHO_SITE	PDOC00006
PS00006	389->393	CK2_PHOSPHO_SITE	PDOC00006
PS00006	480->484	CK2_PHOSPHO_SITE	PDOC00006
PS00006	524->528	CK2_PHOSPHO_SITE	PDOC00006
PS00007	489->497	TYR_PHOSPHO_SITE	PDOC00007
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	80->86	MYRISTYL	PDOC00008

PS00008	195->201	MYRISTYL	PDOC00008
PS00008	250->256	MYRISTYL	PDOC00008
PS00008	490->496	MYRISTYL	PDOC00008
PS00008	573->579	MYRISTYL	PDOC00008
PS00017	247->255	ATP_GTP_A	PDOC00017
PS00029	298->320	LEUCINE_ZIPPER	PDOC00029

Pfam for DKFZphfbr2_23b10.1

```
HMM_NAME            DEAD and DEAH box helicases

HMM                     *gLpPWILRnIyeMGFEkPTPIQQqAIPiILeGRDVMACAQTGSGKTAAF
                         +LP+ +  N+++ G+E PTPIQ+Q IP+ L GRD++A A TGSGKTAAF
Query               209  SLPEVLNHNLKKSGYEVPTPIQMQMIPVGLLGRDILASADTGSGKTAAF   257

HMM                     lIPMLQHIDwdPWpqpPQdPrALILAPTRELAMQIQEEcRkFgkHMngIR
                        L+P++ + + +   ++P    ALIL+PTRELA+QI+++++++ + ++ ++
Query               258 LLPVIMRALFES--KTPS---ALILTPTRELAIQIERQAKELMSGLPRMK   302

HMM                     ImcIYGGtnMRdQMRmLeRGpPHIVIATPGRLIDHIERgtldLDrIeMLV
                         ++++GG+++ +Q+ +L++ +  ++IATPGRL+D+I++ ++ L  ++++V
Query               303 TVLLVGGLPLPPQLYRLQQHV-KVIIATPGRLLDIIKQSSVELCGVKIVV   351

HMM                     MDEADRMLDMGFIDQIRrIMrqIPMpwNRQTMMFSATMPdeIqELARrFM
                         DEAD ML MGF++Q+ +I+  IP   + QT++ SAT+P +I++LA  ++
Query               352 VDEADTMLKMGFQQQVLDILENIP--NDCQTILVSATIPTSIEQLASQLL   399

HMM                     RNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdcLcrLIe*
                        +NP+RI+ ++++L    N++Q++ +VE +  K  +L+++++
Query               400 HNPVRIITGEKNLPCA-NVRQIILWVE-DPAKKKKLFEILN    438


HMM_NAME            Helicases conserved C-terminal domain

HMM                     *EileeWLknl.GIrvmYIHGdMpQeERdeIMddFNnGEynVLIcTDVgg
                         ++L+E  ++  G++ ++IH+ ++Q ER +I++   +G+Y V ++T V+G
Query               458  DLLSEAVQKITGLKSISIHSEKSQIERKNILKGLLEGDYEVVVSTGVLG   506

HMM                     RGIDIPdVNHVINYDMPWNPEqYIQRIGRTgRIG*
                        RG+D+++V++V+N+DMP +++ Y++ +  T  +
Query               507 RGLDLISVRLVVNFDMPSSMDEYVH-QENTYKST    539
```

DKFZphfbr2_23b21
----

group: signal transduction

DKFZphfbr2_23b21.1 encodes a novel 193 amino acid protein which is nearly identical to bovine neurocalcin.

Neurocalcin is a Ca(2+)-binding protein with three putative Ca(2+)-binding domains (EF-hands). In cattle, 6 isoforms are differentially expressed in the central nervous system, retina and adrenal gland. Homology with recoverin indicates involvement in Ca2+ dependent activation of guanylate cyclase.

The new protein can find application in modulating/blocking the guanylate cyclase-pathway.

nearly identical to bovine neurocalcin

complete cds complete cDNA
EST hits

Sequenced by AGOWA

Locus: /map="574.6 cR from top of Chr8 linkage group"

Insert length: 3300 bp
Poly A stretch at pos. 3279, polyadenylation signal at pos. 3249

```
   1 GGGGAGAATC TGGTGGATGC TGGACCTTGC TGCTGCTGCT ACTGCTGTTT
  51 CCAGGGGCTG CAGAGCATGG ACTGTTAAAT CTTGCACTTC TTCTGAGTGA
 101 GCTGAATTCT TGCCGCCAGG ATGGGGAAAC AGAACAGCAA GCTGCGCCCG
 151 GAGGTCATGC AGGACTTGCT GGAAAGCACA GACTTTACAG AGCATGAGAT
 201 CCAGGAATGG TATAAAGGCT TCTTGAGAGA CTGCCCCAGT GGACATTTGT
 251 CAATGGAAGA GTTTAAGAAA ATATATGGGA ACTTTTTCCC TTATGGGGAT
 301 GCTTCCAAAT TTGCAGAGCA TGTCTTCCGC ACCTTCGATG CAAATGGAGA
 351 TGGGACAATA GACTTTAGAG AATTCATCAT CGCCTTGAGT GTAACTTCGA
 401 GGGGGAAGCT GGAGCAGAAG CTGAAATGGG CCTTCAGCAT GTACGACCTG
 451 GACGGAAATG GCTATATCAG CAAGGCAGAG ATGCTAGTGA TCGTGCAGGC
 501 AATCTATAAG ATGGTTTCCT CTGTAATGAA AATGCCTGAA GATGAGTCAA
 551 CCCCAGAGAA AAGAACAGAA AAGATCTTCC GCCAGATGGA CACCAATAGA
 601 GACGGAAAAC TCTCCCTGGA AGAGTTCATC CGAGGAGCCA AAAGCGACCC
 651 GTCCATTGTG CGCCTCCTGC AGTGCGACCC GAGCAGTGCC GGCCAGTTCT
 701 GAGCCCTGCG CCCACCAATC GAATTGTAGA GCTGCTTGTG TTCCCTTTTG
 751 ATTCTTCTTT TTAACAATTT TTTTTTTTTT TTGCCAAACA ATATCAATGG
 801 TGATGCCGTC CCCTGTGCGG TCTGATGCGC CTTCCTCCGT GACGCCTTCA
 851 GCCTCTTTTG TCGTGGATGC TTCGTGGGAA TGCCCAGAGC CCCAGTGTGC
 901 TTGTGGAGAG CATGGACAGA CTTCGTGGTG TTCATTGTTT GATGATTTTT
 951 AATCGTTACT ATTATTTCTT TTTATTCTAA TGTCTCTGTT CTAAAACGTA
1001 AGACTCGGGG GTTGGGGCAA AAGAAGGGAA ACCCATCCAG TCCTGTGATT
1051 CTATTGCAAG CTTCAAGGGG CTTTTGTTTG AAAGACAAAA CTCCCCACCT
1101 GGGTCTGTTG TCACACGTGC CGTAGGGGTG ATGGATGGCA CCGGATGCTG
1151 GATTCCCCAA GAACAAGTTA CCCTCTGGGG TGAGGCTATT CCAGCGAGCT
1201 GGGACATTTC CCCATGGGGG CCCACTCCCC TCTCTTCCCC AGCAGGCTGT
1251 AGTTTCTAAG CTGTGAACAT TTCAAGATAA ATTAACAGAG GAGAGGAAAA
1301 AGATGGCTCA GCTATTTTTT CACAGGTTTA CACTAGTTGA GCTAATATGC
1351 GTGTCTTTGG AAATTAAACA CAAATGGTAA CATATTCCAA AACCAGACCC
1401 ATCTTGTTGC CTATTGTGAT AAAATAAAAA GACGGCTGTA TATAACATAT
1451 TGGGTAATGC AGACCAAATT AAGTGTTTTG CCTTGTTTAA ATGAAATGCA
1501 TGTTTAGTGA GCACTAATAC AATCTTATTC CAGAAGACTG TTTTTAGTAG
1551 CTTATTGTGA AGTAAGACAA CTATAATGAA TGTCTGTCTT GTTTGGAAGT
1601 CATATCTGTC TTTGCACAAA TGTACCAATC GACAAGTATA TTTTATATAT
1651 TCCATAAAAA TACAAAGTAA CCCTGACTAG GGCCCAACTT TAATTTTGAA
1701 TGCATTTCCA GAGTGGCCAT GCCTAGAGGG CAGATGCAGA GCAGGTGGTA
1751 GTGGGACAGG ACAATTGGAG CACAGGAATG TTAACATGTA TGACAGGGGA
1801 CCAGTAGGGT GGTTTCCCTC TCAGGCCCAG CAGCCCATTG ACAGCATTAG
1851 ACTGGCGGCA TGGTGCTTTT CTGAGCAGAT CAATACTCTG CAGACTCGAA
1901 AAAACATCAC ATACATTCTT GGAACTTCCC AGTGGTTTAA TCTATGTGCA
1951 TGGTTAGGGA GCCAGGCCTG GAATATTCAG TTTCCCTGCC CCTGTTAAAG
2001 AATCAGAGGT TGGGCAGTCA TCAAATTCAT CATAAAGACA TGGGCAAGTG
2051 TGTCTGTGGT TTCCAAGGCC CCCCTATGGA GAATCCAAAA GTATTTTCCA
2101 TTGCCGTGCT CTTTGAATGC AGACTTCTAT TTCCAGAAGT GACAGCACAA
2151 GTCTGAGTTG CTGTTTGGTC TGGTGACCTC AGACACACTA ATTTGAATTG
2201 AAAGCTAAGA GTAAAAATTT GCTGGTTACA GGCGAGTCAT ACTCTTGCAA
2251 GTAGTTAGCA AAGGGAGGCC CAAATTCTCA AGGTTGTTGA TGGGGAACTT
2301 GCCACTAAGA GAAGGCAGAG AGGTCCCTAG TGGGTATATT TGCTGCCAAG
2351 CCACTTGCCA AAGAAGAGGA ACCACAGAAA GAGAGACATC ATGACCAGGA
2401 GAAAAATGTG ACTAGACATG CTAACCTCCA GGTTTTTATA TATGACTTGA
2451 GTCTGCTGTA ATTGGCAGCA GAAATCCAAA TTTGTATGGT AGACCAAAAA
2501 GAACCAAATC CATAGGGTGA AATTTTGAGA CCTAGACTCT GTAAAAATAA
```

```
2551 TCCTAGTCTT CCTCCAGGGG TCAGTTCCTC ACAGTGGTTC TGTACCAAAA
2601 CTTGCCAAAT TCCTCCATGG CCAAGTGTTA AAATCTGTGT TTGGAAAATA
2651 GCGAATTAAC CTAAGACACA GAAGGCAGAC TGGGTGAGGA GACCTAGCAT
2701 GCCCTATTGG CAGTGCTCAG GAGCTGCATC CCACTTTTCC CTGCTCTGAA
2751 TCGAAGTCCT AGTTCCTTCC TTTGATTCTC CTTTGGTAGG TGGAATCAGT
2801 TAATGTTTTG AGAAACCTGC CTGGGCTCTG CCCTTAGTCA TGACATCTCG
2851 CTGAGCCAGA CCCACTCTGT TCCTTGGAAC CTAGAGCTGG AGTGAGGAGT
2901 AGAGGTCTCC GGCTATTCCA GAAAGAAAAG TGAGCCACAT GCAGGCTGAT
2951 GAATGCCGAC ACTTCCAGAA TGTATAGAAA TAGTCCCTGT CCTGGCCTGC
3001 CACTGACCCT GTCTGTATTT TCTCGGAGGT TGTTTTTCTC CTTCTCCTTC
3051 CCAGGAAGGT CTTTGTATGT CGAATCCAGT GCACTCAAGT TTGGCCAAGG
3101 GACTCCACAG CACCCAGAGG ACTGCATGCC TCAAGGTTTA TGTCACTCCT
3151 CTGCTGGGCT GTTCATTGTC ATTGCTGTGT TCAGGGACCT TTGGAAATAA
3201 AACCTGTTCT GTCCCAAATA AAACCAGCCT GTGATGTTCA AGGGACTGGA
3251 ATAAAGTGGC TTACGACCTG AAGGATTCTA AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

Entry HS431350 from database EMBL:
human STS WI-15914.
Score = 1308, P = 3.1e-53, identities = 276/285

Entry HSG19929 from database EMBL:
human STS A002C26.
Score = 926, P = 1.5e-35, identities = 186/187

Entry AF052142 from database EMBL:
Homo sapiens clone 24665 mRNA sequence.
Score = 7378, P = 0.0e+00, identities = 1482/1487
3' UTR

Medline entries

93247712:
Neurocalcin family: a novel calcium-binding protein abundant in bovine central nervous system.

94045365:
Distinct regional localization of neurocalcin, a Ca(2+)-binding protein, in the bovine adrenal gland.

96407688:
Crystallization and preliminary X-ray crystallographic studies of recombinant bovine neurocalcin delta.

96066284:
Distribution pattern of three neural calcium-binding proteins (NCS-1, VILIP and recoverin) in chicken, bovine and rat retina.

Peptide information for frame 1

ORF from 121 bp to 699 bp; peptide length: 193
Category: strong similarity to known protein
Prosite motifs: EF_HAND (73-86)
EF_HAND (109-122)
EF_HAND (157-170)

```
  1 MGKQNSKLRP EVMQDLLEST DFTEHEIQEW YKGFLRDCPS GHLSMEEFKK
 51 IYGNFFPYGD ASKFAEHVFR TFDANGDGTI DFREFIIALS VTSRGKLEQK
101 LKWAFSMYDL DGNGYISKAE MLVIVQAIYK MVSSVMKMPE DESTPEKRTE
151 KIFRQMDTNR DGKLSLEEFI RGAKSDPSIV RLLQCDPSSA GQF
```

BLASTP hits

Entry JH0616 from database PIR:
neurocalcin (clone pCalN) - bovine

Score = 1001, P = 5.2e-101, identities = 192/193, positives = 192/193

Entry GGU91630_1 from database TREMBL:
product: "neurocalcin"; Gallus gallus neurocalcin mRNA, complete cds.
Score = 998, P = 1.1e-100, identities = 191/193, positives = 192/193

Entry NECD_BOVIN from database SWISSPROT:
NEUROCALCIN DELTA.
Score = 996, P = 1.8e-100, identities = 191/192, positives = 191/192

Entry S47565 from database PIR:
BDR-1 protein - human
Score = 934, P = 6.6e-94, identities = 174/193, positives = 187/193

Entry I50676 from database PIR:
gene Rem-1 protein - chicken >TREMBL:GGREM1_1 gene: "Rem-1"; G.gallus
rem-1 mRNA
Score = 933, P = 8.4e-94, identities = 174/193, positives = 186/193

Alert BLASTP hits for DKFZphfbr2_23b21, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_23b21, frame 1

Report for DKFZphfbr2_23b21.1

```
[LENGTH]        193
[MW]            22215.30
[pI]            5.35
[HOMOL]         PIR:JH0616 neurocalcin (clone pCalN) - bovine 1e-109
[FUNCAT]        98 classification not yet clear-cut  [S. cerevisiae, YDR373w] 3e-54
[FUNCAT]        30.03 organization of cytoplasm      [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]        03.07 pheromone response, mating-type determination, sex-specific proteins
          [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]        03.01 cell growth      [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]        13.04 homeostasis of other ions      [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]        04.05.01.04 transcriptional control  [S. cerevisiae, YKL190w] 2e-18
[FUNCAT]        30.04 organization of cytoskeleton   [S. cerevisiae, YBR109c] 0.001
[FUNCAT]        08.19 cellular import [S. cerevisiae, YBR109c] 0.001
[FUNCAT]        03.22 cell cycle control and mitosis [S. cerevisiae, YBR109c] 0.001
[FUNCAT]        03.04 budding, cell polarity and filament formation [S. cerevisiae, YBR109c]
0.001
[FUNCAT]        10.02.99 other morphogenetic activities      [S. cerevisiae, YBR109c] 0.001
[FUNCAT]        30.05 organization of centrosome     [S. cerevisiae, YBR109c] 0.001
[BLOCKS]        BL00018
[SCOP]          d1rec__ 1.34.1.5.18 Recoverin [bovine (Bos taurus) 8e-55
[SCOP]          d1jsa__ 1.34.1.5.17 Recoverin [human (Homo sapiens) 5e-58
[SCOP]          d1tcob_ 1.34.1.5.16 Calcineurin regulatory subunit (B-chain 1e-06
[SCOP]          d2mysc_ 1.34.1.5.15 Myosin Regulatory Chain [chicken (Gallu 2e-29
[SCOP]          d1scmc_ 1.34.1.5.14 Myosin Regulatory Chain [bay scallo 5e-33
[SCOP]          d2mysb_ 1.34.1.5.13 Myosin Essential Chain [chicken (Gallu 4e-26
[SCOP]          d1scmb_ 1.34.1.5.12 Myosin Essential Chain [bay scallo 6e-27
[SCOP]          d1clm__ 1.34.1.5.11 Calmodulin [Paramecium tetraurelia 1e-15
[SCOP]          d4cln__ 1.34.1.5.10 Calmodulin [Drosophila melanogaster 2e-16
[SCOP]          d1cfc__ 1.34.1.5.9 Calmodulin [African frog (Xenopus laevis) 2e-16
[SCOP]          d1ahr__ 1.34.1.5.8 Calmodulin [chicken gallus gallus 4e-16
[SCOP]          d3cln__ 1.34.1.5.7 Calmodulin [rat (Rattus rattus) 2e-16
[SCOP]          d1trcb_ 1.34.1.5.6 Calmodulin [bovine (Bos taurus) 8e-08
[SCOP]          d1cll__ 1.34.1.5.5 Calmodulin [human (Homo sapiens) 2e-16
[SCOP]          d1rtpl_ 1.34.1.4.5 Parvalbumin [rat (Rattus rattus) 8e-06
[SCOP]          d5tnc__ 1.34.1.5.2 Troponin C [turkey (Meleagris gallopavo) 3e-13
[SCOP]          d1pvaa_ 1.34.1.4.3 Parvalbumin [pike (Esox lucius) 6e-06
[SCOP]          d1tnp__ 1.34.1.5.1 Troponin C [chicken (Gallus gallus) 9e-11
[EC]            2.7.1.107 Diacylglycerol kinase 2e-08
[PIRKW]         blocked amino end 1e-100
[PIRKW]         phosphotransferase 2e-08
[PIRKW]         duplication 4e-17
[PIRKW]         tandem repeat 7e-06
[PIRKW]         heterodimer 4e-17
[PIRKW]         heart 6e-09
[PIRKW]         zinc 2e-08
[PIRKW]         serine/threonine-specific protein kinase 1e-06
[PIRKW]         muscle contraction 1e-08
[PIRKW]         acetylated amino end 4e-09
[PIRKW]         ATP 2e-08
[PIRKW]         skeletal muscle 6e-09
```

```
[PIRKW]         signal transduction 1e-91
[PIRKW]         protein kinase 2e-08
[PIRKW]         calcium binding 1e-100
[PIRKW]         alternative splicing 2e-13
[PIRKW]         methylated amino acid 1e-09
[PIRKW]         thin filaments 1e-08
[PIRKW]         lipoprotein 1e-101
[PIRKW]         cardiac muscle 6e-09
[PIRKW]         muscle 6e-09
[PIRKW]         myristylation 1e-100
[PIRKW]         EF hand 1e-101
[PIRKW]         retina 2e-51
[SUPFAM]        calcium-dependent protein kinase 2e-08
[SUPFAM]        unassigned calmodulin-related proteins 8e-41
[SUPFAM]        spec-related protein LpS1 7e-06
[SUPFAM]        calmodulin repeat homology 1e-101
[SUPFAM]        human diacylglycerol kinase 2e-08
[SUPFAM]        protein kinase C zinc-binding repeat homology 2e-08
[SUPFAM]        protein kinase homology 2e-08
[SUPFAM]        calmodulin 1e-101
[PROSITE]       EF_HAND 3
[PROSITE]       CK2_PHOSPHO_SITE       7
[PROSITE]       PKC_PHOSPHO_SITE       3
[PFAM]          EF hand
[KW]            All_Alpha
[KW]            3D

SEQ     MGKQNSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCPSGHLSMEEFKKIYGNFFPYGD
1rec-   .......HHHHHHHHHTTTTCCCHHHHHHHHHHHHHHHTTTTEEEHHHHHHHHHHHHTTTTC

SEQ     ASKFAEHVFRTFDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLDGNGYISKAE
1rec-   HHHHHHHHHHHH-----CEEEHHHHHHHHHHHHHHCCCGGGHHHHHHHHHHTTTTCCCCEEHHH

SEQ     MLVIVQAIYKMVSSVMKMPEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKSDPSIV
1rec-   HHHHHHHHHHHCCTTGGGCTTTTTCHHHHHHHHHHHHCCTTTTEECHHHHHHHHHHCHHHH

SEQ     RLLQCDPSSAGQF
1rec-   HHHCCCH......
```

Prosite for DKFZphfbr2_23b21.1

```
PS00005     92->95    PKC_PHOSPHO_SITE      PDOC00005
PS00005    149->152   PKC_PHOSPHO_SITE      PDOC00005
PS00005    158->161   PKC_PHOSPHO_SITE      PDOC00005
PS00006     23->27    CK2_PHOSPHO_SITE      PDOC00006
PS00006     44->48    CK2_PHOSPHO_SITE      PDOC00006
PS00006    106->110   CK2_PHOSPHO_SITE      PDOC00006
PS00006    117->121   CK2_PHOSPHO_SITE      PDOC00006
PS00006    143->147   CK2_PHOSPHO_SITE      PDOC00006
PS00006    158->162   CK2_PHOSPHO_SITE      PDOC00006
PS00006    165->169   CK2_PHOSPHO_SITE      PDOC00006
PS00018     73->86    EF_HAND               PDOC00018
PS00018    109->122   EF_HAND               PDOC00018
PS00018    157->170   EF_HAND               PDOC00018
```

Pfam for DKFZphfbr2_23b21.1

```
HMM_NAME        EF hand

HMM                 *MFrmMDkDGDGyIDFEEFmeMMkem*
                     +FR +D +GDG+IDF EF+ +++
Query           68  VFRTFDANGDGTIDFREFIIALSVT     92

30.75     100   128     1    29 dkfzphfbr2_23b21.1 nearly identical to bovine neurocalcin
  Alignment to HMM consensus:
Query               *EIqEMFrmMDkDGDGyIDFEEFmeMMkem*
                      ++++F+M+D DG+GYI++ E++++++++
  dkfzphfbr2    100  KLKWAFSMYDLDGNGYISKAEMLVIVQAI     128

Query           176     1    29 dkfzphfbr2_23b21.1 nearly identical to bovine neurocalcin
  Alignment to HMM consensus:
HMM                 *EIqEMFrmMDkDGDGyIDFEEFmeMMkem*
                      +++FR MD+++DG+++ EEF++  K+
Query           148  RTEKIFRQMDTNRDGKLSLEEFIRGAKSD     176
```

DKFZphfbr2_23f2

group: brain derived

DKFZphfbr2_23f2 encodes a novel 182 amino acid protein with weak similarity to S. pombe Vps29p.

No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to Vps29p

complete cDNA, complete cds, EST hits
S.cerevisiae and S.pombe Vps29p are involved in vacuolar protein sorting
part of the cDNA is encoded by HSAC2350, splice pattern 4 exons

Sequenced by AGOWA

Locus: /map="12q24"

Insert length: 1016 bp
Poly A stretch at pos. 996, polyadenylation signal at pos. 974

```
   1 GAATGGGGAG GAGCCAGAGG AAGAGGGCGG CGACGGTGGT GGTGACTGAG
  51 CGGAGCCCGG TGACAGGATG TTGGTGTTGG TATTAGGAGA TCTGCACATC
 101 CCACACCGGT GCAACAGTTT GCCAGCTAAA TTCAAAAAAC TCCTGGTGCC
 151 AGGAAAAAATT CAGCACATTC TCTGCACAGG AAACCTTTGC ACCAAAGAGA
 201 GTTATGACTA CCTCAAGACT CTGGCTGGTG ATGTTCATAT TGTGAGAGGA
 251 GACTTCGATG AGAATCTGAA TTATCCAGAA CAGAAAGTTG TGACTGTTGG
 301 ACAGTTCAAA ATTGGTCTGA TCCATGGACA TCAAGTTATT CCATGGGGAG
 351 ATATGGCCAG CTTAGCCCTG TTGCAGAGGC AATTTGATGT GGACATTCTT
 401 ATCTCGGGAC ACACACACAA ATCTGAAGCA TTTGAGCATG AAAATAAATT
 451 CTACATTAAT CCAGGTTCTG CCACTGGGGC ATATAATGCC TTGGAAACAA
 501 ACATTATTCC ATCATTTGTG TTGATGGATA TCCAGGCTTC TACAGTGGTC
 551 ACCTATGTGT ATCAGCTAAT TGGAGATGAT GTGAAAGTAG AACGAATCGA
 601 ATACAAAAAA CCTTAAAGCC AGGCCTGTCT TGATGATTTT TGGTTTTTTT
 651 TCATTGTCCT GTTGAAATCA AGTAATTAAA CATTTAAGAG CCACAAAATT
 701 GTATCACTTT TATAATATTT TGCAGTAAAA TATAATACCA TCTTCTCTGT
 751 TAATACATAA TTGCTCCAAG CTTCCTGTAA ACTATAAGAA TATATTTAGT
 801 TTACAGTATA TGGATTCTAT GAAAAAATGT CCACAACACA GTAATTGGTC
 851 ACTTGTTAAG AAAAATTTAT CCTTGTAAGT ATCTTCAAAG TTGATATTTG
 901 GAACTTTATT CCAAAAGTAG TGCATGTGGA GAAAGAATCT AGACTTTCTT
 951 GTATACATTT TTCTCTTCTC CAGTAATAAA CAATTACCTT TCATTGAAAA
1001 AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HSAC2350 from database EMBLNEW:
Homo sapiens 12q24 PAC P424M6 Length = 167,217

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 68 bp to 613 bp; peptide length: 182
Category: similarity to known protein
Prosite motifs: RGD (60-63)

```
  1 MLVLVLGDLH IPHRCNSLPA KFKKLLVPGK IQHILCTGNL CTKESYDYLK
 51 TLAGDVHIVR GDFDENLNYP EQKVVTVGQF KIGLIHGHQV IPWGDMASLA
101 LLQRQFDVDI LISGHTHKSE AFEHENKFYI NPGSATGAYN ALETNIIPSF
```

151 VLMDIQASTV VTYVYQLIGD DVKVERIEYK KP

BLASTP hits

Entry CEZK1128_6 from database TREMBL:
"ZK1128.1"; Caenorhabditis elegans cosmid ZK1128
Length = 523
Score = 400 (140.8 bits), Expect = 2.3e-37, P = 2.3e-37
Identities = 81/150 (54%), Positives = 106/150 (70%)

Entry S46793 from database PIR:
hypothetical protein YHR012c - yeast (Saccharomyces cerevisiae)
Length = 282
Score = 180 (63.4 bits), Expect = 3.7e-37, Sum P(3) = 3.7e-37
Identities = 35/71 (49%), Positives = 44/71 (61%)

Entry AB011824_1 from database TREMBL:
"Vps29"; Schizosaccharomyces pombe mRNA for Vps29,
partial cds. Schizosaccharomyces pombe (fission yeast)
Length = 176
Score = 189 (66.5 bits), Expect = 2.7e-27, Sum P(2) = 2.7e-27
Identities = 33/72 (45%), Positives = 50/72 (69%)

Alert BLASTP hits for DKFZphfbr2_23f2, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_23f2, frame 2

Report for DKFZphfbr2_23f2.2

[LENGTH]	182
[MW]	20445.84
[pI]	6.29
[HOMOL]	TREMBL:CEZK1128_6 gene: "ZK1128.8"; Caenorhabditis elegans cosmid ZK1128 2e-51
[FUNCAT]	06.04 protein targeting, sorting and translocation [S. cerevisiae, YHR012w] 1e-27
[FUNCAT]	08.13 vacuolar transport [S. cerevisiae, YHR012w] 1e-27
[FUNCAT]	08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YHR012w] 1e-27
[FUNCAT]	30.08 organization of golgi [S. cerevisiae, YHR012w] 1e-27
[FUNCAT]	09.25 vacuolar and lysosomal biogenesis [S. cerevisiae, YHR012w] 1e-27
[FUNCAT]	r general function prediction [M. jannaschii, MJ0623] 1e-16
[BLOCKS]	BL01269D
[BLOCKS]	BL01269A
[PROSITE]	RGD 1
[PROSITE]	MYRISTYL 4
[PROSITE]	PKC_PHOSPHO_SITE 1
[KW]	Alpha_Beta

```
SEQ    MLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHILCTGNLCTKESYDYLKTLAGDVHIVR
PRD    ccceeecccccccccccchhhhhhhhhhcceeeeeeccccccchhhhhhhhhhhhceeeee

SEQ    GDFDENLNYPEQKVVTVGQFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKSE
PRD    cccccccccccceeeeecccceeeeecccccccccchhhhhhhhhhcceeeeecccccc

SEQ    AFEHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQLIGDDVKVERIEYK
PRD    cccccccccccccccccccccccccccceeeeeccccceeeeeeeeeccccceeeeeeeec

SEQ    KP
PRD    cc
```

Prosite for DKFZphfbr2_23f2.2

PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00008	38->44	MYRISTYL	PDOC00008
PS00008	83->89	MYRISTYL	PDOC00008
PS00008	133->139	MYRISTYL	PDOC00008
PS00008	137->143	MYRISTYL	PDOC00008
PS00016	60->63	RGD	PDOC00016

(No Pfam data available for DKFZphfbr2_23f2.2)

DKFZphfbr2_23124
----

group: intracellular transport and trafficking

DKFZphfbr2_23124.2 encodes a novel 348 amino acid protein with similarity to human glycoprotein gp36b and canine VIP36 glycoprotein.

The vesicular protein VIP36 (36 kDa vesicular integral membrane protein) shows homology to leguminous plant lectins. The protein is localized to the Golgi apparatus, endosomal and vesicular structures and the plasma membrane. VIP36 binds to sugar residues of glycosphingolipids and/or glycosylphosphatidyl-inositol anchors and might provide a link between the extracellular/luminal face of glycolipid rafts and the cytoplasmic protein segregation machinery. Gp36 is located within the endoplasmatic reticulum. For the novel protein, a lectin character is predicted. Due to the intracellular localisation of the homolog proteins, it should be involved in intracellular transport and trafficking.

The new protein can find application in modulating/blocking intracellular transport and trafficking.

strong similarity to human GP36b glycoprotein

complete cDNA, complete cds, EST hits
potential start at Bp 29 matches kozak consensua ANNatgG
similarity to lectins,

Sequenced by AGOWA

Locus: /map="2"

Insert length: 2416 bp
Poly A stretch at pos. 2394, no polyadenylation signal found

```
   1 GGGGGATGAA GGGTCGTTGG TGGGAAAGAT GGCGGCGACT CTGGGACCCC
  51 TTGGGTCGTG GCAGCAGTGG CGGCGATGTT TGTCGGCTCG GGATGGGTCC
 101 AGGATGTTAC TCCTTCTTCT TTTGTTGGGG TCTGGGCAGG GGCCACAGCA
 151 AGTCGGGGCG GGTCAAACGT TCGAGTACTT GAAACGGGAG CACTCGCTGT
 201 CGAAGCCCTA CCAGGGTGTG GGCACAGGCA GTTCCTCACT GTGGAATCTG
 251 ATGGGCAATG CCATGGTGAT GACCCAGTAT ATCCGCCTTA CCCCAGATAT
 301 GCAAAGTAAA CAGGGTGCCT TGTGGAACCG GGTGCCATGT TTCCTGAGAG
 351 ACTGGGAGTT GCAGGTGCAC TTCAAAATCC ATGGACAAGG AAAGAAGAAT
 401 CTGCATGGGG ATGGCTTGGC AATCTGGTAC ACAAAGGATC GGATGCAGCC
 451 AGGGCCTGTG TTTGGAAACA TGGACAAATT TGTGGGGCTG GGAGTATTTG
 501 TAGACACCTA CCCCAATGAG GAGAAGCAGC AAGAGCGGGT ATTCCCCTAC
 551 ATCTCAGCCA TGGTGAACAA CGGCTCCCTC AGCTATGATC ATGAGCGGGA
 601 TGGGCGGCCT ACAGAGCTGG GAGGCTGCAC AGCCATTGTC CGCAATCTTC
 651 ATTACGACAC CTTCCTGGTG ATTCGCTACG TCAAGAGGCA TTTGACGATA
 701 ATGATGGATA TTGATGGCAA GCATGAGTGG AGGGACTGCA TTGAAGTGCC
 751 CGGAGTCCGC CTGCCCCGCG GCTACTACTT CGGCACCTCC TCCATCACTG
 801 GGGATCTCTC AGATAATCAT GATGTCATTT CCTTGAAGTT GTTTGAACTG
 851 ACAGTGGAGA GAACCCCAGA AGAGGAAAAG CTCCATCGAG ATGTGTTCTT
 901 GCCCTCAGTG GACAATATGA AGCTGCCTGA GATGACAGCT CCACTGCCGC
 951 CCCTGAGTGG CCTGGCCCTC TTCCTCATCG TCTTTTTCTC CCTGGTGTTT
1001 TCTGTATTTG CCATAGTCAT TGGTATCATA CTCTACAACA AATGGCAGGA
1051 ACAGAGCCGA AAGCGCTTCT ACTGAGCCCT CCTGCTGCCA CCACTTTTGT
1101 GACTGTCACC CATGAGGTAT GGAAGGAGCG GGCACTGGCC TGAGCATGCA
1151 GCCTGGAGAG TGTTCTTGTC TCTAGCAGCT GGTTGGGGAC TATATTCTGT
1201 CACTGGAGTT TTGAATGCAG GGACCCCGCA TTCCCATGGT TGTGCATGGG
1251 GACATCTAAC TCTGGTCTGG GAAGCCACCC ACCCCAGGGC AATGCTGCTG
1301 TGATGTGCCT TTCCCTGCAG TCCTTCCATG TGGGAGCAGA GGTGTGAAGA
1351 GAATTTACGT GGTTGTGATG CCAAAATCAC GGAACAGAAT TTCATAGCCC
1401 AGGCTGCCGT GTTGTTTGAC TCAGAAGGCC CTTCTACTTC AGTTTTGAAT
1451 CCACAAAGAA TTAAAAACTG GTAACACCAC AGGCTTTCTG ACCATCCATT
1501 CGTTGGGTTT TGCATTTGAC CCAACCCTCT GCCTACCTGA GGAGCTTTCT
1551 TTGGAAACCA GGATGGAAAC TTCTTCCCTG CCTTACCTTC CTTTCACTCC
1601 ATTCATTGTC CTCTCTGTGT GCAACCTGAG CTGGGAAAGG CATTTGGATG
1651 CCTCTCTGTT GGGGCCTGGG GCTGCAGAAC ACACCTGCGT TTCGCTGGCC
1701 TTCATTAGGT GGCCCTAGGG AGATGGCTTT CTGCTTTGGA TCACTGTTCC
1751 CTAGCATGGG TCTTGGGTCT ATTGGCATGT CCATGGCCTT CCCAATCAAG
1801 TCTCTTCAGG CCCTCAGTGA AGTTTGGCTA AAGGTTGGTG TAAAAATCAA
1851 GAGAAGCCTG GAAGACACCA TGGATGCCAT GGATTAGCTG TGCAACTGAC
1901 CAGCTCCAGG TTTGATCAAA CCAAAAGCAA CATTTGTCAT GTGGTCTGAC
1951 CATGTGGAGA TGTTTCTGGA CTTGCTAGAG CCTGCTTAGC TGCATGTTTT
2001 GTAGTTACGA TTTTTGGAAT CCCTCTTTGA GTGCTGAAAG TGTAAGGAAG
2051 CTTTCTTCTT ACACCTTGGG CTTGGATATT GCCCAGAGAA GAAATTTGGC
2101 TTTTTTTTCT TAATGGACAA GGGACAGTTG CTGTTCTCAT GTTCCAAGTC
2151 TGAGAGCAAC AGACCCTCAT CATCTGTGCC TGGAAGAGTT CACTGTCATT
2201 GAGCAGCACA GCCTGAGTGC TGGCCTCTGT CAACCCTTAT TCCACTGCCT
```

```
2251 TATTTGACAA GGGGTTACAT GCTGCTCACC TTACTGCCCT GGGATTAAAT
2301 CAGTTACAGG CCAGAGTCTC CTTGGAGGGC CTGGAACTCT GAGTCCTCCT
2351 ATGAACCTCT GTAGCCTAAA TGAAATTCTT AAAATCACCG ATGGAACCAA
2401 AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HS622145 from database EMBL:
human STS WI-6746.
Score = 1079, P = 5.1e-43, identities = 219/223

Entry G42541 from database EMBLNEW:
SHGC-58649 Human Homo sapiens STS genomic, sequence tagged site.
Score = 1091, P = 1.7e-43, identities = 219/220

Medline entries

94265253:
A putative novel class of animal lectins in the secretory pathway homologous to leguminous
lectins.

94208543:
VIP36, a novel component of glycolipid rafts and exocytic carrier vesicles in epithelial cells.

Peptide information for frame 2

ORF from 29 bp to 1072 bp; peptide length: 348
Category: strong similarity to known protein

```
  1 MAATLGPLGS WQQWRRCLSA RDGSRMLLLL LLLGSGQGPQ QVGAGQTFEY
 51 LKREHSLSKP YQGVGTGSSS LWNLMGNAMV MTQYIRLTPD MQSKQGALWN
101 RVPCFLRDWE LQVHFKIHGQ GKKNLHGDGL AIWYTKDRMQ PGPVFGNMDK
151 FVGLGVFVDT YPNEEKQQER VFPYISAMVN NGSLSYDHER DGRPTELGGC
201 TAIVRNLHYD TFLVIRYVKR HLTIMMDIDG KHEWRDCIEV PGVRLPRGYY
251 FGTSSITGDL SDNHDVISLK LFELTVERTP EEEKLHRDVF LPSVDNMKLP
301 EMTAPLPPLS GLALFLIVFF SLVFSVFAIV IGIILYNKWQ EQSRKRFY
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_23124, frame 2

PIR:G01447 GP36b glycoprotein - human, N = 1, Score = 1001, P = 5.9e-101

SWISSPROT:VP36_CANFA VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36 PRECURSOR (VIP36)., N = 1, Score = 990, P = 8.6e-100

TREMBL:CET04G9_2 gene: "T04G9.3"; Caenorhabditis elegans cosmid T04G9., N = 1, Score = 614, P = 6e-60

PIR:S42626 ER-golgi intermediate compartment protein - human, N = 2, Score = 397, P = 1e-42

```
>PIR:G01447 GP36b glycoprotein - human
           Length = 356

  HSPs:

 Score = 1001 (150.2 bits), Expect = 5.9e-101, P = 5.9e-101
 Identities = 197/356 (55%), Positives = 256/356 (71%)

Query:      1 MAATLGPLGSWQQWRRCLSARDG--------SRMLLLLLLLGSGQGPQQVGAGQTFEYLK 52
              MAA  G +  W   RRCL  R G         +  L LLLLGS        +  G + E+LK
Sbjct:      1 MAAE-GWIWRWGWGRRCLG-RPGLLGPGPGPTTPLFLLLLLGSVTA--DITDGNS-EHLK 55
```

```
Query:  53 REHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQ 112
           REHSL KPYQGVG+ S  LW+  G+ M+ +QY+RLTPD +SK+G++WN  PCFL+DWE+
Sbjct:  56 REHSLIKPYQGVGSSSMPLWDFQGSTMLTSQYVRLTPDERSKEGSIWNHQPCFLKDWEMH 115

Query: 113 VHFKIHGQGKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNEEKQQERVF 172
           VHFK+HG GKKNLHGDG+A+WYT+DR+ PGPVFG+ D F GL +F+DTYPN+E   ERVF
Sbjct: 116 VHFKVHGTGKKNLHGDGIALWYTRDRLVPGPVFGSKDNFHGLAIFLDTYPNDETT-ERVF 174

Query: 173 PYISAMVNNGSLSYDHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKH 232
           PYIS MVNNGSLSYDH +DGR TEL GCTA  RN  +DTFL +RY +  LT+M D++ K+
Sbjct: 175 PYISVMVNNGSLSYDHSKDGRWTELAGCTADFRNRDHDTFLAVRYSRGRLTVMTDLEDKN 234

Query: 233 EWRDCIEVPGVRLPRGYYFGTSSITGDLSDNHDVISLKLFELTVERTPEEEKLHRDVFLP 292
           EW++CI++ GVRLP GYYFG S+ TGDLSDNHD+IS+KLF+L VE TP+EE +      P
Sbjct: 235 EWKNCIDITGVRLPTGYYFGASAGTGDLSDNHDIISMKLFQLMVEHTPDEESIDWTKIEP 294

Query: 293 SVDNMKLPEMTAPLP-------PLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK 345
           SV+ +K P+      P       PL+G  +FL++  +L+  V   V+G +++ K QE++ K
Sbjct: 295 SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLLCALLGIVVCAVVGAVVFQKRQERN-K 353

Query: 346 RFY 348
           RFY
Sbjct: 354 RFY 356
```

Pedant information for DKFZphfbr2_23124, frame 2

Report for DKFZphfbr2_23124.2

[LENGTH]	348
[MW]	39711.10
[pI]	8.55
[HOMOL]	PIR:G01447 GP36b glycoprotein - human 1e-101
[PIRKW]	lectin 2e-37
[PIRKW]	transmembrane protein 2e-37
[PIRKW]	endoplasmic reticulum 2e-37
[PIRKW]	Golgi apparatus 2e-37
[PROSITE]	AMIDATION 1
[PROSITE]	MYRISTYL 5
[PROSITE]	CK2_PHOSPHO_SITE 2
[PROSITE]	GLYCOSAMINOGLYCAN 1
[PROSITE]	PKC_PHOSPHO_SITE 3
[PROSITE]	ASN_GLYCOSYLATION 1
[KW]	Alpha_Beta
[KW]	SIGNAL_PEPTIDE 39
[KW]	LOW_COMPLEXITY 7.76 %

```
SEQ  MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKP
SEG  ........................xxxxxxx............................
PRD  cccccccccccccccccccccchhhhhhhhhhcccccccccccchhhhhhhhhhhccc

SEQ  YQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQ
SEG  ............................................................
PRD  cccccccccceeeccccccccccceeeecchhhhhccccccccccchhhhhhhheeeeecc

SEQ  GKKNLHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTYPNEEKQQERVFPYISAMVN
SEG  ............................................................
PRD  ccccccccceeeeeecccccccccccccccccceeeeeecccccccccccccccceeeeeec

SEQ  NGSLSYDHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEV
SEG  ............................................................
PRD  ccccccccccccccccccccccccccccceeeehhhhhheeeeecccccccccccccc

SEQ  PGVRLPRGYYFGTSSITGDLSDNHDVISLKLFELTVERTPEEEKLHRDVFLPSVDNMKLP
SEG  ............................................................
PRD  ccccccccccccccccccccchhhhhhhhhhhhcccccccccccccccccccccc

SEQ  EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
SEG  ...........xxxxxxxxxxxxxxxxxxx.................
PRD  ccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccc
```

Prosite for DKFZphfbr2_23124.2

PS00001	181->185	ASN_GLYCOSYLATION	PDOC00001
PS00002	35->39	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	19->22	PKC_PHOSPHO_SITE	PDOC00005

PS00005	268->271	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00006	279->283	CK2_PHOSPHO_SITE	PDOC00006
PS00008	43->49	MYRISTYL	PDOC00008
PS00008	63->69	MYRISTYL	PDOC00008
PS00008	65->71	MYRISTYL	PDOC00008
PS00008	96->102	MYRISTYL	PDOC00008
PS00008	198->204	MYRISTYL	PDOC00008
PS00009	120->124	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_23124.2)

DKFZphfbr2_23n16
----

group: signal transduction

DKFZphfbr2_23n16.1 encodes a novel 292 amino acid protein with weak similarity to putative phosphatidylinositol-4-phosphate 5-kinase of Arabidopsis thaliana.

The novel proteins contains a WW domain which has been originally described as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. This domain is frequently associated with other domains typical for proteins in signal transduction processes. Examples of proteins containing the WW domain are Dystrophin, Utrophin, vertebrate YAP protein (binds the SH3 domain of the Yes oncoprotein), murine NEDD-4 (embryonic development and differentiation of the central nervous system), IQGAP (human GTPase activating protein acting on ras). Therefore the new protein should be involved in intracellular signal transduction.

The new protein can find application in modulating/blocking intracellular signal transduction pathways.

similarity to putative phosphatidylinositol-4-phosphate 5-kinase

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 2936 bp
Poly A stretch at pos. 2916, polyadenylation signal at pos. 2873

```
   1 GGGGGCGCTC CCGAGAAAGA GTGAGGGCGC GACGCGCACC AACGGTGGAG
  51 GGATGTTTCA GCAGCCCCTG AGAAGGAAGA GGAGGAAGCT GAGGGCCCGC
 101 TGAGGGCGCA GGACCTGAGG GAGTCCTACA TCCAGCTCGT CCAGGGTGTG
 151 CAGGAGTGGC AGGATGGTTG CATGTACCAG GGGGAGTTTG GGTTGAACAT
 201 GAAGCTTGGA TATGGCAAAT TCTCTTGGCC CACAGGCGAG TCATACCATG
 251 GGCAGTTTTA CCGGGACCAC TGCCATGGCC TGGGTACCTA CATGTGGCCA
 301 GATGGCTCCA GTTTCACGGG CACATTTTAC CTCAGCCACC GAGAAGGCTA
 351 CGGCACCATG TACATGAAGA CACGGCTTTT CCAGACTCAC TGCCACAACG
 401 ACATTGTCAA CCTTCTCCTG GACTGTGGGG CCGACGTGAA CAAGTGCTCA
 451 GATGAGGGTC TCACGGCACT CAGCATGTGT TTCCTCCTCC ACTACCCCGC
 501 CCAGTCCTTC AAGCCCAATG TTGCTGAACG GACCATACCT GAGCCCCAGG
 551 AACCTCCAAA ATTCCCAGTT GTTCCAATCC TTTCATCATC ATTTATGGAC
 601 ACAAACCTGG AGTCTCTGTA CTATGAGGTG AACGTGCCTT CCCAGGGTAG
 651 CTATGAGCTG AGGCCACCGC CAGCACCACT GCTCCTGCCA CGCGTCTCAG
 701 GCAGCCACGA GGGCGGCCAC TTCCAGGACA CCGGGCAGTG TGGGGGGTCC
 751 ATAGACCACA GGAGCAGCTC TCTGAAGGGG GACTCCCCGT TGGTGAAGGG
 801 CAGCCTTGGC CATGTGGAAA GCGGGCTTGA GGACGTGTTG GGAGACACAG
 851 ACCGGGGCAG TCTGTGCAGT GCTGAGACGA AATTTGAGTC CAACTTGTGT
 901 GTGTGCGACT TCTCCATCGA GCTCTCGCAG GCCATGCTGG AGAGAAGCGC
 951 CCAGTCCCAC AGCTTGCTGA AGATGGCCTC GCCCTCACCG TGCACCAGCA
1001 GCTTCGACAA AGGGACCATG CGGAGGATGG CGCTGTCCAT GATCGAGTAG
1051 GTCCTGGCAC CAGCTGGTGG GGGTGGAGGG CCACCATCAG GGCTGAATCC
1101 TATGCTCAGC AGACCCACGT CTCTTCCCTG TGCCAGTGGG AGGCGTTGTG
1151 TCTGGAGATG TGTGTCTGAA TGTGTGAGCA TCCCTGTGTC GGTGGCTCCA
1201 TGCCATGGCC AGCCCTGTGG GGGTGCCACG GTGACGGGCT GTTTTCAGTG
1251 CCACCCCAGC CCTGTGGGGG TGCCACGGTG ACGGGCTGTT TTCAGTACCA
1301 CGCCAGCCCT GCTTTGGCCT TTGGCACTGG CCTGAAGTGT CTCTGTGGGA
1351 GCCTCAGCAG GGGCCACTGT CAGGGGTCCT ATCCTAGCCA TAGTGCACGT
1401 GAGTGACACC TGCCTGGGCA GCTCTCACAC CCCTGCTGTC CACCCTGTCT
1451 ATACCAGTGT GTCTCAAAAT GTGGTCTATG CACCCCCGGG GGTCCAAGAC
1501 CCTTTCAGGG AGTCTGTGGG GTCAAAATGA TTCTCTTGAT AACCCTGAGA
1551 CTCTGTTAGC CTTCTCCTTG TGTTGATGTT GGTGGATGGT ATGAAGACAG
1601 GGCCGTGCAG ACCACCAGCC CCCAGCGTGC AGGGCAGCAG TGCCCGGCCT
1651 GCTTGGGGGC ATGGTATTCC TTCACCACGG TGTGCACTTG CGGGGATGCC
1701 TGTCTCACTG AAGAATGCCT TTGACTAAGC AGAAAAGCAA TGACAAATTG
1751 CATTAAATCT TGCTCCTTGC GTACACACCC CTCGAATATT CTGGGTCGGA
1801 AAACATGGGA AGGACACTGA TGTGTGTCTG CCACAGACCA AGGCACACCG
1851 CTTCCCCGCA AGAAGCGCTT CCCCCAGGGC CAGAGTAGCA ACAGAATGCG
1901 GCATCTTCCC AACCTCCTGC CCCATTTTTG ATTGGAAGAA TGACCACTGG
1951 TATGTGGCTG TTCATTCTCC TGAACACAGC CTGCCACTTT AAGGAAAACA
2001 TATGACACTA TTTGTTGCTG GCGAAATTTA CATTTTCAAG TGAATAGCAG
2051 AATTCTGGAC ACTTGCCACC ACCACCAAAA CCTTCATAGC TTCCCTTAAC
2101 TTTGAGACAT GGGTGTTCAG AGGTTTTTCA CGTGAGATGG CGTTAGCAGC
2151 GCAGTTTTGT GATACTGCCT GAAGACATGC CGACAGTGCC CAGATCTCTT
```

```
2201 CTATTGGTGA GCCAGCTTTT CCCACACGGC CAAGTTCTGA TGTTGAACCA
2251 TTGCCAGGTG GGTGAAGATC CATTGACAGT GAGAGGTGGG CCCGTGGGCT
2301 TCAGTGCAGC CAGGCGCAGA AGGCTGGTTC ATGAGTGTCC AGCTCCGCCA
2351 GGTAGCTAGC TCACCACCCC CAGCCTGGGT TCATGTAGTT CAAATAGGAA
2401 GACCACGATG ATCAGAAAGG CTGCTCAAAT ACTCCTTCGT CCAGCCGCGT
2451 ACCTGGGGGA GGCTGAATCT CCACTCACTT CCACCAAGGC TGTGCAGAGC
2501 AGATAGGGGA ATCCAGCAAA GGTGGAAAAC AGTGCCATCC TTCTCCCCAA
2551 CTGGTTTTGT TTTGTAAAAT AACTTTTTGT GACAGTGTTA CTTATTAGTA
2601 ACATGCAGTG GGTTTGTTAT GGTTAACAAG TTGGTGAGCA TTATTGAGAG
2651 GTGAAGCCAG CTGAGCTTCT GGGTTGGGTG GGGACTTGGA GAACTTTTGT
2701 GTCTAGCTAA AGGATTGTAA ATGCACCAAT CAATGCTCAG TGTCTAGCTA
2751 AAGGATTGTA AATGCACCAA TCAGCACTCT GTAAAATTGA CCAATCAGCG
2801 TTCTGTAAAA TGGACCAATC AGTGGTCTGT AAAATGGACC AGTCAGCAGG
2851 ATGTGGGCGG GGCCAAAAAA GGGAATAAAA GCTGGCCACC GCCAGGCTCC
2901 CCACCAGCCT GCAGCGAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 172 bp to 1047 bp; peptide length: 292
Category: similarity to unknown protein
Prosite motifs: WW_DOMAIN_1 (19-24)

```
  1 MYQGEFGLNM KLGYGKFSWP TGESYHGQFY RDHCHGLGTY MWPDGSSFTG
 51 TFYLSHREGY GTMYMKTRLF QTHCHNDIVN LLLDCGADVN KCSDEGLTAL
101 SMCFLLHYPA QSFKPNVAER TIPEPQEPPK FPVVPILSSS FMDTNLESLY
151 YEVNVPSQGS YELRPPPAPL LLPRVSGSHE GGHFQDTGQC GGSIDHRSSS
201 LKGDSPLVKG SLGHVESGLE DVLGDTDRGS LCSAETKFES NLCVCDFSIE
251 LSQAMLERSA QSHSLLKMAS PSPCTSSFDK GTMRRMALSM IE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_23n16, frame 1

TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for AtPIP5K1, complete cds., N = 2, Score = 138, P = 1.1e-06

TREMBL:AF019380_1 product: "putative phosphatidylinositol-4-phosphate 5-kinase"; Arabidopsis thaliana putative phosphatidylinositol-4-phosphate 5-kinase mRNA, complete cds., N = 2, Score = 138, P = 1.4e-06

PIR:T02098 probable phosphatidylinositol-4-phosphate 5-kinase - Arabidopsis thaliana, N = 2, Score = 135, P = 6.7e-06

```
>TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for
     AtPIP5K1, complete cds.
            Length = 683

  HSPs:

 Score = 138 (20.7 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
 Identities = 23/61 (37%), Positives = 35/61 (57%)

Query:     1 MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGY 60
             MY+G++       G GKFSWP+G +Y G+F       G GT+    DG ++ GT+     + G+
Sbjct:    34 MYEGDWKRGKASGKGKFSWPSGATYEGEFKSGRMEGFGTFTGADGDTYRGTWVADRKHGH 93

Query:    61 G 61
             G
Sbjct:    94 G 94
```

```
 Score = 112 (16.8 bits), Expect = 9.7e-04, Sum P(2) = 9.7e-04
 Identities = 19/51 (37%), Positives = 27/51 (52%)

Query:    12 LGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGYGT 62
             +G GK+ W  G  Y G + R    G G + WP G+++ G F     EG+GT
Sbjct:    22 IGSGKYLWKDGCMYEGDWKRGKASGKGKFSWPSGATYEGEFKSGRMEGFGT 72

 Score = 97 (14.6 bits), Expect = 4.4e-02, Sum P(2) = 4.3e-02
 Identities = 19/60 (31%), Positives = 32/60 (53%)

Query:     2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGYG 61
             Y+GEF       G+G F+    G++Y G +  D  HG G   + +G  + GT+  + ++G G
Sbjct:    58 YEGEFKSGRMEGFGTFTGADGDTYRGTWVADRKHGHGQKRYANGDFYEGTWRRNLQDGRG 117

 Score = 93 (14.0 bits), Expect = 1.2e-01, Sum P(2) = 1.1e-01
 Identities = 18/62 (29%), Positives = 34/62 (54%)

Query:     2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGYG 61
             Y+G +   + K G+G+   +  G+ Y G + R+   G G Y+W +G+ +TG + +     G G
Sbjct:    81 YRGTWVADRKHGHGQKRYANGDFYEGTWRRNLQDGRGRYVWRNGNQYTGEWRIGVISGKG 140

Query:    62 TM 63
              +
Sbjct:   141 LL 142

 Score = 91 (13.7 bits), Expect = 2.0e-01, Sum P(2) = 1.8e-01
 Identities = 18/51 (35%), Positives = 24/51 (47%)

Query:     2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTF 52
             Y GE+ + +  G G    WP G  Y G +       G G + W DGSS  G +
Sbjct:   127 YTGEWRIGVISGKGLLVWPNGNRYEGLWENGIPKGNGVFTWSDGSSCVGAW 177

 Score = 90 (13.5 bits), Expect = 2.6e-01, Sum P(2) = 2.3e-01
 Identities = 17/60 (28%), Positives = 31/60 (51%)

Query:     2 YQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGYG 61
             Y+G +   N++ G G++ W  G  Y G++      G G  +WP+G+ + G +      +G G
Sbjct:   104 YEGTWRRNLQDGRGRYVWRNGNQYTGEWRIGVISGKGLLVWPNGNRYEGLWENGIPKGNG 163

 Score = 45 (6.8 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
 Identities = 14/62 (22%), Positives = 26/62 (41%)

Query:   215 VESGLEDVLGDTDRGSLCSAETKFESNLCVCDF--SIELSQAMLERSAQSHSLLKMASPS 272
             V+SG   + G+     +C  E+  E+    CD   ++E S    +R +      +    +
Sbjct:   205 VDSGAGSLGGEKVFPRICIWESDGEAGDITCDIIDNVEASMIYRDRISVDRDGFRQFKKN 264

Query:   273 PC 274
             PC
Sbjct:   265 PC 266
```

Pedant information for DKFZphfbr2_23n16, frame 1

Report for DKFZphfbr2_23n16.1

```
[LENGTH]       292
[MW]           32214.44
[pI]           5.51
[HOMOL]        TREMBL:AB005902_1 product: "AtPIP5K1"; Arabidopsis thaliana mRNA for AtPIP5K1,
complete cds. 7e-08
[BLOCKS]       BL01137A Hypothetical YBL055c/yjjV family proteins
[PROSITE]      WW_DOMAIN_1    1
[PROSITE]      MYRISTYL       5
[PROSITE]      CK2_PHOSPHO_SITE      7
[PROSITE]      PKC_PHOSPHO_SITE      5
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY     4.11 %

SEQ    MYQGEFGLNMKLGYGKFSWPTGESYHGQFYRDHCHGLGTYMWPDGSSFTGTFYLSHREGY
SEG    ............................................................
PRD    cccccccccccccccceeeccccccccccccccccccccccccccccccceeeeecccc

SEQ    GTMYMKTRLFQTHCHNDIVNLLLDCGADVNKCSDEGLTALSMCFLLHYPAQSFKPNVAER
SEG    ............................................................
PRD    ccccchhhhhheeeccccchhhhhcccccccccccccchhhhhhhhcccccccccccceee

SEQ    TIPEPQEPPKFPVVPILSSSFMDTNLESLYYEVNVPSQGSYELRPPPAPLLLPRVSGSHE
```

```
SEG     ..........................................xxxxxxxxxxxx......
PRD     eccccccccceeeeeeeecccccccccccceeeeeecccccccccccccccccccccccc

SEQ     GGHFQDTGQCGGSIDHRSSSLKGDSPLVKGSLGHVESGLEDVLGDTDRGSLCSAETKFES
SEG     ............................................................
PRD     ccccccccccccccccccccccccccceeeccccccccccccccccccccccceeeeecccc

SEQ     NLCVCDFSIELSQAMLERSAQSHSLLKMASPSPCTSSFDKGTMRRMALSMIE
SEG     ....................................................
PRD     cccccchhhhhhhhhhhhhhhhhhhhhccccccccccccccchhhhhhccc
```

Prosite for DKFZphfbr2_23n16.1

PS00005	55->58	PKC_PHOSPHO_SITE	PDOC00005
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	200->203	PKC_PHOSPHO_SITE	PDOC00005
PS00005	226->229	PKC_PHOSPHO_SITE	PDOC00005
PS00005	282->285	PKC_PHOSPHO_SITE	PDOC00005
PS00006	55->59	CK2_PHOSPHO_SITE	PDOC00006
PS00006	121->125	CK2_PHOSPHO_SITE	PDOC00006
PS00006	140->144	CK2_PHOSPHO_SITE	PDOC00006
PS00006	144->148	CK2_PHOSPHO_SITE	PDOC00006
PS00006	217->221	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	276->280	CK2_PHOSPHO_SITE	PDOC00006
PS00008	45->51	MYRISTYL	PDOC00008
PS00008	86->92	MYRISTYL	PDOC00008
PS00008	177->183	MYRISTYL	PDOC00008
PS00008	188->194	MYRISTYL	PDOC00008
PS00008	229->235	MYRISTYL	PDOC00008
PS01159	19->44	WW_DOMAIN_1	PDOC50020

(No Pfam data available for DKFZphfbr2_23n16.1)

DKFZphfbr2_23o24
----

group: brain derived

DKFZphfbr2_23o24 encodes a novel 139 amino acid protein with similarity to CAAX-box proteins.

The CAAX box is a prenyl group binding site found in a number of eukaryotic proteins, such as which is found in Ras- and ras-like proteins such as Rho, Rab, Rac, Ral, and Rap, as well as in nuclear lamins A and B, some G protein alpha and gamma subunits and some dnaJ-like proteins. These proteins are posttranslationally modified at this site by the attachment of either a farnesyl or a geranyl-geranyl group to a cysteine residue.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to lectins

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 3564 bp
Poly A stretch at pos. 3541, no polyadenylation signal found

```
   1 GAATGGCTCC GCAGATGGCC GGCACTGAGA GCCAGCAAGA AGCGGAGGAG
  51 ATGGGCCTTC AGCAGGGGGT TGCGGGGGGA GCTTTAAACT GAGCCCTGTA
 101 AACATGGCAG AACTGCTCAG TGGGAGACTC TCAGCACAGA CGGTCATGGG
 151 GAAGTGAGTG CAGTTCATTT GTAATCTTGT TGTCGAGTTC TGGGTTTTTT
 201 TTGTTTGTTT CGTAACTTTA AAGGTATGCA CTTTATATAG ATTTATTTAT
 251 TTGCTGGGAC CGTTACTCAG AGTTCCTAGA AATGTACACA GCTTTTTTAC
 301 CAGGGTTACT CCTCAGAATC ACTTGTCACT TCTTTAAATG AATGAATGAA
 351 TGTGCCAGGC CCTATGCCTG GAGGTTGGGA GCTTCATCTA CATCACATTC
 401 TAACAGGTGA CCACTGGGGT AAGCACTGTG TGACTGCAAA GCCAGGGTGT
 451 GTTTCCATCA ACACCCAGAT GACCGTGCCT ATGTGCCCCT GTTGTCCTCC
 501 CTCCAGGACT GCCTCCTCAC CCCACCCCTT TCTGCAGCTC CTCATCTAAA
 551 CATCTCGCCT GGTGAGGTCA CGGCTTAGCC TGTTGGCCAG TGGCCCCACC
 601 ACCATCCTTC CCCCTGTGCA GATTGGAGGA GGCCAGGTCT CTCCCCTTAG
 651 CTCCTATGTC CCCTTCACCC CCCATGGCAC AGATGAGACA TTCACAGAGT
 701 TTGCAGATGA TGGAAGAGAA GACTCCAGGT TGCCAGGTGT GTCCACTCTC
 751 AGGAACCCCC AGCCCAAGCC TCACTGCTCG TGTTCCCAGC CAACCCCAGC
 801 ACGGGGGATA CGCCGGTGCT GTTTCCCTGC TCAGATACAA CCAGTTACCA
 851 GAAACGACCT CACCCCTCCA ACCACTTTCC AAGGTGCCAG GACAGAGAAG
 901 CCCTTCACTG GCCCACCCAG GGCAGTTGAC AGAGGGATGC CCTCCTTGGA
 951 GGGGAGCCTC ACCTCTACCC ACAGGGCCGC GGCCTTGTCC TGGATTCTCA
1001 CCGGGGCAGT CACGTCAGGA TGGAGAGGTC CCATGTCAGC CAGTTCTTTG
1051 GTGGGGGTCA TGTAGTCTGA AATGACCTGC CGATGGTCCA GGCTGAGCCA
1101 GGGAAGCTGA GCCTGGGTGC CTTTTTGGTG CCTACTCTGA CTTGAGTTGG
1151 ATTCATGCCA CAGACCCACC TTCTTGAGCA ACAACACATA TAGCCACCAA
1201 CACAAGAGCC AGGCACACAC TGAGCAGAGA AAGTCCCTGT CGCCTCACCA
1251 CCCAAAAACT CCAGCTTTGC AGAGACCAAG GTTCTTCTCT ACCTTTGCAG
1301 AAGCCTCTGT GACCAAACCC GGAGCTTGCC CTTCTGAGGC CTCTAGCATT
1351 TCTCCAGGTG TTTTTCAGAG GACTTGGTTT AAATTTGTTC ACCCCAAATG
1401 TGGTCTTTCC CGGATCATGA AAGGATCTGC CGCAAAGGTG AATCTGAGTC
1451 TCCTCAGAGT CATATGAGAC TGAAACTGCT TATAACATTT CCGTGACCTA
1501 ATAAGTCTTC CAAAAATGTA GGGTATTAAG AGTTTAGTGA CATTAAAAAG
1551 TTTAGTCGAA AATATCGTGA TTCAGGTATA TTTAGACATT TGATTCATGC
1601 CAAATTGCCA CTGTTAACAG AAAACACACC CCAAGCACAT TAATGCCTAG
1651 ATATTTCAAA CCCTTTTCTG CCCACACATT CTTAAAAATA ATATACTGAG
1701 AAATCTATAT ACAGGTTTTT TTTTAATTAG CTTGGAAAAG AGCAGTTGTA
1751 TTCTGTTTGA ACAGCTGCTA ATGTCAATTC CTGTGGGAAG AAAGACCAAA
1801 GAACATGGAG TTACACCAAG AATTTTAAAA CAAAGACGCT GTCCCTTTCC
1851 TGAGCACCGT GCAGCCAAGA CTGAGAGATC AGTCTGAGAC CTGTGATTAA
1901 GGAGTGTTTT CTACATAGCG TATAATTATG GAGCCACACA AGTGGGCCAT
1951 TACTCTGTTG AGTGCTTCAT GTTTGAGGTA TTTTCGTGTT CCAACTTACA
2001 TTAAAGTGTT TATAAAACAG GAAAAATCCA CGAGCAGGTA TTGACACTAT
2051 CCATATTAGA TCATCACAAA ATTATATATA TAGCAGAGTC ATAAACAATG
2101 AGAAACGGTC TTCCCACACT TGCTTTAAAT GGCCATGACC TAGTGTTTAG
2151 GGAAAGCAGT AAAATCAGCG AGGAGCTCGT GGGAAAAATG AGACGGGCCC
2201 TGAGGGGGTG ACTCATGGGC CAAGCAGGGC CACACAGGTA CCAGGCCGCC
2251 ACGTCCTCTC CTGCCTCTCA CTCTCTGGAG ACTGGACTTC CTTTACTGCC
2301 TCCTTTCTGA CATTTCCTAG ACATCAGACT TTGCTACTTA GTACACAAAC
2351 GGGGTTCCCT TTTAAATTTG TTCACTCTAG TTAGCATTTG CAGAAGCTGT
2401 GAAAAATTAC AGAGAGATGA TGTGTTGGGT AAGAGATGGT TTAAAAGTCC
```

```
2451 AGCTTGCTGT TTTTCATTAA GTGTCTTGAA AATGAGTAAG TGGCGTTCCT
2501 GGAGGGGAAC AATCATATAA TTCCGCAGGG TGGGTCTAAA CTTGTTTTCT
2551 GATAGTGTTT AGCAGCTCAT GGCTCTGAGG GCACCTGATA ACACAGCAGC
2601 CAGGCGCTGA TGAGAAGTGT GTGCCAGACA GACCCGAGTG TGGCTTGGCT
2651 CTTGCCTTAT GTTCCTTTCT CTGTTCAGAG AAGCGTGAGA TGAGATTTTG
2701 TGATTATATT GCACTCCTTG GGCTGACTTT CCCATGCACA GAATGTTTTA
2751 CACATCCTGA TAGCTGAGCT GAAAATGCAA AGAGAAGGGA AAATGCCTTA
2801 AATTGTTCTG GCTAATTTAG AAGCAGCAGG CCTTGGAAGT CTTTGTCCTG
2851 TGTCCCTGAA CAAATCTTAT GGGAGCTCTG GTACCTATGC CAGAAAATGC
2901 ACATAGGCAC AACACTTTTA CATACACGTT CACACACCCC ACCCTTATGG
2951 AGAACTTTTT TCTAAATAAG AGAAAGAAAA ATTTTAAGAC TTACAAGTTA
3001 TGTTTAGGTA TTTTACATGG TTCAGAAAAC AAGACATGAA GCGGTATAAA
3051 CTGAGAAGTC TTGTTCCCAC AACCCCACGT GCCAGGTACA CATAACCATT
3101 TTTATTCACC TCTAGCTTGT GCTTCCAATG TTTGTTAGGC ATATGTAAAT
3151 AAGTGAATAG ATAAGCATTT CTCCCTCCTT TTGCTGACAT GAGTGGTGGC
3201 ATGTTTTGCC CCTGGCTTTT ATCCCTTGAC CCCATTCCAG TACCTAGAGA
3251 CCTGCTTCAT TTTTTTAGAT GTGTAATACT TCATGTGTGC GTGTGCCTTA
3301 GTGATTAACT CGTGCACTGT GCAGGGACAT CGGGCTGGGA TCAGTTTGTT
3351 CACTGATATA TACAGCGCTG CGGGAGATAC CCTCACATGT GTATCATTTG
3401 GTCCATGTGC AGGTGTGTCT GGAAGATAGA ATTCTAGGCG TAGAATTGAT
3451 AGGTTAAATG TATTTATAGG GAAAAAATCA ATATAAAACT TTGCGTGTAA
3501 TGATATTTGC GTGCTTTTTT TTTTAATTTT TTTACCCAAA TAGTAAAAAA
3551 AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 656 bp to 1072 bp; peptide length: 139
Category: similarity to known protein

```
  1 MSPSPPMAQM RHSQSLQMME EKTPGCQVCP LSGTPSPSLT ARVPSQPQHG
 51 GYAGAVSLLR YNQLPETTSP LQPLSKVPGQ RSPSLAHPGQ LTEGCPPWRG
101 ASPLPTGPRP CPGFSPGQSR QDGEVPCQPV LWWGSCSLK
```

BLASTP hits

Entry CEEGAP7_1 from database TREMBL:
gene: "EGAP7.1"; Caenorhabditis elegans cosmid EGAP7.
Score = 123, P = 2.3e-07, identities = 35/103, positives = 44/103

Entry MMBPC35_1 from database TREMBL:
Mouse carbohydrate binding protein 35 mRNA, 3' end.
Score = 113, P = 2.2e-06, identities = 40/103, positives = 44/103

Entry A28651 from database PIR:
galactose-specific lectin - mouse >TREMBL:MMMAC2A_1 Mouse mRNA for Mac-2 antigen
Score = 113, P = 2.2e-06, identities = 40/103, positives = 44/103

Alert BLASTP hits for DKFZphfbr2_23o24, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_23o24, frame 2

Report for DKFZphfbr2_23o24.2

[LENGTH]	139	
[MW]	14748.91	
[pI]	8.90	
[PROSITE]	PRENYLATION	1

[PROSITE]	MYRISTYL	1
[PROSITE]	CK2_PHOSPHO_SITE	1
[PROSITE]	PROKAR_LIPOPROTEIN	1
[PROSITE]	PKC_PHOSPHO_SITE	1
[KW]	All_Alpha	

```
SEQ  MSPSPPMAQMRHSQSLQMMEEKTPGCQVCPLSGTPSPSLTARVPSQPQHGGYAGAVSLLR
PRD  ccccchhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccchhhhhhhh

SEQ  YNQLPETTSPLQPLSKVPGQRSPSLAHPGQLTEGCPPWRGASPLPTGPRPCPGFSPGQSR
PRD  hhcccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  QDGEVPCQPVLWWGSCSLK
PRD  ccccccccccccccccccc
```

Prosite for DKFZphfbr2_23o24.2

PS00005	40->43	PKC_PHOSPHO_SITE	PDOC00005
PS00006	119->123	CK2_PHOSPHO_SITE	PDOC00006
PS00008	50->56	MYRISTYL	PDOC00008
PS00013	126->137	PROKAR_LIPOPROTEIN	PDOC00013
PS00294	136->140	PRENYLATION	PDOC00266

(No Pfam data available for DKFZphfbr2_23o24.2)

DKFZphfbr2_23o5
----

group: brain derived

DKFZphfbr2_23o5 encodes a novel 360 amino acid protein with no known similarity

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

potential start at Bp 24 matchs Kozak consensus ANNatgG

Sequenced by AGOWA

Locus: /map="7q21-q22"

Insert length: 1736 bp
Poly A stretch at pos. 1714, polyadenylation signal at pos. 1680

```
   1 GGGGGAGGAT CAAAGTAGGC AAGATGGCGT CGAGCGGCGG GGAGCCAGGG
  51 AGTTTATTTG ATCACCACGT CCAGAGGGCG GTATGCGACA CACGGGCCAA
 101 ATATCGAGAG GGACGACGGC CTCGTGCTGT GAAGGTATAT ACAATCAATT
 151 TGGAATCTCA GTACTTATTA ATACAAGGAG TTCCTGCTGT GGGAGTCATG
 201 AAGGAATTAG TTGAGCGATT CGCTTTATAT GGTGCAATTG AACAGTACAA
 251 TGCTCTAGAT GAATACCCAG CAGAAGACTT TACTGAAGTT TATCTTATTA
 301 AATTTATGAA CTTACAAAGT GCAAGGACAG CCAAGAGAAA AATGGATGAA
 351 CAGAGTTTCT TCGGTGGATT GCTTCATGTG TGCTATGCTC CAGAATTTGA
 401 AACAGTTGAA GAAACTAGAA AAAAACTACA AATGCGGAAG GCATATGTAG
 451 TAAAAACTAC TGAAAATAAA GACCATTACG TGACAAAGAA GAAATTGGTT
 501 ACAGAGCATA AAGACACAGA GGATTTTAGA CAAGACTTCC ACTCAGAGAT
 551 GTCTGGATTT TGTAAAGCTG CTTTGAACAC TTCTGCAGGG AACTCAAATC
 601 CTTATCTTCC GTATTCCTGT GAATTGCCTT TATGTTATTT CTCCTCAAAA
 651 TGTATGTGTT CATCCGGGGG ACCTGTAGAC AGAGCACCAG ACTCCTCTAA
 701 GGATGGTAGA AACCATCATA AAACAATGGG GCATTATAAC CACAATGACT
 751 CTTTGCGGAA AACACAGATA AACTCTTTGA AAAACTCAGT GGCCTGCCCT
 801 GGTGCACAAA AGGCTATTAC GTCTTCAGAG GCAGTTGACA GATTTATGCC
 851 TAGGACAACA CAACTGCAGG AGCGCAAAAG AAGAAGAGAA GATGATCGTA
 901 AACTTGGAAC TTTTCTTCAA ACAAACCCAA CTGGTAATGA GATTATGATT
 951 GGACCTCTGT TACCAGACAT CTCTAAAGTG GATATGCACG ATGACTCATT
1001 GAATACAACG GCGAATTTAA TTCGGCATAA ACTTAAAGAG GTATTTCATC
1051 TGTGCCAAAG CCTCCAGAGG ACAAGCCAGA AGATGTACAT ACAAGTCATC
1101 CATTAAAACA AAGAAGAAGA ATATAGAGTG CCAGCAGCAA CTTAGTATTT
1151 TCTAAAAAGA ACATTTATTA TTTATTTTTA GCCTGTCATT TTAATTCTTC
1201 AAGAGATTTT ACTGCTGGTA TTTTTTGATG CACTCCTCTT TGTAATTTCA
1251 TTCAAGCCAT TTGTCTAAAG TCATTTCTTT GTTTTTTGGG AGATGGAGTC
1301 TTGCTCTGTT GCCCAGGCTG GAATGCAGTG GCGTGATCTC GGCTCACTGC
1351 AACCTCCACC TCCCGGGTTC AAGCGATTCT CCTGCCTCAG CCTCCTGAGT
1401 ATCTGGGATT ACAGGCGTGC ACCACCATGC CTGGCTAAGT TTTGTGTTTT
1451 TTTTAGTAGA GATGGGTTTT CACCATATTG GTCAGGCTGG TCTCGAACTC
1501 CTGACCTTGT GATACACCTG CCTCAGCCTC CCAAAGGGAT GAGCCACCGC
1551 GCCTGGCCCA TTTCTTCTTT TTTTGACCCA TACTTAATGT TGCAGAAACT
1601 ATTCTTGTCA TAACATTATC TCTCATGTAC AGTAATTATA TGTAAATTAA
1651 TTGAAGCAAA TATGGAAACT TTACAATAGA AATAAAGATA GGCAGCCAGC
1701 GTCTGTTTCC AATTATAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry AC005156 from database EMBL:
Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.
Score = 2897, P = 2.4e-154, identities = 583/586
2 exons covering Bp 465-1723

Medline entries

No Medline entry

Peptide information for frame 3

```
ORF from 24 bp to 1103 bp; peptide length: 360
Category: similarity to unknown protein


    1 MASSGGEPGS LFDHHVQRAV CDTRAKYREG RRPRAVKVYT INLESQYLLI
   51 QGVPAVGVMK ELVERFALYG AIEQYNALDE YPAEDFTEVY LIKFMNLQSA
  101 RTAKRKMDEQ SFFGGLLHVC YAPEFETVEE TRKKLQMRKA YVVKTTENKD
  151 HYVTKKKLVT EHKDTEDFRQ DFHSEMSGFC KAALNTSAGN SNPYLPYSCE
  201 LPLCYFSSKC MCSSGGPVDR APDSSKDGRN HHKTMGHYNH NDSLRKTQIN
  251 SLKNSVACPG AQKAITSSEA VDRFMPRTTQ LQERKRRRED DRKLGTFLQT
  301 NPTGNEIMIG PLLPDISKVD MHDDSLNTTA NLIRHKLKEV FHLCQSLQRT
  351 SQKMYIQVIH

                              BLASTP hits

No BLASTP hits available

             Alert BLASTP hits for DKFZphfbr2_23o5, frame 3

TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome
II BAC F15K20 genomic sequence, complete sequence., N = 2, Score = 114,
P = 3.6e-11


>TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome II
     BAC F15K20 genomic sequence, complete sequence.
            Length = 227

  HSPs:

 Score = 114 (17.1 bits), Expect = 3.6e-11, Sum P(2) = 3.6e-11
 Identities = 21/41 (51%), Positives = 29/41 (70%)

Query:   103 AKRKMDEQSFFGGLLHVCYAPEFETVEETRKKLQMRKAYVV 143
             AKRK+DE SF G  L + YAPE+E V +T+ KL+ R+  V+
Sbjct:    51 AKRKLDESSFLGNRLQISYAPEYENVNDTKDKLESRRKEVL 91

 Score = 107 (16.1 bits), Expect = 2.6e-10, Sum P(2) = 2.6e-10
 Identities = 50/191 (26%), Positives = 83/191 (43%)

Query:   103 AKRKMDEQSFFGGLLHVCYAPEFETVEETRKKLQMRKAYVVKTTENKDHYVTKKKLVTEH 162
             AKRK+DE SF G  L + YAPE+E V +T+ KL+ R+  V+      +    T +  VT+
Sbjct:    51 AKRKLDESSFLGNRLQISYAPEYENVNDTKDKLESRRKEVLARLNPQKEKSTSQ--VTKL 108

Query:   163 KDTEDFRQDFHSEMSGFCKAALNTSAGNSNPYLPYSCELPLCYFSSKCMCSSGGPVDRAP 222
                  + D  S       +   +  GN+ P     S +    YF+S  M  +   V
Sbjct:   109 AGPALTQTDNVSSQRREMEYQFHR--GNA-PVTRVSSDQE--YFASSSMNQTVKTV---- 159

Query:   223 DSSKDGRNHHKTMGHYNHNDSLRKTQINSLKNSVACPGAQKAITSSEAVDRFMPRTTQLQ 282
                  K  +   + +   +H   + ++  N  +      P +Q     S     R  P ++Q+Q
Sbjct:   160 -REKLNKTREENISSLSHCKQIEESG-NQKRLQ---PSSQTQPEESGNQKRLQP-SSQIQ 213

Query:   283 -ERKRRREDDRK 293
              + KR R D+R+
Sbjct:   214 PDLKRTRVDNRR 225

 Score = 102 (15.3 bits), Expect = 3.6e-11, Sum P(2) = 3.6e-11
 Identities = 22/55 (40%), Positives = 38/55 (69%)

Query:    26 KYREGRRPRAVKVYTINLESQYLLIQGVPAVGVMKELVERFALYGAIEQY--NALDE 80
             +Y++     P AV+VYT+  ES+Y++++ VPA+G    +L+  F   YG +E++     LDE
Sbjct:     3 RYKD-ETP-AVRVYTVCDESRYMIVRNVPALGCGDDLMRLFMTYGEVEEFAKRKLDE 57


             Pedant information for DKFZphfbr2_23o5, frame 3
             ----------------------------------------------

                      Report for DKFZphfbr2_23o5.3


[LENGTH]         360
[MW]             41105.85
[pI]             8.89
[HOMOL]          TREMBL:AC005824_10 gene: "F15K20.11"; Arabidopsis thaliana chromosome II BAC
F15K20 genomic sequence, complete sequence. 5e-12
[PROSITE]        AMIDATION       1
[PROSITE]        MYRISTYL        2
[PROSITE]        CK2_PHOSPHO_SITE       7
```

```
[PROSITE]       PKC_PHOSPHO_SITE        9
[PROSITE]       ASN_GLYCOSYLATION       3
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY      4.17 %

SEQ   MASSGGEPGSLFDHHVQRAVCDTRAKYREGRRPRAVKVYTINLESQYLLIQGVPAVGVMK
SEG   ............................................................
PRD   cccccccccceeeecceeeeehhhhhhhhhcccccceeeeeeeccccceeeeeeeccccchhhh

SEQ   ELVERFALYGAIEQYNALDEYPAEDFTEVYLIKFMNLQSARTAKRKMDEQSFFGGLLHVC
SEG   ............................................................
PRD   hhhhhhhhhhhhhhhhhhhcccccccceeeeeeehhhhhhhhhhhhhhhhhcccccccceeee

SEQ   YAPEFETVEETRKKLQMRKAYVVKTTENKDHYVTKKKLVTEHKDTEDFRQDFHSEMSGFC
SEG   ............................................................
PRD   ecchhhhhhhhhhhhhhhhhheeeeccccceeeeeeeeeeeecccccchhhhhhhhhhcccce

SEQ   KAALNTSAGNSNPYLPYSCELPLCYFSSKCMCSSGGPVDRAPDSSKDGRNHHKTMGHYNH
SEG   ............................................................
PRD   eeeeccccccccccccccccccccceeeeccccccccccccccccccccccccccccccccccc

SEQ   NDSLRKTQINSLKNSVACPGAQKAITSSEAVDRFMPRTTQLQERKRRREDDRKLGTFLQT
SEG   .......................................xxxxxxxxxxxxxxx......
PRD   ccccceeeeccccccccccccccccceeeeeecceeeeeecccccchhhhhhhhhhhccceeeeeeec

SEQ   NPTGNEIMIGPLLPDISKVDMHDDSLNTTANLIRHKLKEVFHLCQSLQRTSQKMYIQVIH
SEG   ............................................................
PRD   cccccceeeecccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhcchhhhhhhccc
```

Prosite for DKFZphfbr2_23o5.3

PS00001	185->189	ASN_GLYCOSYLATION	PDOC00001
PS00001	241->245	ASN_GLYCOSYLATION	PDOC00001
PS00001	327->331	ASN_GLYCOSYLATION	PDOC00001
PS00005	99->102	PKC_PHOSPHO_SITE	PDOC00005
PS00005	102->105	PKC_PHOSPHO_SITE	PDOC00005
PS00005	131->134	PKC_PHOSPHO_SITE	PDOC00005
PS00005	154->157	PKC_PHOSPHO_SITE	PDOC00005
PS00005	207->210	PKC_PHOSPHO_SITE	PDOC00005
PS00005	224->227	PKC_PHOSPHO_SITE	PDOC00005
PS00005	243->246	PKC_PHOSPHO_SITE	PDOC00005
PS00005	251->254	PKC_PHOSPHO_SITE	PDOC00005
PS00005	351->354	PKC_PHOSPHO_SITE	PDOC00005
PS00006	4->8	CK2_PHOSPHO_SITE	PDOC00006
PS00006	10->14	CK2_PHOSPHO_SITE	PDOC00006
PS00006	127->131	CK2_PHOSPHO_SITE	PDOC00006
PS00006	224->228	CK2_PHOSPHO_SITE	PDOC00006
PS00006	266->270	CK2_PHOSPHO_SITE	PDOC00006
PS00006	303->307	CK2_PHOSPHO_SITE	PDOC00006
PS00006	317->321	CK2_PHOSPHO_SITE	PDOC00006
PS00008	5->11	MYRISTYL	PDOC00008
PS00008	260->266	MYRISTYL	PDOC00008
PS00009	29->33	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_23o5.3)

DKFZphfbr2_2a2
----

group: brain derived

DKFZphfbr2_2a2.3 encodes a novel 167 amino acid protein with weak similarity to human 52K autoantigen Ro/SS-A

The novel protein contains a C3HC4 Zinc finger "RING finger" motive.
This domain is probably involved in mediating protein-protein interactions.
Proteins containing a RING-finger are: mammalian V(D)J recombination activating protein (RAG1), mouse rpt-1, human rfp, human 52 Kd Ro/SS-A protein and others.

No informative BLAST results; no predictive prosite, pfam or SCOP motife

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to 52K autoantigen Ro/SS-A - human

complete cDNA, complete cds, few EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1376 bp
Poly A stretch at pos. 1355, polyadenylation signal at pos. 1340

```
   1 GGGGACTCCA AATTAGAAAG GGGACGTCTA GTGGGTTGCC CGGGAGGGGT
  51 GGCGGGAGCG GTCCTGGAAA TAATCTGTCC TCTGTCGCCG GGAACTGGCG
 101 AGGTAGTTCC TTCGCGGTGG AGAGACCTGG AATGGCCAAA TATCAAGGTG
 151 AAGTTCAAAG TTTGAAACTG GATGATGATT CAGTTATAGA AGGAGTAAGC
 201 GACCAAGTAC TTGTGGCAGT TGTGGTCAGT TTCGCTTTGA TTGCTACCCT
 251 GGTATATGCA CTTTTCAGAA ATGTACATCA AAACATTCAC CCAGAAAACC
 301 AGGAGCTAGT AAGGGTACTT CGAGAACAGC TTCAAACAGA ACAGGATGCA
 351 CCTGCTGCCA CTCGACAGCA GTTCTACACT GACATGTACT GTCCCATCTG
 401 CCTGCACCAA GCCTCCTTCC CGGTGGAGAC CAACTGTGGA CATCTTTTTT
 451 GTGGTGCCTG CATTATTGCT TACTGGCGAT ATGGTTCATG GCTTGGGGCA
 501 ATCAGTTGTC CAATCTGTAG ACAAACGGTA ACCTTACTCC TAACAGTATT
 551 TGGTGAAGAT GATCAGTCTC AGGATGTTCT GAGATTGCAT CAGGATATTA
 601 ATGATTATAA CCGGAGATTC TCAGGGCAAC CCTGATCTAT TATGGAGAGA
 651 ATTATGGATC TACCCACTTT ACTGAGGCAT GCATTCAGGG AAATGTTTTC
 701 AGTCGGGGGC CTTTTCTGGA TGTTTCGCAT CAGGATAATA CTTTGTTTAA
 751 TGGGAGCTTT TTTCTATCTT ATATCACCTC TAGATTTTGT ACCTGAAGCC
 801 TTGTTTGGAA TTCTAGGCTT TCTAGATGAT TTCTTTGTCA TCTTTTTATT
 851 GCTTATCTAC ATCTCTATTA TGTATCGAGA AGTGATAACC CAAAGGCTAA
 901 CTAGATGAAA AAGGAAACAA AACTGAGTTT ACTAGGATAT CTGAGCTAAT
 951 GTAGAACATC AAACAGAAGG ACCCATGGCA GTATAAAGCA ATGAAGCAAT
1001 GGAGTATTAT CTCACAAATA TAAAACCACT ATAAGACAAA CATTTGATTA
1051 TCATTTGACA AATACCTAGG TATAACTGGA ATTTCATGT TTGAAGTTCT
1101 AATATTAAGT TTAGAATTAT AATGATCTAC AGTTGTATCT TGATTCTATG
1151 TTGTCTGGAA AAAATATGGA ATTATATAAA AAGGGATGCT TTTATATATT
1201 TTTCTTTTCC CCAGAATTAC TTAGATTAAT TAGATGTATA GTAAAATATT
1251 GTTAAATGTC AGTTTATCCA TCTTATCCTT CTCAGCAGGT ACCTATATGA
1301 TAATATATAG CTGTGAAACT CATCTAAATA TTTTTGTTCC AATAAAATAT
1351 TATATACTAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 132 bp to 632 bp; peptide length: 167
Category: similarity to known protein
Classification: unset

Prosite motifs: ZINC_FINGER_C3HC4 (102-112)

```
  1 MAKYQGEVQS LKLDDDSVIE GVSDQVLVAV VVSFALIATL VYALFRNVHQ
 51 NIHPENQELV RVLREQLQTE QDAPAATRQQ FYTDMYCPIC LHQASFPVET
101 NCGHLFCGAC IIAYWRYGSW LGAISCPICR QTVTLLLTVF GEDDQSQDVL
151 RLHQDINDYN RRFSGQP
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2a2, frame 3

TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid Y38F1A, N = 1, Score = 194, P = 2e-15

PIR:T05222 hypothetical protein F17I5.130 - Arabidopsis thaliana, N = 1, Score = 159, P = 1.4e-10

TREMBLNEW:AB025011_1 gene: "TRIF"; product: "Trif-d"; Mus musculus mRNA for Trif-d, complete cds., N = 1, Score = 108, P = 2.6e-06

PIR:A37241 52K autoantigen Ro/SS-A - human, N = 1, Score = 115, P = 5e-05

>TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid Y38F1A
Length = 283

HSPs:

Score = 194 (29.1 bits), Expect = 2.0e-15, P = 2.0e-15
Identities = 52/149 (34%), Positives = 78/149 (52%)

```
Query:    16 DSVIEGVSDQVLVAVVVSFALIATLVYALFRNVHQNIHPENQELVRVLREQLQTEQDAPA 75
             D  +E ++ Q+ +A+ V F ++  +  A       Q        E      R Q+ T++
Sbjct:    41 DPDVE-LATQITMAIAVIF-IVKAIFDAWQSRRRQRAASRMDENAE--RNQIITQRRISE 96

Query:    76 ATRQQFYTDMYCPICLHQASFPVETNCGHLFCGACIIAYWRYGSWLGA-ISCPICRQTVT 134
             A  Q  +     CPICL  ASFPV T+CGH+FC  CII YW+     +      C +CR T
Sbjct:    97 ALHQSSHE---CPICLANASFPVLTDCGHIFCCECIIQYWQQSKAIVTPCDCAMCRSTFY 153

Query:   135 LLLTV----FGEDDQSQDVLRLHQ-DINDYNRRFS 164
             +LL V      G  +++ D ++ +   I+DYNRRFS
Sbjct:   154 MLLPVHWPTMGTSEETDDHIQENNIRIDDYNRRFS 188
```

Pedant information for DKFZphfbr2_2a2, frame 3

Report for DKFZphfbr2_2a2.3

```
[LENGTH]     167
[MW]         18941.65
[pI]         4.91
[HOMOL]      TREMBL:CEY38F1A_8 gene: "Y38F1A.2"; Caenorhabditis elegans cosmid Y38F1A 1e-13

[FUNCAT]     06.10 assembly of protein complexes  [S. cerevisiae, YDR265w] 1e-04
[FUNCAT]     30.19 peroxisomal organization       [S. cerevisiae, YDR265w] 1e-04
[FUNCAT]     99 unclassified proteins    [S. cerevisiae, YLR323c] 2e-04
[BLOCKS]     BL00518 Zinc finger, C3HC4 type, proteins
[PROSITE]    ZINC_FINGER_C3HC4     1
[PFAM]       Zinc finger, C3HC4 type (RING finger)
[KW]         Irregular
[KW]         3D
[KW]         LOW_COMPLEXITY     6.59 %
```

```
SEQ    MAKYQGEVQSLKLDDDSVIEGVSDQVLVAVVVSFALIATLVYALFRNVHQNIHPENQELV
SEG    .....................xxxxxxxxxxx............................
1rmd-  ............................................................

SEQ    RVLREQLQTEQDAPAATRQQFYTDMYCPICLHQASFPVETNCGHLFCGACIIAYWRYGSW
SEG    ............................................................
1rmd-  ...................HHHHHHBTTTTEETTTEEEETTTEEEEHHHHH---HHHHH

SEQ    LGAISCPICRQTVTLLLTVFGEDDQSQDVLRLHQDINDYNRRFSGQP
```

```
SEG     ................................................................
1rmd-   HCCB-TTTTT..........................................................
```

Prosite for DKFZphfbr2_2a2.3

```
PS00518     102->112    ZINC_FINGER_C3HC4      PDOC00449
```

Pfam for DKFZphfbr2_2a2.3

```
HMM_NAME       Zinc finger, C3HC4 type (RING finger)

HMM               *CPICFcTFQlDyPWPFdePmMlPCgHsFCypCIrrW...........CP
                   CPIC      L+        P++++CGH+FC +CI+ +            CP
Query           87 CPIC-----LHQ---ASFPVETNCGHLFCGACIIAYWRYGSWLGAISCP   127

HMM               mC*
                  +C
Query          128 IC     129
```

DKFZphfbr2_2b17
----

group: transmembrane protein

DKFZphfbr2_2b17 encodes a novel 285 amino acid protein with similarity to D. melanogaster 30K protein.

The protein contains 3 transmembrane regions.
No informative BLAST results; no predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to Drosophila hypothetical 30K protein

complete cDNA, complete cds, EST hits
TRANSMEMBRANE 3

Sequenced by Qiagen

Locus: unknown

Insert length: 1426 bp
Poly A stretch at pos. 1345, polyadenylation signal at pos. 1330

```
   1 GGGGGTATTT CCAAGGACTC CAAAGCGAGG CCGGGGACTG AAGGTGTGGG
  51 TGTCGAGCCC TCTGGCAGAG GGTTAACCTG GGTCAAATGC ACGGATTCTC
 101 ACCTCGTACA GTTACGCTCT CCCGCGGCAC GTCCGCGAGG ACTTGAAGTC
 151 CTGAGCGCTC AAGTTTGTCC GTAGGTCGAG AGAAGGCCAT GGAGGTGCCG
 201 CCACCGGCAC CGCGGAGCTT TCTCTGTAGA GCATTGTGCC TATTTCCCCG
 251 AGTCTTTGCT GCCGAAGCTG TGACTGCCGA TTCGGAAGTC CTTGAGGAGC
 301 GTCAGAAGCG GCTTCCCTAC GTCCCAGAGC CCTATTACCC GGAATCTGGA
 351 TGGGACCGCC TCCGGGAGCT GTTTGGCAAA GATGAACAGC AGAGAATTTC
 401 AAAGGACCTT GCTAATATCT GTAAGACGGC GGCTACAGCA GGCATCATTG
 451 GCTGGGTGTA TGGGGGAATA CCAGCTTTTA TTCATGCTAA ACAACAATAC
 501 ATTGAGCAGA GCCAGGCAGA AATTTATCAT AACCGGTTTG ATGCTGTGCA
 551 ATCTGCACAT CGTGCTGCCA CACGAGGCTT CATTCGTTAT GGCTGGCGCT
 601 GGGGTTGGAG AACTGCAGTG TTTGTGACTA TATTCAACAC AGTGAACACT
 651 AGTCTGAATG TATACCGAAA TAAAGATGCC TTAAGCCATT TTGTAATTGC
 701 AGGAGCTGTC ACGGGAAGTC TTTTTAGGAT AAACGTAGGC CTGCGTGGCC
 751 TGGTGGCTGG TGGCATAATT GGAGCCTTGC TGGGCACTCC TGTAGGAGGC
 801 CTGCTGATGG CATTTCAGAA GTACTCTGGT GAGACTGTTC AGGAAAGAAA
 851 ACAGAAGGAT CGAAAGGCAC TCCATGAGCT AAAACTGGAA GAGTGGAAAG
 901 GCAGACTACA AGTTACTGAG CACCTCCCTG AGAAAATTGA AAGTAGTTTA
 951 CAGGAAGATG AACCTGAGAA TGATGCTAAG AAAATTGAAG CACTGCTAAA
1001 CCTTCCTAGA AACCCTTCAG TAATAGATAA ACAAGACAAG GACTGAAAGT
1051 GCTCTGAACT TGAAACTCAC TGGAGAGCTG AAGGGAGCTG CCATGTCCGA
1101 TGAATGCCAA CAGACAGGCC ACTCTTTGGT CAGCCTGCTG ACAAATTTAA
1151 GTGCTGGTAC CTGTGGTGGC AGTGGCTTGC TCTTGTCTTT TTCTTTTCTT
1201 TTTAACTAAG AATGGGGCTG TTGTACTCTC ACTTTACTTA TCCTTAAATT
1251 TAAATACATA CTTATGTTTG TATTAATCTA TCAATATATG CATACATGAA
1301 TATATCCACC CACCTAGATT TTAAGCAGTA AATAAAACAT TTCGCAAAAG
1351 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HSG19630 from database EMBL:
human STS A001T27.
Score = 961, P = 1.2e-36, identities = 193/194

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 189 bp to 1043 bp; peptide length: 285
Category: similarity to unknown protein

```
  1 MEVPPPAPRS FLCRALCLFP RVFAAEAVTA DSEVLEERQK RLPYVPEPYY
 51 PESGWDRLRE LFGKDEQQRI SKDLANICKT AATAGIIGWV YGGIPAFIHA
101 KQQYIEQSQA EIYHNRFDAV QSAHRAATRG FIRYGWRWGW RTAVFVTIFN
151 TVNTSLNVYR NKDALSHFVI AGAVTGSLFR INVGLRGLVA GGIIGALLGT
201 PVGGLLMAFQ KYSGETVQER KQKDRKALHE LKLEEWKGRL QVTEHLPEKI
251 ESSLQEDEPE NDAKKIEALL NLPRNPSVID KQDKD
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2b17, frame 3

PIR:JQ1024 hypothetical 30K protein (DmRP140 5' region) - fruit fly (Drosophila melanogaster), N = 1, Score = 312, P = 6.1e-28

```
>PIR:JQ1024 hypothetical 30K protein (DmRP140 5' region) - fruit fly
     (Drosophila melanogaster)
          Length = 261

  HSPs:

 Score = 312 (46.8 bits), Expect = 6.1e-28, P = 6.1e-28
 Identities = 68/231 (29%), Positives = 125/231 (54%)

Query:    30 ADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKDEQQRISKDLANICKTAATAGIIGW 89
             AD  V +E +     ++        E+G +RL+++F  DE    I  +L ++ +       +IG
Sbjct:    23 ADEIVDKENKTYKAFLASKPPEETGLERLKQMFTIDEFGSIFSELNSVYQAGFLGFLIGA 82

Query:    90 VYGGIPAFIHAKQQYIEQSQAEIYHNRFDAVQSAHRAATRGFIRYGWRWGWRTAVFVTIF 149
             +YGG+      A   ++E +QA  + + FDA +       T  F + G++WGWR  +F T +
Sbjct:    83 IYGGVTQSRVAYMNFMENNQATAFKSHFDAKKKLQDQFTVNFAKGGFKWGWRVGLFTTSY 142

Query:   150 NTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAF 209
               + T ++VYR K ++ ++ AG++TGSL+++++GLRG+ AGGIIG  LG   G   +
Sbjct:   143 FGIITCMSVYRGKSSIYEYLAAGSITGSLYKVSLGLRGMAAGGIIGGFLGGVAGVTSLLL 202

Query:   210 QKYSGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPEKIESSLQEDEPE 260
               K SG +++E             ++  ++K RL   E++ +  +   +++ PE
Sbjct:   203 MKASGTSMEE-----------VRYWQYKWRLDRDENIQQAFKKLTEDENPE 242
```

Pedant information for DKFZphfbr2_2b17, frame 3

Report for DKFZphfbr2_2b17.3

```
[LENGTH]        285
[MW]            32177.88
[pI]            8.65
[HOMOL]         PIR:JQ1024 hypothetical 30K protein (DmRP140 5' region) - fruit fly (Drosophila
melanogaster) 7e-20
[PROSITE]       MYRISTYL        7
[PROSITE]       CK2_PHOSPHO_SITE        5
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            SIGNAL_PEPTIDE 25
[KW]            TRANSMEMBRANE  3
[KW]            LOW_COMPLEXITY     5.96 %

SEQ   MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRE
SEG   ............................................................
PRD   cccccccceeeeeeeeeehhhhhhhhhhhhhhhhhhhhhhhhhccccccccccchhhhhh
MEM   ............................................................

SEQ   LFGKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEIYHNRFDAV
SEG   ............................................................
PRD   hhccchhhhhhhhhhhhhhhhhhccceeeecccccchhhhhhhhhhhhhhhhhhhhhhhh
MEM   ...........MMMMMMMMMMMMMMMMMMMMMMMMMMMMM..................

SEQ   QSAHRAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFR
SEG   ............................................................
PRD   hhhhhhhhhhhcccccccccceeeeeeeeccccccceeeccccccccceeeeecccccceee
MEM   .................MMMMMMMMMMMMMMMMMMMMMMMMMMM................M

SEQ   INVGLRGLVAGGIIGALLGTPVGGLLMAFQKYSGETVQERKQKDRKALHELKLEEWKGRL
```

```
SEG    ..xxxxxxxxxxxxxxxxx.........................................
PRD    eeccccccccccEeeeeccccccchhhhhhhccchhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM    MMMMMMMMMMMMMMMMMMMMMMMMMMMM................................

SEQ    QVTEHLPEKIESSLQEDEPENDAKKIEALLNLPRNPSVIDKQDKD
SEG    .............................................
PRD    ccccccccchhhhhccccccchhhhhhhhhccccccceeeccccc
MEM    .............................................
```

Prosite for DKFZphfbr2_2b17.3

PS00001	153->157	ASN_GLYCOSYLATION	PDOC00001
PS00006	53->57	CK2_PHOSPHO_SITE	PDOC00006
PS00006	108->112	CK2_PHOSPHO_SITE	PDOC00006
PS00006	216->220	CK2_PHOSPHO_SITE	PDOC00006
PS00006	253->257	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	172->178	MYRISTYL	PDOC00008
PS00008	187->193	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00008	195->201	MYRISTYL	PDOC00008
PS00008	199->205	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_2b17.3)

DKFZphfbr2_2b5
----

group: cell structure and motility

DKFZphfbr2_2b5 encodes a novel 957 amino acid protein with strong similarity to collagens.

The novel protein contains the typical (xxG)n repeat of collagen proteins and a Pfam von Willebrand factor type A domain. Therefore, the protein seems to be a new collagen alpha chain.

The new protein can find application in modulation of connective tissue, bone and cartilage development and maintainance.

similarity to collagen proteins

shows typical (xxG)n repeat of collagen proteins
[PFAM] von Willebrand factor type A domain

Sequenced by Qiagen

Locus: /map="6"

Insert length: 4160 bp
Poly A stretch at pos. 4141, polyadenylation signal at pos. 4119

```
   1 GGGGGCCCGC TGCAGGGAGA ACGGACTCCG GGCGGAGGGC AGCCAATCCG
  51 TTTCAGCGCA GGTCTTGCTC GGGTTGGGCT TGCCACTGCC TGGAACATAC
 101 CTGTCCCCCT GGCGCAACAC TCAGCTGGCT GCGACCGCAA CCCCGAGCCT
 151 GGACACTGCG CCAGGAATCC TAAAACCAAA ATATTAGAAC GAAAACAGAA
 201 ACATGGCTCA CTATATTACA TTTCTCTGCA TGGTTTTGGT GCTGCTTCTT
 251 CAGAATTCTG TGTTAGCTGA AGATGGGGAA GTAAGATCAA GTTGTCGTAC
 301 TGCTCCGACA GATTTAGTTT TCATCTTAGA TGGCTCTTAT AGTGTTGGCC
 351 CAGAAAACTT TGAAATAGTG AAAAAGTGGC TTGTCAATAT CACAAAAAAC
 401 TTTGACATAG GGCCGAAGTT TATTCAAGTT GGAGTGGTTC AATATAGTGA
 451 CTACCCTGTG CTGGAGATTC CTCTCGGAAG CTATGATTCA GGAGAACATT
 501 TGACGGCAGC AGTGGAATCC ATACTCTACT TAGGAGGAAA CACAAAGACA
 551 GGGAAGGCCA TCCAGTTTGC GCTCGATTAC CTTTTTGACA AGTCCTCACG
 601 ATTTCTGACT AAGATAGCAG TGGTACTTAC GGATGGCAAG TCCCAAGATG
 651 ACGTCAAGGA TGCAGCTCAA GCAGCAAGAG ATAGTAAGAT AACATTATTT
 701 GCTATTGGTG TTGGTTCAGA AACAGAAGAT GCCGAACTTA GAGCTATTGC
 751 CAACAAGCCT TCGTCTACTT ATGTGTTTTA TGTGGAAGAC TATATTGCAA
 801 TATCCAAAAT AAGGGAAGTG ATGAAGCAGA AACTTTGTGA AGAATCTGTC
 851 TGTCCAACAC GAATTCCAGT GGCAGCTCGT GATGAAAGGG GATTTGATAT
 901 TCTTTTGGGT TTAGATGTAA ATAAAAAGGT TAAGAAAAGA ATACAGCTTT
 951 CACCAAAAAA GATAAAAGGA TATGAAGTAA CATCAAAAGT TGATTTATCA
1001 GAACTCACAA GCAATGTTTT CCCAGAAGGT CTTCCTCCAT CATATGTATT
1051 TGTGTCTACT CAAAGATTTA AAGTCAAGAA AATTTGGGAT TTATGGAGAA
1101 TATTAACTAT TGATGGAAGG CCACAAATAG CAGTTACCTT AAATGGTGTG
1151 GACAAAATCT TATTATTTAC AACAACCAGC GTAATTAATG GCTCACAAGT
1201 GGTTACCTTT GCTAACCCTC AAGTTAAGAC GTTGTTTGAT GAAGGCTGGC
1251 ACCAAATTCG TCTCTTAGTA ACAGAACAAG ATGTGACTTT GTATATTGAT
1301 GACCAACAAA TTGAAAACAA GCCCTTACAT CCAGTTTTAG GGATCTTGAT
1351 CAATGGGCAA ACCCAAATTG GAAAATATTC TGGAAAAGAA GAAACTGTTC
1401 AGTTTGATGT CCAAAAGTTG CGAATCTACT GTGACCCAGA ACAGAACAAC
1451 CGGGAGACAG CATGTGAGAT TCCTGGATTT AATGGAGAGT GCCTTAATGG
1501 TCCCAGTGAT GTAGGTTCAA CTCCAGCTCC CTGTATTTGT CCTCCGGGAA
1551 AACCAGGACT TCAAGGCCCC AAAGGTGACC CTGGACTGCC TGGGAACCCT
1601 GGCTACCCTG GACAACCTGG TCAAGATGGT AAGCCTGGAT ATCAGGGAAT
1651 TGCAGGGACA CCAGGTGTTC CAGGATCTCC AGGAATACAA GGAGCTCGAG
1701 GACTACCAGG TTACAAAGGA GAACCAGGGC GAGATGGTGA CAAGGGTGAT
1751 CGTGGACTTC CTGGTTTTCC TGGGCTTCAT GGCATGCCAG GATCAAAGGG
1801 TGAAATGGGT GCCAAAGGAG ACAAAGGATC ACCTGGATTT TATGGCAAAA
1851 AGGGTGCAAA AGGTGAAAAG GGGAATGCTG GCTTCCCTGG CCTCCCTGGA
1901 CCTGCTGGAG AACCAGGAAG ACATGGAAAG GATGGATTAA TGGGTAGTCC
1951 CGGTTTCAAG GGAGAAGCAG GATCCCCTGG TGCTCCGGGG CAGGATGGAA
2001 CACGGGGAGA GCCTGGAATC CCAGGATTTC CTGGAAACCG AGGATTAATG
2051 GGCCAAAAGG GAGAAATTGG GCCTCCAGGA CAGCAAGGAA AAAAAGGAGC
2101 CCCAGGGATG CCTGGTTTAA TGGGAAGCAA TGGCTCACCA GGCCAGCCTG
2151 GAACACCGGG ATCTAAGGGA AGCAAAGGTG AACCTGGAAT TCAAGGGATG
2201 CCTGGGGCTT CAGGGCTCAA GGGAGAACCA GGAGCAACGG GTTCCCCAGG
2251 AGAACCAGGA TACATGGGTT TACCCGGGAT TCAAGGAAAA AAGGGGGACA
2301 AAGGAAATCA AGGTGAAAAA GGTATTCAGG GTCAAAAGGG AGAAAATGGA
2351 AGACAGGGAA TTCCAGGGCA ACAGGGAATT CAAGGCCATC ATGGTGCAAA
2401 AGGAGAGAGA GGTGAAAAGG GAGAACCTGG TGTCCGAGGT GCCATTGGAT
2451 CAAAAGGAGA ATCTGGGGTG GATGGCTTGA TGGGGCCCGC AGGTCCTAAG
2501 GGCAACCTGG GGATCCAGGG TCCTCAGGGA CCCCCAGGTT TGGATGGGAA
2551 GCCCGGAAGA GAGTTTTCAG AACAATTTAT TCGACAAGTT TGCACAGATG
```

```
2601 TAATAAGAGC CCAGCTACCA GTCTTACTTC AGAGTGGAAG AATTAGAAAT
2651 TGTGATCATT GCCTGTCCCA ACATGGCTCC CCGGGTATTC CTGGGCCACC
2701 TGGTCCGATA GGCCCAGAGG GTCCCAGAGG ATTACCTGGT TTGCCAGGAA
2751 GAGATGGTGT TCCTGGATTA GTGGGTGTCC CTGGACGTCC AGGTGTCAGA
2801 GGATTAAAAG GCCTACCAGG AAGAAATGGG GAAAAAGGGA GCCAAGGGTT
2851 TGGGTATCCT GGAGAACAAG GTCCTCCTGG TCCCCCAGGT CCAGAGGGCC
2901 CTCCTGGAAT AAGCAAAGAA GGTCCTCCAG GAGACCCAGG TCTCCCTGGC
2951 AAAGATGGAG ACCATGGAAA ACCTGGAATC CAAGGGCAAC CAGGCCCCCC
3001 AGGCATCTGC GACCCATCAC TATGTTTTAG TGTAATTGCC AGAAGAGATC
3051 CGTTCAGAAA AGGACCAAAC TATTAGTGTC TGATGCCTCA TTCAGCAGCC
3101 TAGGCATGGT GCTTTTTCTG TGGTCTTTTG CATCTCAGGA AGATAACCAA
3151 CAGTATCCCT TGAAAAGAAA CTTAAGTACC TCGGTGTTTT TATTTTTTTT
3201 TTCTTATGGA AAAAAATATA AAAGATCACA TATACTGATT TTAAAGGCTC
3251 CTCAGTCATT TGGAGCCCTT GGATTAGCAG CATTAATTAA ATCTCAAGGG
3301 TTTCTTGTAA AGTCCATTTA TGTTAATCAA AGTTGAATAT AAAAATCCAC
3351 CATTGCCTGT TAGCCAGTCA GTTTTAGTCA CTGTGAAATA TTTCACATTC
3401 AGCCTCCATG CAGTAGAGAT TTGAGTTTAA TTTCATGTCC ATGTGACTTT
3451 CATGTTTCCT ATCTCATAGC TCATGCTACT ACATAAGCCA AAACATGTAT
3501 CTCATCATTG GAAGTAAGAT CAGGGCTGAT ATTCACCTGG GATAGACAGT
3551 ATTGGTGAAC TACTCATTTA CTACAGTGTC TCAGCCTTGA TAAAGGGCAG
3601 TGGATTGCCT GTTGTTCGGT GTTGTGAATA GCACCTCTGA ATAAGATTAG
3651 AGTGTTTCTT AATTCATTTC AAACTCTAAA ATTAGATTAA TGGTGGTGCT
3701 AAGAAAGAGT ATTAATTACT TTGGGAATGG TCAAAATTAA CATTAAAAAC
3751 ATTTTAGACA AAAAGTTTCA TTGTACATTC AAAGAAAATG TAAGTTTGGA
3801 AGTACTAAAA GACTATTTTA TACTTGTTGA TTAATCGGAA TGTTTGTTGT
3851 ATGCCTTCAT TTTCCATTTC ACTTATATGT GCATGTCCAT ATATGTTAAT
3901 TTTCATTGTA GCAAAGCTAA TGGAAATAAA GCTAATGCTC TAGTTGAAAG
3951 AAAAGGAAAA CTCCTGAAAT CCTAGAATGT CTTGTTATTT TTAGCTGACT
4001 GTAAAATATT ATGAACAGTC TTTGTGTATT GTGCTTAATG CTTTTGTAAG
4051 AAACAGAATT TGAAATATTT CATCCTTGTC ATGCTCAAAA TTTTGTTACA
4101 TGCTTGTTAT TCAGAGTATA ATAAAGTTTT GTACAGGCCT GAAAAAAAAA
4151 AAAAAAAAAA
```

BLAST Results

Entry HS682J15 from database EMBLNEW:
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 682J15
Score = 6240, P = 0.0e+00, identities = 1256/1263
13 exons matching Bp 2015-4118

Entry HS708F5 from database EMBLNEW:
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 708F5
Score = 2775, P = 1.0e-221, identities = 739/912
10 exons matching Bp 5-1745

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 203 bp to 3073 bp; peptide length: 957
Category: similarity to known protein

```
  1 MAHYITFLCM VLVLLLQNSV LAEDGEVRSS CRTAPTDLVF ILDGSYSVGP
 51 ENFEIVKKWL VNITKNFDIG PKFIQVGVVQ YSDYPVLEIP LGSYDSGEHL
101 TAAVESILYL GGNTKTGKAI QFALDYLFDK SSRFLTKIAV VLTDGKSQDD
151 VKDAAQAARD SKITLFAIGV GSETEDAELR AIANKPSSTY VFYVEDYIAI
201 SKIREVMKQK LCEESVCPTR IPVAARDERG FDILLGLDVN KKVKKRIQLS
251 PKKIKGYEVT SKVDLSELTS NVFPEGLPPS YVFVSTQRFK VKKIWDLWRI
301 LTIDGRPQIA VTLNGVDKIL LFTTTSVING SQVVTFANPQ VKTLFDEGWH
351 QIRLLVTEQD VTLYIDDQQI ENKPLHPVLG ILINGQTQIG KYSGKEETVQ
401 FDVQKLRIYC DPEQNNRETA CEIPGFNGEC LNGPSDVGST PAPCICPPGK
451 PGLQGPKGDP GLPGNPGYPG QPGQDGKPGY QGIAGTPGVP GSPGIQGARG
501 LPGYKGEPGR DGDKGDRGLP GFPGLHGMPG SKGEMGAKGD KGSPGFYGKK
551 GAKGEKGNAG FPGLPGPAGE PGRHGKDGLM GSPGFKGEAG SPGAPGQDGT
601 RGEPGIPGFP GNRGLMGQKG EIGPPGQQGK KGAPGMPGLM GSNGSPGQPG
651 TPGSKGSKGE PGIQGMPGAS GLKGEPGATG SPGEPGYMGL PGIQGKKGDK
701 GNQGEKGIQG QKGENGRQGI PGQQGIQGHH GAKGERGEKG EPGVRGAIGS
751 KGESGVDGLM GPAGPKGQPG DPGPQGPPGL DGKPGREFSE QFIRQVCTDV
801 IRAQLPVLLQ SGRIRNCDHC LSQHGSPGIP GPPGPIGPEG PRGLPGLPGR
```

```
851 DGVPGLVGVP GRPGVRGLKG LPGRNGEKGS QGFGYPGEQG PPGPPGPEGP
901 PGISKEGPPG DPGLPGKDGD HGKPGIQGQP GPPGICDPSL CFSVIARRDP
951 FRKGPNY
```

BLASTP hits

Entry HSCOL7A1X_1 from database TREMBL:
gene: "COL7A1"; product: "collagen type VII"; Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.
Score = 949, P = 3.4e-122, identities = 237/553, positives = 281/553

Entry CA17_HUMAN from database SWISSPROT:
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN). >TREMBL:HSCOL7A1_1 gene: "COL7A1"; product: "alpha-1 type VII collagen"; Human alpha-1 type VII collagen (COL7A1) mRNA, complete cds.
Score = 949, P = 3.6e-122, identities = 237/553, positives = 281/553

Alert BLASTP hits for DKFZphfbr2_2b5, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2b5, frame 2

Report for DKFZphfbr2_2b5.2

[LENGTH]	957
[MW]	99413.38
[pI]	8.49
[HOMOL]	PIR:A40020 collagen alpha 1(XII) chain precursor - chicken 9e-90
[BLOCKS]	BL01119B Copper-fist domain proteins
[BLOCKS]	BL00313B
[BLOCKS]	BL01113A C1q domain proteins
[BLOCKS]	BL00420A Speract receptor repeat proteins domain proteins
[SCOP]	d1zoob_ 3.45.1.1.1 Integrin CD11a/CD18 (LFA-1) [Human (Hom 2e-58
[SCOP]	d1ido__ 3.45.1.1.2 Integrin CR3 (CD11b/CD18), alpha subunit [Huma 8e-62
[EC]	3.1.1.7 Acetylcholinesterase 7e-24
[PIRKW]	blocked amino end 1e-43
[PIRKW]	duplication 7e-46
[PIRKW]	cornea 1e-35
[PIRKW]	lung 2e-40
[PIRKW]	leukocyte 1e-42
[PIRKW]	skin 1e-40
[PIRKW]	transmembrane protein 1e-37
[PIRKW]	cartilage 3e-59
[PIRKW]	hydroxylysine 4e-62
[PIRKW]	connective tissue 3e-43
[PIRKW]	triple helix 5e-82
[PIRKW]	homotrimer 2e-37
[PIRKW]	bone 6e-40
[PIRKW]	Alport syndrome 1e-42
[PIRKW]	laminin binding 2e-40
[PIRKW]	liver 2e-40
[PIRKW]	glycoprotein 5e-82
[PIRKW]	carboxylic ester hydrolase 7e-24
[PIRKW]	disulfide bond 7e-46
[PIRKW]	cell binding 7e-46
[PIRKW]	heterotrimer 4e-62
[PIRKW]	calcium binding 8e-28
[PIRKW]	alternative splicing 5e-82
[PIRKW]	coiled coil 5e-82
[PIRKW]	basement membrane 7e-46
[PIRKW]	trimer 5e-82
[PIRKW]	pyroglutamic acid 3e-43
[PIRKW]	hydroxyproline 4e-62
[PIRKW]	extracellular matrix 5e-82
[PIRKW]	chondroitin sulfate proteoglycan 6e-41
[PIRKW]	sulfoprotein 7e-39
[PIRKW]	kidney 1e-42
[PIRKW]	angiogenesis inhibitor 6e-36
[PIRKW]	Ehlers-Danlos syndrome 2e-40
[SUPFAM]	fibronectin type III repeat homology 5e-82
[SUPFAM]	scavenger receptor cysteine-rich domain homology 1e-37
[SUPFAM]	C-type lectin homology 6e-30
[SUPFAM]	collagen alpha 2(I) chain 5e-40
[SUPFAM]	collagen alpha 1(I) chain 6e-44

```
[SUPFAM]        fibrillar collagen carboxyl-terminal homology 6e-44
[SUPFAM]        animal Kunitz-type proteinase inhibitor homology 2e-38
[SUPFAM]        fibronectin type II repeat homology 6e-21
[SUPFAM]        complement C1q carboxyl-terminal homology 1e-38
[SUPFAM]        collagen alpha 3(VI) chain 2e-31
[SUPFAM]        collagen alpha 1(IV) chain 7e-46
[SUPFAM]        collagen alpha 1(VI) chain 2e-37
[SUPFAM]        von Willebrand factor type C repeat homology 6e-44
[SUPFAM]        unassigned collagens 4e-62
[SUPFAM]        von Willebrand factor type A repeat homology 5e-82
[SUPFAM]        collagen alpha 1(XIV) chain 5e-82
[SUPFAM]        pulmonary surfactant protein D 6e-30
[SUPFAM]        collagen alpha 1(V) chain 7e-39
[SUPFAM]        collagen alpha 1(VIII) chain 1e-38
[SUPFAM]        EGF homology 1e-35
[PROSITE]       AMIDATION       3
[PROSITE]       MYRISTYL        14
[PROSITE]       CK2_PHOSPHO_SITE        13
[PROSITE]       PKC_PHOSPHO_SITE        8
[PROSITE]       ASN_GLYCOSYLATION       2
[PFAM]          von Willebrand factor type A domain
[KW]            Irregular
[KW]            3D
[KW]            SIGNAL_PEPTIDE 23
[KW]            LOW_COMPLEXITY    24.24 %

SEQ     MAHYITFLCMVLVLLLQNSVLAEDGEVRSSCRTAPTDLVFILDGSYSVGPENFEIVKKWL
SEG     ............................................................
1atzB   ................................CCCEEEEEEEECCCCCCHHHHHHHHHHH

SEQ     VNITKNFDIGPKFIQVGVVQYSDYPVLEIPLGSYDSGEHLTAAVESILYLGGNTKTGKAI
SEG     ............................................................
1atzB   HHHHHHCCBTTTTEEEEEEEEETTTEEEEETTTTTTHHHHHHHHHHCCCCCCCCCHHHHH

SEQ     QFALDYLFDKSSRFLTKIAVVLTDGKSQDDVKDAAQAARDSKITLFAIGVGSETEDAELR
SEG     ............................................................
1atzB   HHHHHHHHCCTTTTTEEEEEEEECCCTTTTHHHHHHHHHHCEEEEEEEEECCCCCHHHHH

SEQ     AIANKPSSTYVFYVEDYIAISKIREVMKQKLCEESVCPTRIPVAARDERGFDILLGLDVN
SEG     ............................................................
1atzB   HHHGGGGGGGCECCHHHHHHHHHCHHHHHHHH............................

SEQ     KKVKKRIQLSPKKIKGYEVTSKVDLSELTSNVFPEGLPPSYVFVSTQRFKVKKIWDLWRI
SEG     ............................................................
1atzB   ............................................................

SEQ     LTIDGRPQIAVTLNGVDKILLFTTTSVINGSQVVTFANPQVKTLFDEGWHQIRLLVTEQD
SEG     ............................................................
1atzB   ............................................................

SEQ     VTLYIDDQQIENKPLHPVLGILINGQTQIGKYSGKEETVQFDVQKLRIYCDPEQNNRETA
SEG     ............................................................
1atzB   ............................................................

SEQ     CEIPGFNGECLNGPSDVGSTPAPCICPPGKPGLQGPKGDPGLPGNPGYPGQPGQDGKPGY
SEG     ..........................xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
1atzB   ............................................................

SEQ     QGIAGTPGVPGSPGIQGARGLPGYKGEPGRDGDKGDRGLPGFPGLHGMPGSKGEMGAKGD
SEG     xx..........................................................
1atzB   ............................................................

SEQ     KGSPGFYGKKGAKGEKGNAGFPGLPGPAGEPGRHGKDGLMGSPGFKGEAGSPGAPGQDGT
SEG     ......xxxxxxxxxxxxx.........................................
1atzB   ............................................................

SEQ     RGEPGIPGFPGNRGLMGQKGEIGPPGQQGKKGAPGMPGLMGSNGSPGQPGTPGSKGSKGE
SEG     ................xxxxxxxxxxxxxxxxxxxxxx......................
1atzB   ............................................................

SEQ     PGIQGMPGASGLKGEPGATGSPGEPGYMGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGI
SEG     .......................................xxxxxxxxxxxxxxxxxxxxx
1atzB   ............................................................

SEQ     PGQQGIQGHHGAKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQGPPGL
SEG     xxxxxxxxxxx.............................xxxxxxxxxxxxxxxxxxxx
1atzB   ............................................................

SEQ     DGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDHCLSQHGSPGIPGPPGPIGPEG
SEG     xxxxx.......................................xxxxxxxxxxxxxxxx
```

```
latzB   ............................................................

SEQ     PRGLPGLPGRDGVPGLVGVPGRPGVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGP
SEG     xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.......xxxxxxxxxxxxxxxxxxx
latzB   ............................................................

SEQ     PGISKEGPPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPFRKGPNY
SEG     xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx......................
latzB   .........................................................
```

Prosite for DKFZphfbr2_2b5.2

PS00001	62->66	ASN_GLYCOSYLATION	PDOC00001
PS00001	329->333	ASN_GLYCOSYLATION	PDOC00001
PS00005	30->33	PKC_PHOSPHO_SITE	PDOC00005
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00005	131->134	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	260->263	PKC_PHOSPHO_SITE	PDOC00005
PS00005	286->289	PKC_PHOSPHO_SITE	PDOC00005
PS00005	393->396	PKC_PHOSPHO_SITE	PDOC00005
PS00005	811->814	PKC_PHOSPHO_SITE	PDOC00005
PS00006	147->151	CK2_PHOSPHO_SITE	PDOC00006
PS00006	172->176	CK2_PHOSPHO_SITE	PDOC00006
PS00006	261->265	CK2_PHOSPHO_SITE	PDOC00006
PS00006	343->347	CK2_PHOSPHO_SITE	PDOC00006
PS00006	357->361	CK2_PHOSPHO_SITE	PDOC00006
PS00006	393->397	CK2_PHOSPHO_SITE	PDOC00006
PS00006	419->423	CK2_PHOSPHO_SITE	PDOC00006
PS00006	531->535	CK2_PHOSPHO_SITE	PDOC00006
PS00006	600->604	CK2_PHOSPHO_SITE	PDOC00006
PS00006	657->661	CK2_PHOSPHO_SITE	PDOC00006
PS00006	681->685	CK2_PHOSPHO_SITE	PDOC00006
PS00006	750->754	CK2_PHOSPHO_SITE	PDOC00006
PS00006	754->758	CK2_PHOSPHO_SITE	PDOC00006
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	112->118	MYRISTYL	PDOC00008
PS00008	236->242	MYRISTYL	PDOC00008
PS00008	276->282	MYRISTYL	PDOC00008
PS00008	380->386	MYRISTYL	PDOC00008
PS00008	494->500	MYRISTYL	PDOC00008
PS00008	527->533	MYRISTYL	PDOC00008
PS00008	596->602	MYRISTYL	PDOC00008
PS00008	638->644	MYRISTYL	PDOC00008
PS00008	650->656	MYRISTYL	PDOC00008
PS00008	653->659	MYRISTYL	PDOC00008
PS00008	665->671	MYRISTYL	PDOC00008
PS00008	743->749	MYRISTYL	PDOC00008
PS00008	746->752	MYRISTYL	PDOC00008
PS00009	547->551	AMIDATION	PDOC00009
PS00009	628->632	AMIDATION	PDOC00009
PS00009	694->698	AMIDATION	PDOC00009

Pfam for DKFZphfbr2_2b5.2

```
HMM_NAME        von Willebrand factor type A domain

HMM                 *DIVFLIDGSdSIGpqNFNrMKDFIeRMMERMDIgPDwIRVGVVQYSdNP
                     D+VF++DGS S+GP NF+++K+ ++++  ++DIGP+ I+VGVVQYSD P
Query            37  DLVFILDGSYSVGPENFEIVKKWLVNITKNFDIGPKFIQVGVVQYSDYP    85

HMM                 RqEmrFmFNDYQNKeEILQaIqqMMyWMgggTNTGeAIQYVvrNMFweer
                      E  +++  Y + E++++A+  ++ ++GG T+TG AIQ++++++F +++
Query            86 VLE--IPLGSYDSGEHLTAAVESIL-YLGGNTKTGKAIQFALDYLFDKSS   132

HMM                 GmRWenvPQVMIIITDGRSQDDIRDpIneMrrmaGIqvFaIGIGNhDNnn
                    +      +++++++TDG+SQDD++D+++++R+   I+ FAIG+G
Query           133 RF----LTKIAVVLTDGKSQDDVKDAAQAARD-SKITLFAIGVGSETE--   175

HMM                 WeELReIASePdEdHVFyVdDFeeLdnMqeqL*
                     +ELR IA++P++ +VFYV+D+ +++ ++E +
Query           176 DAELRAIANKPSSTYVFYVEDYIAISKIREVM    207
```

DKFZphfbr2_2c1
----

group: brain derived

DKFZphfbr2_2c1 encodes a novel 697 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 3973 bp
Poly A stretch at pos. 3914, polyadenylation signal at pos. 3900

```
   1 GGGGGGATTT CGGCGGCGGA AACATGGCGG TCGCGGCCGG GCCGGTAACG
  51 GAGAAAGTTT ACGCCGACAC TGGCCTGTAT TAGCGCGTAT GGCCTCGGGC
 101 CCTCGTTCCC CAAGGCGTGC CGCCTCCCTG TTCTCAGTCG CAGGCTGAAG
 151 CCTTGTCTGC TCTCCTCCTT TTTGGTTTGG TTTTGGAACT GACTCCGAGG
 201 GTTGGGAGAG CGCGTTGGTG GCGACGGCCG AGTCAGATCA CTATAAACAA
 251 AATTTCCACA AGAGAAAATG TTGAAATAGG AGTTGCGGAT ACATTGGATA
 301 TACTGGATGA AATACAAGCG GTTAATTTTT GTAACGTGAG GGAAAAGCCC
 351 ACATTGCTGG TTACATGTGT AAATCACTGC GTTATTGCTT TAGTCATTGT
 401 CTCTATTTAG CAATGACAAG ACTGGAAGAA GTAAATAGAG AAGTGAACAT
 451 GCATTCTTCA GTGCGGTATC TTGGCTATTT AGCCAGAATC AATTTATTGG
 501 TTGCTATATG CTTAGGTCTA TACGTAAGAT GGGAAAAAAC AGCAAATTCC
 551 TTAATTTTGG TAATTTTTAT TCTTGGTCTT TTTGTTCTTG GAATCGCCAG
 601 CATACTCTAT TACTATTTTT CAATGGAAGC AGCAAGTTTA AGTCTCTCCA
 651 ATCTTTGGTT TGGATTCTTG CTTGGCCTCC TATGTTTTCT TGATAATTCA
 701 TCCTTTAAAA ATGATGTAAA AGAAGAATCA ACCAAATATT TGCTTCTAAC
 751 ATCCATAGTG TTAAGGATAT TGTGCTCTCT GGTGGAGAGA ATTTCTGGCT
 801 ATGTCCGTCA TCGGCCCACT TTACTAACCA CAGTTGAATT TCTGGAGCTT
 851 GTTGGATTTG CCATTGCCAG CACAACTATG TTGGTGGAGA AGTCTCTGAG
 901 TGTCATTTTG CTTGTTGTAG CTCTGGCTAT GCTGATTATT GATCTGAGAA
 951 TGAAATCTTT CTTAGCTATT CCAAACTTAG TTATTTTTGC AGTTTTGTTA
1001 TTTTTTTCCT CATTGGAAAC TCCCAAAAAT CCGATTGCTT TTGCGTGTTT
1051 TTTTATTTGC CTGATAACTG ATCCTTTCCT TGACATTTAT TTTAGTGGAC
1101 TTTCAGTAAC TGAAAGATGG AAACCCTTTT TGTACCGTGG AAGAATTTGC
1151 AGAAGACTTT CAGTCGTTTT TGCTGGAATG ATTGAGCTTA CATTTTTTAT
1201 TCTTTCCGCA TTCAAACTTA GAGACACTCA CCTCTGGTAT TTTGTAATAC
1251 CTGGCTTTTC CATTTTTGGA ATTTTCAGGA TGATTTGTCA TATTATTTTT
1301 CTTTTAACTC TTTGGGGATT CCATACCAAA TTAAATGACT GCCATAAAGT
1351 ATATTTTACT CACAGGACAG ATTACAATAG CCTTGATAGA ATCATGGCAT
1401 CCAAAGGGAT GCGCCATTTT TGCTTGATTT CAGAGCAGTT GGTGTTCTTT
1451 AGTCTTCTTG CAACAGCGAT TTTGGGAGCA GTTTCCTGGC AGCCAACAAA
1501 TGGAATTTTC TTGAGCATGT TCCTAATCGT TTTGCCATTG GAATCCATGG
1551 CTCATGGGCT CTTCCATGAA TTGGGTAACT GTTTAGGAGG AACATCTGTT
1601 GGATATGCTA TTGTGATTCC CACCAACTTC TGCAGTCCTG ATGGTCAGCC
1651 AACACTGCTT CCCCCAGAAC ATGTACAGGA GTTAAATTTG AGGTCTACTG
1701 GCATGCTCAA TGCTATCCAA AGATTTTTTG CATATCATAT GATTGAGACC
1751 TATGGATGTG ACTATTCCAC AAGTGGACTG TCATTTGATA CTCTGCATTC
1801 CAAACTAAAA GCTTTCCTCG AACTTCGGAC AGTGGATGGA CCCAGACATG
1851 ATACGTATAT TTTGTATTAC AGTGGGCACA CCCATGGTAC AGGAGAGTGG
1901 GCTCTAGCAG GTGGAGATAC ACTACGCCTT GACACACTTA TAGAATGGTG
1951 GAGAGAAAAG AATGGTTCCT TTTGTTCCCG GCTTATTATC GTATTAGACA
2001 GCGAAAATTC AACCCCTTGG GTGAAAGAAG TGAGGAAAAT TAATGACCAG
2051 TATATTGCAG TGCAAGGAGC AGAGTTGATA AAAACAGTAG ATATTGAAGA
2101 AGCTGACCCG CCACAGCTAG GTGACTTTAC AAAAGACTGG GTAGAATATA
2151 ACTGCAACTC CTGTAATAAC ATCTGCTGGA CTGAAAAGGG ACGCACAGTG
2201 AAAGCAGTAT ATGGTGTGTC AAAACGGTGG AGTGACTACA CTCTGCATTT
2251 GCCAACGGGA AGCGATGTGG CCAAGCACTG GATGTTACAC TTTCCTCGTA
2301 TTACATATCC CCTAGTGCAT TTGGCAAATT GGTTATGCGG TCTGAACCTT
2351 TTTTGGATCT GCAAAACTTG TTTTAGGTGC TTGAAAAGAT TAAAAATGAG
2401 TTGGTTTCTT CCTACTGTGC TGGACACAGG ACAAGGCTTC AAACTTGTCA
2451 AATCTTAATT TGGACCCCAA AGCGGGATAT TAATAAGCAC TCATACTACC
2501 AATTATCACT AACTTGCCAT TTTTTGTATG CTGTATTTTT ATTTGTGGAA
2551 AATACCTTGC TACTTCTGTA GCTGCTCTCA CTTTGTCTTT TCTTAAGTAA
2601 TTATGGTATA TATAAGGCGT TGGGAAAAAA CATTTTATAA TGAAAGTATG
2651 TAGGGAGTCA AATGCTTACT GTAAATGCAT AAGAGACGTT AAAAATAACA
2701 CTGCACTTTC AGGAATGTTT GCTTATGGTC CTGATTAGAA AGAAACAGTT
```

```
2751 GTCTATGCTC TGCAATGGTC AATGATGAAT TACTAATGCC TTATTTTCTA
2801 GGCATATAAT AATAGTTTAG AGAATGTAGA CCAGATAAAT TTGTTTACTG
2851 TTTTAAGAAA ACTACCAGTT TACTTACAGA AGATTCTTTT TTCCAAACAG
2901 TAGGTTTCAT CCAAGACCAT TTGAAGAACT GCAAACTCTT TCTCTTAGAA
2951 AAGAAAGAGG GCAGCCTAAA ATAAACGCAA AATTTGCTTA TACTCCATCA
3001 CATTCAGATG TCTTGGTTGT GACTTATTAC CAGTGTGGCA GAGAACCCAA
3051 GTTACATTTT AGATCAAAAT ATTCTTTATG TAGGTATTGT TAAAAGGCTA
3101 GAGCCTACAA GTTGCTCTTC CATGCGTTGG TCAGGGGGCC CTGAAAACAC
3151 TGGTAATATT AAGAGTCTTT CTCAGGGTAA CTTAATGTTT TCTTAATGAA
3201 CAGTGTTTCC AGCTACAAAT TCTTCCAATA AATTGTCTTC CTTTTTGAAA
3251 AGTACTCTCA TAGAAGAAAT TTAGCAATTT CTCGTTGACT GACTCAGTCT
3301 ATTTTAAGTA TTCAGAAAAG ATTTTGATCC CCATTGAGTT AATGCTCTGC
3351 CTTGAAAATT ATTTTTCTGA TCCTTGTTAG TGATAACATT TTTTTTCTAC
3401 TGAAGGTCAG AGGATAGGAA ACAAGTATTT CTCTTCTGGT ATACATGTAA
3451 TGTATTCTGT AAAAAAGTAT TCATATTGGC AATTTTAGTT AGGCATAATA
3501 TTGTGGTTGT AATTTTTAAA ACTTAGTGTT TTGTCTGATT AAAGCAGGCA
3551 CTGATCAGGG TATCTCCTAA GAGGTAATTC ACTTCTTATT CCTTTCCAAT
3601 AATTATTACA TTCTAAATTT TCATCTATGA GAAATAACAA ACAAGAAGGG
3651 AATAGAATTA AATTGGGGTA TAATCTAATC TTCATTGTTT AAATGGTTTG
3701 CCTTCTCACC ATTGAAGCCA TTTTTTTATA GCCTCAGAAA GAGGAAATAA
3751 TGCCTCCACC ATTTTCTACC TGGTGACTTG AAAATTGAAC TTTTAAGTTA
3801 GGAAGAAGTT AGAGTCAGGG AACTTGTATA CCACTATCTA TGCAGCATTG
3851 TTATAGTCTG ATTATTTCTG TGTTTTGAAT ATGATTTTCC TAATGCTCTA
3901 AATAAAATTT TGTTAAAAAT CAAAAAAAAA AAAAAAAAAA CTTATCGATA
3951 CCGTCGACCT CGATGATGTC GAC
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 365 bp to 2455 bp; peptide length: 697
Category: putative protein
Classification: unset

```
  1 MCKSLRYCFS HCLYLAMTRL EEVNREVNMH SSVRYLGYLA RINLLVAICL
 51 GLYVRWEKTA NSLILVIFIL GLFVLGIASI LYYYFSMEAA SLSLSNLWFG
101 FLLGLLCFLD NSSFKNDVKE ESTKYLLLTS IVLRILCSLV ERISGYVRHR
151 PTLLTTVEFL ELVGFAIAST TMLVEKSLSV ILLVVALAML IIDLRMKSFL
201 AIPNLVIFAV LLFFSSLETP KNPIAFACFF ICLITDPFLD IYFSGLSVTE
251 RWKPFLYRGR ICRRLSVVFA GMIELTFFIL SAFKLRDTHL WYFVIPGFSI
301 FGIFRMICHI IFLLTLWGFH TKLNDCHKVY FTHRTDYNSL DRIMASKGMR
351 HFCLISEQLV FFSLLATAIL GAVSWQPTNG IFLSMFLIVL PLESMAHGLF
401 HELGNCLGGT SVGYAIVIPT NFCSPDGQPT LLPPEHVQEL NLRSTGMLNA
451 IQRFFAYHMI ETYGCDYSTS GLSFDTLHSK LKAFLELRTV DGPRHDTYIL
501 YYSGHTHGTG EWALAGGDTL RLDTLIEWWR EKNGSFCSRL IIVLDSENST
551 PWVKEVRKIN DQYIAVQGAE LIKTVDIEEA DPPQLGDFTK DWVEYNCNSC
601 NNICWTEKGR TVKAVYGVSK RWSDYTLHLP TGSDVAKHWM LHFPRITYPL
651 VHLANWLCGL NLFWICKTCF RCLKRLKMSW FLPTVLDTGQ GFKLVKS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2c1, frame 2

PIR:A71148 hypothetical protein PH0395 - Pyrococcus horikoshii, N = 1,
Score = 96, P = 0.12

```
>PIR:A71148 hypothetical protein PH0395 - Pyrococcus horikoshii
          Length = 288
```

HSPs:

Score = 96 (14.4 bits), Expect = 1.3e-01, P = 1.2e-01
Identities = 59/234 (25%), Positives = 116/234 (49%)

```
Query:    77 IASILYYYFSMEAASLSLSNLWFGFLL--GL--LCFLDNSSFKNDVKEESTKYLLLTSIV 132
             ++ +LYY F+  A    ++  L  G+LL    +  L +L N +     V+ +  K  +  ++
Sbjct:    57 LSLVLYYLFAFSALK-TIIFLALGYLLMNSIYELGYLMNDTISRRVEGKVHKVRVKLTVF 115

Query:   133 LRILCSLVERISGYVRHRPTLLTTVEFLELVGFAIASTTMLVEKSLSVILLVVALAMLII 192
               +L +L    I  YV      ++ T+ FL+LVG    ++  +L E +L ++ L+  L     +
Sbjct:   116 DSLLIALSRAI--YV-----VIFTLVFLKLVGLQYSTQVILAEVTLFLVFLLYDLTPKHV 168

Query:   193 DLRMKSFLAIPNLVIFAVLLFFSSLET-PKNPIAFACFFICLITDPFLDIYFSGLSVTER 251
                 M SF  +  +  F +LL F    T  +N I  +  FI  I   F   ++   +  +
Sbjct:   169 RTVMLSF-PLKFMKAFVLLLPFIITGTLVENVITLS--FILPIAVRFSQAHYLKTACKDN 225

Query:   252 WKPFLYRGRICRRLSVVFAGMIEL-TFFILSAFK-LRDTHLW-YFVIPGFSIFGIFRMIC 308
               P  ++ R+  R S+++  +  L TF +L +F  L +T L   ++IP F++  +  ++
Sbjct:   226 -PPRDFKRRV-ERFSMMYLQVTSLSTFTVLVSFVYLGNTDLLRQYLIP-FAVNVVLILLS 282

Query:   309 HI 310
             ++
Sbjct:   283 YL 284
```

Pedant information for DKFZphfbr2_2c1, frame 2

Report for DKFZphfbr2_2c1.2

```
[LENGTH]        697
[MW]            79741.46
[pI]            8.41
[KW]            TRANSMEMBRANE  11
[KW]            LOW_COMPLEXITY      9.76 %

SEQ     MCKSLRYCFSHCLYLAMTRLEEVNREVNMHSSVRYLGYLARINLLVAICLGLYVRWEKTA
SEG     ............................................................
PRD     ccceeehhhhhhhhhhhhhhhhhhhhhccceeeehhhhhhhhhhhhhhhhhhhhcccccc
MEM     ..................................MMMMMMMMMMMMMMMMMM........

SEQ     NSLILVIFILGLFVLGIASILYYYFSMEAASLSLSNLWFGFLLGLLCFLDNSSFKNDVKE
SEG     ..xxxxxxxxxxxxxxx.............xxxxxxxxxxxxxxxxxxxxxxx.......
PRD     ccceeeecccccchhhhchhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccc
MEM     ...MMMMMMMMMMMMMMMMM..........MMMMMMMMMMMMMMMMMM............

SEQ     ESTKYLLLTSIVLRILCSLVERISGYVRHRPTLLTTVEFLELVGFAIASTTMLVEKSLSV
SEG     ...............................xxxxxxxxxxxx.............xxxx
PRD     cchhhhhhhhhhhhhhhhhhhhceeeeccccccchhhhhhhhhhhhhhhhhhhhhhhhhh
MEM     ....MMMMMMMMMMMMMMMMM....................................MMM

SEQ     ILLVVALAMLIIDLRMKSFLAIPNLVIFAVLLFFSSLETPKNPIAFACFFICLITDPFLD
SEG     xxxxxxxxxxxxxx..............................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhcccccccccchhhhhhhhhccccccee
MEM     MMMMMMMMMMMMMM...MMMMMMMMMMMMMMMMM........MMMMMMMMMMMMMMMMM.

SEQ     IYFSGLSVTERWKPFLYRGRICRRLSVVFAGMIELTFFILSAFKLRDTHLWYFVIPGFSI
SEG     ............................................................
PRD     eeecccccccccccceeeccccccccchhhhhhhhhhhhhhhhhhcccccceeeeeecccccc
MEM     .........................MMMMMMMMMMMMMMMMM.................M

SEQ     FGIFRMICHIIFLLTLWGFHTKLNDCHKVYFTHRTDYNSLDRIMASKGMRHFCLISEQLV
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhcccccccceeeeeeecccccchhhhhhhcccchhhhhhhhh
MEM     MMMMMMMMMMMMMMMM..........................................MM

SEQ     FFSLLATAILGAVSWQPTNGIFLSMFLIVLPLESMAHGLFHELGNCLGGTSVGYAIVIPT
SEG     ............................................................
PRD     hhhhhhhhhhhcccccccchhhhhhhheeehhhhhhhhcccccccccccceeeeeeeeec
MEM     MMMMMMMMMMMMMMM....MMMMMMMMMMMMMMMMM........................

SEQ     NFCSPDGQPTLLPPEHVQELNLRSTGMLNAIQRFFAYHMIETYGCDYSTSGLSFDTLHSK
SEG     ............................................................
PRD     cccccccccccccccccccccccccchhhhhhhhhhhhhhhhcccccccccccccchhhhhh
MEM     ............................................................

SEQ     LKAFLELRTVDGPRHDTYILYYSGHTHGTGEWALAGGDTLRLDTLIEWWREKNGSFCSRL
SEG     ............................................................
PRD     hhhhhhhhcccccccceeeeeeccccccccccccceeecccchhhhhhhhhhccccceeee
MEM     ............................................................

SEQ     IIVLDSENSTPWVKEVRKINDQYIAVQGAELIKTVDIEEADPPQLGDFTKDWVEYNCNSC
```

```
SEG      ............................................................
PRD      eeeeecccccccchhhhhcccеeeeecccеeeeeeeeeccccccccccccceeeeccccc
MEM      ............................................................

SEQ      NNICWTEKGRTVKAVYGVSKRWSDYTLHLPTGSDVAKHWMLHFPRITYPLVHLANWLCGL
SEG      ............................................................
PRD      cceeeecccceeeeeeeeecccccceeeeccccchhhhhhccccccchhhhhhhhhcc
MEM      ............................................................

SEQ      NLFWICKTCFRCLKRLKMSWFLPTVLDTGQGFKLVKS
SEG      .....................................
PRD      eeeeeehhhhhhhhhhhhhhcceeeeccccccccccc
MEM      .....................................
```

(No Prosite data available for DKFZphfbr2_2c1.2)

(No Pfam data available for DKFZphfbr2_2c1.2)

DKFZphfbr2_2c17
----

group: signal transduction

DKFZphfbr2_2c17.3 encodes a novel 446 amino acid protein with similarity to yeast YMR131c and mammalian retinoblastoma-binding protein RbAp46

The protein contains 1 WD-40 repeat, which is typical for the beta-transducin subunit of G-proteins. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

The new protein can find application in modulating/blocking G-protein-dependent pathways.

similarity to YMR131c and retinoblastoma-binding protein RbAp46

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2248 bp
Poly A stretch at pos. 2230, polyadenylation signal at pos. 2200

```
   1 TGGGGAAGAT GGCGGCGCGC AAGGGTCGGC GTCGCACGTG TGAAACCGGG
  51 GAACCCATGG AAGCCGAGTC CGGCGACACA AGTTCCGAGG GCCCGGCCCA
 101 GGTCTACCTG CCCGGCCGGG GGCCGCCGCT ACGCGAAGGG GAGGAGCTGG
 151 TCATGGACGA GGAGGCCTAT GTGCTCTACC ACCGAGCGCA GACTGGCGCC
 201 CCCTGTCTCA GCTTTGACAT AGTCCGGGAT CACCTGGGAG ACAACCGGAC
 251 AGAGCTTCCT CTTACACTTT ACTTGTGTGC TGGGACCCAG GCTGAGAGCG
 301 CCCAGAGCAA CAGACTGATG ATGCTTCGGA TGCACAATCT GCATGGGACA
 351 AAGCCCCCAC CCTCAGAGGG CAGTGATGAA GAAGAAGAGG AGGAAGATGA
 401 AGAGGATGAA GAAGAGCGGA AACCTCAGCT GGAGCTGGCC ATGGTGCCCC
 451 ACTATGGTGG CATCAACCGA GTTCGGGTGT CATGGCTGGG TGAAGAGCCT
 501 GTGGCTGGGG TGTGGTCAGA GAAGGGCCAG GTGGAGGTGT TTGCGCTGCG
 551 GCGGCTTCTG CAGGTGGTGG AGGAGCCCCA GGCCCTGGCA GCCTTCCTCC
 601 GGGATGAGCA GGCCCAAATG AAGCCCATCT TCTCCTTCGC TGGACACATG
 651 GGCGAGGGCT TTGCCCTTGA CTGGTCCCCC CGGGTGACCG GTCGCCTGCT
 701 GACCGGTGAC TGTCAAAAGA ACATCCACCT CTGGACACCT ACGGACGGCG
 751 GCTCCTGGCA CGTGGACCAG CGGCCATTCG TGGGCCACAC ACGCTCTGTG
 801 GAGGACCTGC AGTGGTCACC GACTGAGAAC ACGGTGTTTG CCTCCTGCTC
 851 AGCTGACGCC TCCATCCGCA TCTGGGACAT CCGGGCAGCC CCCAGCAAGG
 901 CCTGCATGCT CACCACAGTC ACCGCCCATG ATGGGGACGT CAATGTCATC
 951 AGCTGGAGCC GCCGGGAGCC CTTCCTGCTC AGTGGCGGGG ATGATGGGGC
1001 CCTCAAGATC TGGGACCTTC GGCAGTTCAA GTCTGGTTCC CCAGTGGCCA
1051 CCTTCAAGCA GCACGTGGCC CCCGTGACCT CCGTCGAGTG GCACCCCCAG
1101 GACAGCGGGG TCTTTGCAGC CTCGGGTGCA GACCACCAGA TCACACAGTG
1151 GGACCTGGCA GTGGAGCGGG ACCCTGAGGC GGGCGACGTG GAGGCCGACC
1201 CCGGACTGGC CGACCTCCCG CAGCAGCTGC TGTTCGTGCA CCAGGGCGAG
1251 ACCGAGCTGA AGGAGCTGCA CTGGCACCCG CAGTGCCCAG GGCTCCTGGT
1301 CAGCACGGCG CTGTCAGGCT TCACCATCTT CCGCACCATC AGCGTCTGAG
1351 GCGTCCCACT GGCTCTGATC TTGCTTCCTG CTTGGAAACT GAAGTCGAAT
1401 TGGGCTCCCC TGGAAGGGGT TCATTCAGGT CTGTTGACTG AGACTGGCCG
1451 GCCTGTGGGC TGCCGTGATG GATTCTGTTT GACGTATTGT TCTCTAGAAG
1501 GCCTGGCTCT GATCCAGTGA CCCCTCTCAC CAAAGAACTC GGTTTAACCA
1551 GGGCTCTGTA AGACCACTCC CACCCAGAGA CTTGTGTGGC CTGGTGTGGC
1601 CTGTGTGTCG GATTCCTTCC TGTCAGCTGT GACCCATTTG ACCTGTGTCC
1651 CCAGAACCCA GTTTTTTGTT TGTTTGTTTG AGACGGAGTC TTGGTCTGTC
1701 GCCCAGGCTG GAGTGCAGTA GCACGATCTT GGCTCACTGC AACCTCCGCC
1751 TCCTGGGTTA AAGTGATTCT CTCAGCTCAG TCTCCCAGGT AGCTGGGATT
1801 ACAGGCATGT GCCACCACAC CCCGTTAATT TTTGTATTTT TAGTAGAGAC
1851 GGGGTTTCAC CATGTTGGCC AGGCTGGTCT CAAATTCTTG ATCTCAAGTG
1901 ATCTGTCCGC CCCGGCCTCC CAGAGTGCTG GGTTGGGATT ACAGGCGTGA
1951 GCCACCGCGT CCGGCTCAGG ACCCAGTTTT GGCTGCTGGT TCCCAGCAGG
2001 GGACTCGGGG GATATACAGT GGCTGCACCA AATTGGAGGT GTGGGTTCCT
2051 CCAACACAAT TTGCTTCTGC CCGTTGTCTT CCTGCCAGCT GGGTTTGGCC
2101 AGGATTTCTC CGTGTGGGGG CTACATGCGA CCCTCTCCCC TCCTCCCTGA
2151 CTTTAGAGGC TGGTGCTGTG TCGGGAGGAA GGTCAGGGCT CCTGAGCAGC
2201 AATAAAGGAC CAGGAAGAGG CCTGAGGTGG AAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 9 bp to 1346 bp; peptide length: 446
Category: similarity to known protein
Classification: unset
Prosite motifs: WD_REPEATS (323-338)

```
  1 MAARKGRRRT CETGEPMEAE SGDTSSEGPA QVYLPGRGPP LREGEELVMD
 51 EEAYVLYHRA QTGAPCLSFD IVRDHLGDNR TELPLTLYLC AGTQAESAQS
101 NRLMMLRMHN LHGTKPPPSE GSDEEEEEED EEDEEERKPQ LELAMVPHYG
151 GINRVRVSWL GEEPVAGVWS EKGQVEVFAL RRLLQVVEEP QALAAFLRDE
201 QAQMKPIFSF AGHMGEGFAL DWSPRVTGRL LTGDCQKNIH LWTPTDGGSW
251 HVDQRPFVGH TRSVEDLQWS PTENTVFASC SADASIRIWD IRAAPSKACM
301 LTTVTAHDGD VNVISWSRRE PFLLSGGDDG ALKIWDLRQF KSGSPVATFK
351 QHVAPVTSVE WHPQDSGVFA ASGADHQITQ WDLAVERDPE AGDVEADPGL
401 ADLPQQLLFV HQGETELKEL HWHPQCPGLL VSTALSGFTI FRTISV
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2c17, frame 3

TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat protein"; Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence., N = 1, Score = 910, P = 2.7e-91

PIR:S53061 hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae), N = 1, Score = 691, P = 4.3e-68

PIR:I49367 retinoblastoma-binding protein mRbAp46 - mouse, N = 1, Score = 338, P = 1.1e-30

PIR:I39181 retinoblastoma-binding protein RbAp46 - human, N = 1, Score = 338, P = 1.1e-30

```
>TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat
     protein"; Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence,
     complete sequence.
            Length = 469

  HSPs:

 Score = 910 (136.5 bits), Expect = 2.7e-91, P = 2.7e-91
 Identities = 195/442 (44%), Positives = 259/442 (58%)

Query:    18 EAESGDTSSEGPAQVYLPGRGPPLREGEELVMDEEAYVLYHRAQTGAPCLSFDIVRDHLG 77
             EA S +  S  P +V+ PG    L +GEEL  D  AY   H    G PCLSFDI+ D LG
Sbjct:    18 EASSSEIPSI-PTRVWQPGVDT-LEDGEELQCDPSAYNSLHGFHVGWPCLSFDILGDKLG 75

Query:    78 DNRTELPLTLYLCAGTQAESAQSNRLMMLRMHNLHGTKP---PPSEGSDEEEEEEDEED- 133
              NRTE P TLY+ AGTQAE A  N + + ++ N+ G +    P + G+ E+E+E+DE+D
Sbjct:    76 LNRTEFPHTLYMVAGTQAEKAAHNSIGLFKITNVSGKRRDVVPKTFGNGEDEDEDDEDDS 135

Query:   134 --------EEERKPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFALRRLLQ 185
                     E  + P.+++  V H+G +NR+R        +   W++ G V+V+ +   L
Sbjct:   136 DSDDDDGDEASKTPNIQVRRVAHHGCVNRIRAMPQNSH-ICVSWADSGHVQVWDMSSHLN 194

Query:   186 VVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPRVTGRLLTGDCQKNIHLWTPT 245
              + E +              P+ +F+GH  EG+A+DWSP   GRLL+GDC+  IHLW P
Sbjct:   195 ALAESETEGKDGTSPVLNQAPLVNFSGHKDEGYAIDWSPATAGRLLSGDCKSMIHLWEPA 254

Query:   246 DGGSWHVDQRPFVGHTRSVEDLQWSPTENTVFASCSADASIRIWDIRAAPSKACMLTTVT 305
              G SW VD  PF GHT SVEDLQWSP E  VFASCS D S+ +WDIR   S A      +
Sbjct:   255 SG-SWAVDPIPFAGHTASVEDLQWSPAEENVFASCSVDGSVAVWDIRLGKSPAL---SFK 310

Query:   306 AHDGDVNVISWSRREPFLL-SGGDDGALKIWDLRQFKSGSPV-ATFKQHVAPVTSVEWHP 363
             AH+ DVNVISW+R    +L SG DDG   I DLR  K G  V A F+ H  P+TS+EW
Sbjct:   311 AHNADVNVISWNRLASCMLASGSDDGTFSIRDLRLIKGGDAVVAHFEYHKHPITSIEWSA 370
```

```
Query:  364 QDSGVFAASGADHQITQWDLAVERDPE------AGDVEADPGLADLPQQLLFVHQGETEL 417
            ++   A +  D+Q+T WDL++E+D E      A   E      DLP QLLFVHQG+ +L
Sbjct:  371 HEASTLAVTSGDNQLTIWDLSLEKDEEEEAEFNAQTKELVNTPQDLPPQLLFVHQGQKDL 430

Query:  418 KELHWHPQCPGLLVSTALSGFTIFRTISV 446
            KELHWH Q PG+++STA  GF I    ++
Sbjct:  431 KELHWHNQIPGMIISTAGDGFNILMPYNI 459
```

Pedant information for DKFZphfbr2_2c17, frame 3

Report for DKFZphfbr2_2c17.3

[LENGTH] 446
[MW] 49447.38
[pI] 4.82
[HOMOL] TREMBL:AC005917_14 gene: "F3P11.14"; product: "putative WD-40 repeat protein"; Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence. 1e-90
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YMR131c] 4e-65
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YEL056w] 4e-15
[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YEL056w] 4e-15
[FUNCAT] 06.07 protein modification (glycolsylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YEL056w] 4e-15
[FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YBR195c] 2e-13
[FUNCAT] 10.04.09 regulation of g-protein activity [S. cerevisiae, YBR195c] 2e-13
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YBR195c] 2e-13
[FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YBR195c] 2e-13
[FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YBR195c] 2e-13
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YPR178w] 1e-11
[FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPR178w] 1e-11
[FUNCAT] 06.13 proteolysis [S. cerevisiae, YGL003c] 4e-09
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YGL003c] 4e-09
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YDL145c] 5e-09
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL145c] 5e-09
[FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YBR198c TAF90 - TFIID subunit] 6e-09
[FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YMR116c] 5e-08
[FUNCAT] 02.16 fermentation [S. cerevisiae, YMR116c] 5e-08
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YLR429w] 3e-07
[FUNCAT] 30.19 peroxisomal organization [S. cerevisiae, YDR142c] 3e-06
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YDR142c] 3e-06
[FUNCAT] 08.10 peroxisomal transport [S. cerevisiae, YDR142c] 3e-06
[FUNCAT] 03.13 meiosis [S. cerevisiae, YLR129w] 4e-06
[FUNCAT] 08.01 nuclear transport [S. cerevisiae, YER107c] 4e-06
[FUNCAT] 03.01 cell growth [S. cerevisiae, YKL021c] 4e-06
[FUNCAT] 04.07 rna transport [S. cerevisiae, YER107c] 4e-06
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YCR057c] 2e-05
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YCR057c] 2e-05
[FUNCAT] 01.01.04 regulation of amino-acid metabolism [S. cerevisiae, YIL046w] 2e-05
[FUNCAT] 06.13.01 cytoplasmic degradation [S. cerevisiae, YIL046w] 2e-05
[FUNCAT] 04.01.04 rrna processing [S. cerevisiae, YLL011w] 3e-05
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YOR212w] 5e-05
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YOR212w] 5e-05
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YOR212w] 5e-05
[BLOCKS] BL00678
[SCOP] d2trcb_ 2.51.3.1.1 Transducin (heterotrimeric G protein), gamm 5e-29
[PIRKW] plasma 6e-07
[PIRKW] duplication 4e-12
[PIRKW] hormone 6e-07
[PIRKW] transmembrane protein 1e-07
[PIRKW] stomach 6e-07
[PIRKW] actin binding 1e-07
[PIRKW] leucine zipper 1e-07
[PIRKW] signal transduction 2e-06
[PIRKW] heterotrimer 2e-06
[PIRKW] peripheral membrane protein 6e-07
[PIRKW] GTP binding 2e-06
[SUPFAM] WD repeat homology 1e-63
[SUPFAM] yeast coatomer complex alpha chain 1e-07
[SUPFAM] GTP-binding regulatory protein beta chain 4e-07
[SUPFAM] PRL1 protein 8e-09

```
[SUPFAM]        MSI1 protein 4e-12
[SUPFAM]        coatomer complex beta' chain 1e-09
[PROSITE]       WD_REPEATS     1
[PFAM]          WD domain, G-beta repeats
[KW]            All_Beta
[KW]            3D
[KW]            LOW_COMPLEXITY     3.14 %
```

```
SEQ     MAARKGRRRTCETGEPMEAESGDTSSEGPAQVYLPGRGPPLREGEELVMDEEAYVLYHRA
SEG     ............................................................
1gotB   ............................................................

SEQ     QTGAPCLSFDIVRDHLGDNRTELPLTLYLCAGTQAESAQSNRLMMLRMHNLHGTKPPPSE
SEG     ............................................................
1gotB   ............................................................

SEQ     GSDEEEEEEDEEDEEERKPQLELAMVPHYGGINRVRVSWLGEEPVAGVWSEKGQVEVFAL
SEG     ..xxxxxxxxxxxxxx............................................
1gotB   ............................................................

SEQ     RRLLQVVEEPQALAAFLRDEQAQMKPIFSFAGHMGEGFALDWSPRVTGRLLTGDCQKNIH
SEG     ............................................................
1gotB   ...........................EEECCCCCEEEEEETTT-TCEEEEEEETTTEEE

SEQ     LWTPTDGGSWHVDQRPFVGHTRSVEDLQWSPTENTVFASCSADASIRIWDIRAAPSKACM
SEG     ............................................................
1gotB   EEETTTT----CEEEEEECCCCCEEEEEEEETTTCE-EEEEETTTEEEEEEETTT--TEEEE

SEQ     LTTVTAHDGDVNVISWSRREPFLLSGGDDGALKIWDLRQFKSGSPVATFKQHVAPVTSVE
SEG     ............................................................
1gotB   EECBTTBTCCEEEEEEETTTTTEEEEEEETTTEEEEEE......................

SEQ     WHPQDSGVFAASGADHQITQWDLAVERDPEAGDVEADPGLADLPQQLLFVHQGETELKEL
SEG     ............................................................
1gotB   ............................................................

SEQ     HWHPQCPGLLVSTALSGFTIFRTISV
SEG     ..........................
1gotB   ..........................
```

Prosite for DKFZphfbr2_2c17.3

```
PS00678     323->338   WD_REPEATS           PDOC00574
```

Pfam for DKFZphfbr2_2c17.3

```
HMM_NAME        WD domain, G-beta repeats

HMM                 *MrGHnnWVWCVaFSPDGrWFIvSGSWDgTCRLWD*
                     ++GH+  V ++ +SP  + +++S S D ++R+WD
Query           257  FVGHTRSVEDLQWSPTENTVFASCSADASIRIWD    290

24.88     304   336     1     34 dkfzphfbr2_2c17.3 similarity to YMR131c and retinoblastoma-
binding protein RbAp46
  Alignment to HMM consensus:
Query               *MrGHnnWVWCVaFSPDGrWFIvSGSWDgTCRLWD*
                     + H+++V+ +++S    + ++SG++DG +++WD
  dkfzphfbr2   304   VTAHDGDVNVISWSRREPF-LLSGGDDGALKIWD    336
```

DKFZphfbr2_2c18
----

group: brain associated

DKFZphfbr2_2c18 encodes a novel 302 amino acid protein with weak similarity to cyclin-dependent kinase p130-PITSLRE.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

weak similarity to cyclin-dependent kinase p130-PITSLRE

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2835 bp
Poly A stretch at pos. 2817, polyadenylation signal at pos. 2796

```
   1 TGGGGCGGAC GGCGAGGGAG TCCAGAGCCT TGAGCCCGGT GCTCCTCCCT
  51 CGCGCAGCGG TGGCTCTGCG GCCGCTGGAG TAAACACTGC CTTTGTTCCC
 101 TAGCGCCTCG TCTTTCGTCG CCCCGTGCCC TCACGCCGCC GGGCTCTGGC
 151 CGGCCCGCCC TCGGTCCTTG AACCCCATTT CGGCTCGTGC CGTGCGGATG
 201 CAGCTGCCGG GCCTGGGTTT GGGCATTGAG CGGGAGGAGG AGGAGGAGCG
 251 GCGGCGCCTG GGCGGCATGC GATGGGGAAC TGCTGCTGGA CGCAGTGCTT
 301 CGGACTGCTT CGCAAGGAAG CGGGGCGGCT GCAGCGAGTA GGCGGCGGCG
 351 GAGGATCCAA GTATTTTAGA ACATGCTCAA GAGGTGAGCA CTTGACAATA
 401 GAGTTTGAGA ATCTAGTAGA AAGTGATGAA GGGGAGAGCC CAGGAAGCAG
 451 TCATAGGCCT CTTACTGAGG AAGAAATTGT TGACCTAAGA GAAAGGCATT
 501 ATGATTCCAT TGCCGAAAAA CAAAAAGATC TTGATGAGAA AATTCAAAAA
 551 GAGTTAGCCT TACAAGAAGA GAAGTTAAGA CTAGAAGAAG AAGCTTTATA
 601 CGCTGCACAG CGTGAAGCAG CCAGGGCAGC AAAGCAGCGA AAGCTCTTGG
 651 AGCAAGAAAG GCAGAGAATT GTGCAGCAAT ATCATCCTTC CAACAATGGA
 701 GAATATCAAA GTTCAGGACC AGAAGATGAC TTCGAATCTT GTTTGAGAAA
 751 TATGAAGTCA CAGTATGAAG TTTTTCGAAG TAGTAGACTC TCATCAGATG
 801 CTACAGTTTT GACACCAAAT ACAGAAAGCA GTTGTGATTT AATGACCAAA
 851 ACTAAATCAA CTAGTGGAAA TGACGACAGC ACATCCTTAG ATCTAGAGTG
 901 GGAAGATGAA GAAGGAATGA ATAGAATGCT TCCAATGAGA GAACGTTCCA
 951 AAACAGAGGA AGACATTCTA CGGGCAGCAC TTAAGTATAG CAACAAGAAG
1001 ACTGGAAGTA ATCCTACATC AGCCTCTGAT GATTCCAATG GGCTGGAGTG
1051 GGAAAATGAT TTTGTTAGTG CCGAAATGGA TGATAATGGA AATTCCGAGT
1101 ATTCTGGATT TGTAAATCCT GTATTAGAAC TGTCTGATTC TGGCATAAGG
1151 CATTCTGACA CAGATCAACA GACTCGATAG GGTAAAATTG TGTGACCTTG
1201 TTTATCAGTT ATGACCAAAT GTTAAAAACC AACTAGAATG TATAAGTGAT
1251 TGTGCTTAGC CTTTTTGTAA GGGAGATGTG TAAGAAACCA TGCTGTAAAT
1301 GCTTATTTTA TTACAAAGGA GTAGGGATGA TAGGATCTGA ATTGATACAG
1351 AATTAAGTGC AATTTCATCA TCTGCCTTCT GCTTTTCAAG ACCAATTTAA
1401 TGGTCCTGTC ATGTTACTGA TTAAATTTAC TTTGTCTTGT CTTTATAGCA
1451 TTTCTGTTTA CTATGGTAGA TTTCCACTTT CAATTTTTAA AATTAATTTT
1501 ACTTTGAATG ATTTATGAAG CCTATTTCAT TGTCTAACTA TGAAAATATT
1551 AAGACTTTTT TGTTAATTCT CAGCCGATGT GAAGGAAGCA TGAGGAGGGA
1601 TCGTCAGACT CAGATTTAGA ATAGTGTTCC CGTTTCCAGC ATTATTTATT
1651 TCTATGACTT CTTTGGATTT TATTATCTAA TAGTAAGTAC AGTTGATGTG
1701 GGTAGATGAC TCTAAGAAAT GCTGAAGTAT CGGCATTACA TGTGTTTATT
1751 TACATGTCCT AGTTTGATAA TGTTGATTCA ATCTGAACAA AAGATAATAT
1801 AAAAATAACC CTTCAGAGTT TGGACATTTC AAGTTGGTAA TAATAAAAAA
1851 TAATATTTAA GAAGATATAT ATATATATAT ATTTAGTTTT TTCCACTTCA
1901 TTTTACATGC CACTATATTG ACTTTAATTG ATATACAGTA TTAAGTTTTT
1951 AGGTGCCATT ATTTTTAAAA AATTCTATAT TTCCAATGAA CGATGTTAGA
2001 TTTTACACAG AACATATTCT CTGCATGATT TCAGAAAAGA AAATCTAAAA
2051 AGGTAATACG GGTATTTCAA ATAAAATCCT TTCTGGTATG AAAGGCTCCA
2101 TTGATTTTAT TAAGCCTTCC TTTACCTTGT AGTACAAGGT GCTTTAATGG
2151 GATAGAACTA AGCATATCAA TATCTATAAC TGCATTTTGT GCTAGACAAT
2201 TACTGTTCTT TTCTCTAAAA TGTATATGTC AATTTACAAG GCCAGGGATA
2251 GAAAACACTC CATAATTGCT TTCCTTGATT TTGCTGAGGA TTTGGTATGA
2301 TTTTAGTAAG CAAACTGTTT TTTGGTTTTT CCTTAATGTT TTTAATTTTT
2351 TTTCCTCTTG CAACAATGAC GGTGCATGTT CTTATAAATA TAGGAAGGTC
2401 CAGATATAAA TAGTAACCTA AAGTTCTTGC TGTGCTTAAA AAAAAAAATC
2451 ATGTGGCTCT TTCAATATTT GAACTGCTAA GCAATGACAT CTGTAGTTTT
2501 ATCTCCTTTT TTATGTCATA GAAATTAATA TGATACTTTA AATATGTAAA
2551 TATAATACAT TGGTAATGCT ATTATTTATA TCTGTCTTAA CATAATTTAA
2601 GTTGTAGCTG TGTCTTGGAA ATATTTTTAA GGTAATCTAT ATTCACATTG
2651 CCTGTGTTAA TGCTTTTTAA GGTTTGTATA CATCAGATGT ATATTTTTGG
```

```
2701 TTTGGCATAA GCTACGATTG TAATTTTTCT TGGCTTTTTG TTCATAAAGA
2751 ATTTTTTGAA GGAATGGTAA CAAATGGTAA TTTACAAATG GTTGTGAATA
2801 AACACATTTT TACACTTAAA AAAAAAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 272 bp to 1177 bp; peptide length: 302
Category: similarity to known protein

```
  1 MGNCCWTQCF GLLRKEAGRL QRVGGGGGSK YFRTCSRGEH LTIEFENLVE
 51 SDEGESPGSS HRPLTEEEIV DLRERHYDSI AEKQKDLDEK IQKELALQEE
101 KLRLEEEALY AAQREAARAA KQRKLLEQER QRIVQQYHPS NNGEYQSSGP
151 EDDFESCLRN MKSQYEVFRS SRLSSDATVL TPNTESSCDL MTKTKSTSGN
201 DDSTSLDLEW EDEEGMNRML PMRERSKTEE DILRAALKYS NKKTGSNPTS
251 ASDDSNGLEW ENDFVSAEMD DNGNSEYSGF VNPVLELSDS GIRHSDTDQQ
301 TR
```

BLASTP hits

Entry A55817 from database PIR:
cyclin-dependent kinase p130-PITSLRE - mouse
Length = 783
Score = 123 (43.3 bits), Expect = 0.00013, P = 0.00013
Identities = 53/197 (26%), Positives = 96/197 (48%)

Alert BLASTP hits for DKFZphfbr2_2c18, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2c18, frame 2

Report for DKFZphfbr2_2c18.2

```
[LENGTH]      302
[MW]          34281.39
[pI]          4.73
[PROSITE]     MYRISTYL        5
[PROSITE]     CK2_PHOSPHO_SITE      12
[PROSITE]     TYR_PHOSPHO_SITE      2
[PROSITE]     PKC_PHOSPHO_SITE      3
[KW]          All_Alpha
[KW]          LOW_COMPLEXITY    13.58 %
[KW]          COILED_COIL       13.58 %
```

```
SEQ    MGNCCWTQCFGLLRKEAGRLQRVGGGGGSKYFRTCSRGEHLTIEFENLVESDEGESPGSS
SEG    .......................xxxxx................................
PRD    cccccccccchhhhhhhhhheeeccccccccceeeecccccccchhhhhhhhcccccccccc
COILS  ............................................................

SEQ    HRPLTEEEIVDLRERHYDSIAEKQKDLDEKIQKELALQEEKLRLEEEALYAAQREAARAA
SEG    ..............................xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD    ccchhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ............................CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ    KQRKLLEQERQRIVQQYHPSNNGEYQSSGPEDDFESCLRNMKSQYEVFRSSRLSSDATVL
SEG    xxxxxxx.....................................................
PRD    hhhhhhhhhhhhhhhhhcccccccccccccccccchhhhhhhhhhheeeeeccccccceeee
COILS  CCCCCCCCC...................................................
```

```
SEQ     TPNTESSCDLMTKTKSTSGNDDSTSLDLEWEDEEGMNRMLPMRERSKTEEDILRAALKYS
SEG     ............................................................
PRD     cccccccccccccccccccccccchhhhhhhccccccchhhhhhhcchhhhhhhhhhhhc
COILS   ............................................................

SEQ     NKKTGSNPTSASDDSNGLEWENDFVSAEMDDNGNSEYSGFVNPVLELSDSGIRHSDTDQQ
SEG     ............................................................
PRD     cccccccccccccccccccccccceeeeccccccccccccceeeeccccccccccccccc
COILS   ............................................................

SEQ     TR
SEG     ..
PRD     cc
COILS   ..
```

Prosite for DKFZphfbr2_2c18.2

PS00005	60->63	PKC_PHOSPHO_SITE	PDOC00005
PS00005	170->173	PKC_PHOSPHO_SITE	PDOC00005
PS00005	240->243	PKC_PHOSPHO_SITE	PDOC00005
PS00006	36->40	CK2_PHOSPHO_SITE	PDOC00006
PS00006	65->69	CK2_PHOSPHO_SITE	PDOC00006
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	148->152	CK2_PHOSPHO_SITE	PDOC00006
PS00006	163->167	CK2_PHOSPHO_SITE	PDOC00006
PS00006	186->190	CK2_PHOSPHO_SITE	PDOC00006
PS00006	198->202	CK2_PHOSPHO_SITE	PDOC00006
PS00006	204->208	CK2_PHOSPHO_SITE	PDOC00006
PS00006	226->230	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00006	250->254	CK2_PHOSPHO_SITE	PDOC00006
PS00006	295->299	CK2_PHOSPHO_SITE	PDOC00006
PS00007	103->111	TYR_PHOSPHO_SITE	PDOC00007
PS00007	103->111	TYR_PHOSPHO_SITE	PDOC00007
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	25->31	MYRISTYL	PDOC00008
PS00008	199->205	MYRISTYL	PDOC00008
PS00008	245->251	MYRISTYL	PDOC00008
PS00008	291->297	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_2c18.2)

DKFZphfbr2_2d15
----

group: differentiation/development

DKFZphfbr2_2d15 encodes a novel 438 amino acid protein similarity to Mus musculus testis-specific Y-encoded-like protein (Tspyl1).

The TSPY genes are arranged in clusters on the Y chromosome of many mammalian species. TSPY is believed to function in early spermatogenesis and is a candidate for GBY, the putative gonadoblastoma-inducing gene on the Y. The novel protein is a new member of the TSPY-SET-NAP1L1 family, which represents proteins closely related to TSPY. Therefore, the new protein seems to be involved in early spermatogenesis.

The new protein can find application in modulating early spermatogenesis.

strong similarity to testis-specific Y-encoded-like protein

complete cDNA, complete cds, EST hits
localisation: primer B does not match perfect

Sequenced by Qiagen

Locus: /map="729.2 cR from top of Chr6 linkage group"

Insert length: 3229 bp
Poly A stretch at pos. 3206, polyadenylation signal at pos. 3184

```
   1 GGAGACTGTA GGGTGGGCGG TGCGAGCGGC GGTTAGCTCC CAGTTCGGCC
  51 TCTGAGGAAA ACGGGCGTTC GCCTGCGGTT GGTCCGACTG TTAGCAACAT
 101 GAGCGGCCTG GATGGGGTCA AGAGGACCAC TCCCCTCCAA ACCCACAGCA
 151 TCATTATTTC TGACCAAGTC CCGAGCGACC AGGACGCACA CCAGTACCTG
 201 AGGCTCCGCG ACCAAAGCGA GGCGACACAG GTGATGGCGG AGCCGGGTGA
 251 GGGAGGCTCG GAGACCGTCG CGCTCCCGCC TTCACCGCCT TCAGAGGAGG
 301 GGGGCGTACC CCAGGATCCC GCGGGCCGTG GCGGTACTCC CCAGATCCGA
 351 GTTGTTGGGG GTCGCGGTCA TGTGGCGATC AAAGCCGGGC AGGAAGAGGG
 401 CCAGCCTCCC GCCGAAGGCC TGGCAGCCGC TTCTGTGGTG ATGGCAGCCG
 451 ACCGCAGCCT GAAAAAGGGC GTTCAGGGTG GAGAGAAGGC CCTAGAAATC
 501 TGTGGCGCCC AGAGATCCGC GTCTGAGCTG ACGGCGGGGG CGGAGGCTGA
 551 GGCGGAGGAG GTGAAGACAG GAAAGTGCGC CACCGTCTCA GCAGCCGTGG
 601 CTGAGAGGGA GAGCGCTGAG GTGGTGGTGA AGGAAGGCCT GGCGGAGAAG
 651 GAGGTAATGG AGGAGCAGAT GGAGGTAGAG GAGCAGCCGC CAGAAGGTGA
 701 AGAAATAGAA GTGGCGGAGG AGGATAGATT GGAGGAGGAG GCGAGGGAGG
 751 AAGAAGGGCC CTGGCCTTTG CATGAGGCTC TCCGCATGGA CCCTCTGGAG
 801 GCCATCCAGC TGGAACTGGA CACTGTGAAT GCTCAGGCCG ACAGGGCCTT
 851 CCAACAGCTG GAGCACAAGT TTGGGCGGAT GCGTCGACAC TACCTGGAGC
 901 GGAGGAACTA CATCATTCAG AATATCCCGG GCTTCTGGAT GACTGCTTTT
 951 CGAAACCACC CCCAGTTGTC CGCCATGATT AGGGGCCAAG ATGCAGAGAT
1001 GTTAAGGTAC ATAACCAATT TAGAGGTGAA GGAACTCAGA CACCCTAGAA
1051 CCGGTTGCAA GTTCAAGTTC TTCTTTAGAA GAAACCCCTA CTTCAGAAAC
1101 AAGCTGATTG TCAAGGAATA TGAGGTAAGA TCCTCCGGCC GAGTGGTGTC
1151 TCTTTCTACT CCAATTATAT GGCGCAGGGG GCATGAACCC CAGTCCTTCA
1201 TTCGCAGAAA CCAAGACCTC ATCTGCAGCT TCTTCACTTG GTTTTCAGAC
1251 CACAGCCTTC CAGAGTCCGA CAAAATTGCT GAGATTATTA AAGAGGATCT
1301 GTGGCCAAAT CCACTGCAAT ACTACCTGTT GCGTGAAGGA GTCCGTAGAG
1351 CCCGACGTCG CCCGCTAAGG GAGCCTGTAG AGATCCCCAG GCCCTTTGGG
1401 TTCCAGTCTG GTTAACATTT GCCCTTGGGA ATACTCCTGC ACAAGGTCTC
1451 CTACCACCTT CTGCTGGACC TGTGCTTGGG CATCAGCAAT GAGTATGCCT
1501 TCTATTGTGC TTTGTTTTTG CTGACTTTTC TGCACCCTGT TTCCTTTGGA
1551 TATTCAGTTC TCTCAACCTC AAGATTGAGA CGGTGGTGGG TATGCTTCTC
1601 CACTTCCATA TGACCTTCAT GCTGTTCTGG AATATCACAT GCTACGAGGT
1651 CATCCTTCAC ACTACTTGTA AGCCAAGCAA ATGATACTGT AGATTGTACT
1701 GCCTTTATCT GCACTGCTTG GACCCTGTTT ATTCCCAGGG CCTCTGAACT
1751 GGTTGCTGTC ACTTGGATTT CTAGCTTTGG GAGCCTGTTC CACCTACTCA
1801 GCTCTGCATT GAGCAGTATG GGCACATGCC CTGTGGACAG TTACTGGACG
1851 TTAATGAACT CAGAGGAGAA AAGCAGTGAG CCACTTGTTC TGTGTGATTT
1901 ATGGTACTTC ATTGCTCTTC CTTCACCTCT AGTCACTTTC TATTGCTACC
1951 TGCCCTACAT TGGCTCCTGC CAAGGTCCCT CTCTCTCCCT GTTTTCCTTT
2001 TTTTTTTTTT TTTTTTTTTT TTTTGAGACG GAGGACGGAG TCTTGCTCTG
2051 TCGCCCAGGT TGGAGTGCAG TGGCGCGATC TCGGCTCACT GCAACCTCCA
2101 CCTCCCGGGT TCAAGCGATT CTCCTGCCTC AGCCTCCCGA GTAGCTGGGA
2151 CTACAGGCGC GCGCCGCCAC GCCCGGCTAA TTTTTATATT TTTAGTAGAG
2201 ACGGGGTTTC ACCATGCTGG CCAGGCTGGT CTCGAACCCC GACCTCGTGA
2251 TCCGCCCTCC TTAGCCTCCC AATCCTCTCT TAAAAAAGTG ATAGCTCAGA
2301 AATATTTGTA AAAGCAAGGT TTTTATTTCA TTTTGGCTCT GTCATTTTCA
2351 GAGGCAAAGA AGTTGGCCTG TAAAATAGAG TGCTAGAGCT CTTACGCCCC
2401 TCCCCTTCTT CCCAACTTCC TACTTCCTAG CCCTTTTATC AACTCCTAGA
2451 ATAGTTAAAG AGAGACACAT CTAGATGGGA TGAAAGGTGC CCTAAGCAGG
```

```
2501 AGAAACTGAA CAAAAGGCTA GAGGCATGGG CCAGGTAAAA ATTGGGCCTA
2551 GAGTGAAGAC TGTGCTGCCG TTAAGAGCTT TCGAGGAAGG AGTACTTACT
2601 CCCCAATGAT GATGAATGGA GAAATACTTT TCAGGGAGAA TTGAAGGGGT
2651 TAAAGTGTTA AATATGTTGC CTAGACAAGG GTTCTTTAAA GAAAGACAGC
2701 GCAACTTTGA ATGCTTTCTT ACTTGTTTTG TGACCTAATT TATGTGGAAG
2751 ATTGTTATTT CATTAGGATT TAGTAAAATT TTTTTTTCTG ATTCTAAACT
2801 TATTGTGAAA ATTGAGCTGT ACAGATATTC TTTTGATTTC AATTGGGAAC
2851 ATTTGGAAGA ACAACAGTCT TACTTGCCTG TACAATATAG AGACATATGA
2901 ATAGTCATAA CAGTTTTCAA CTTGTTCTTG TTTCTGTTAA ACTATATTCC
2951 TAGAAACATA GTTTGAACAA CTTGGTCTTT GTTAGGCTTG TCAAATTGCC
3001 TTCATGGAAA AATAATCTAC AAAAGTATGG TTTAATTGAT TGTCTTACAT
3051 GATAATTTTC CCTGGCAACA ACTTAGTAAG TGATATATCT TTTTTCCTAA
3101 ATTGCTTAAA TACTGTGAAA TTGCTCTGAC AAATTGGAAG TGTACCATTG
3151 GCATATTTGT CTTCCTTTTT ATGCATGATG GTAAAATAAA AGCATGTTGT
3201 TCTGCTAAGA AAAAAAAAAA AAAAAAAAA
```

BLAST Results

Entry AF042181 from database EMBLNEW:
Homo sapiens testis-specific Y-encoded-like protein (TSPYL) mRNA, partial cds.
Score = 3411, P = 6.9e-148, identities = 685/687

Entry HS938343 from database EMBL:
human STS WI-11947.
Score = 1195, P = 2.1e-46, identities = 273/299

Medline entries

98399864:
Murine and human TSPYL genes: novel members of the TSPY-SET-NAP1L1 family

Peptide information for frame 3

ORF from 99 bp to 1412 bp; peptide length: 438
Category: strong similarity to known protein
Classification: Differentiation/Development

```
  1 MSGLDGVKRT TPLQTHSIII SDQVPSDQDA HQYLRLRDQS EATQVMAEPG
 51 EGGSETVALP PSPPSEEGGV PQDPAGRGGT PQIRVVGGRG HVAIKAGQEE
101 GQPPAEGLAA ASVVMAADRS LKKGVQGGEK ALEICGAQRS ASELTAGAEA
151 EAEEVKTGKC ATVSAAVAER ESAEVVVKEG LAEKEVMEEQ MEVEEQPPEG
201 EEIEVAEEDR LEEEAREEEG PWPLHEALRM DPLEAIQLEL DTVNAQADRA
251 FQQLEHKFGR MRRHYLERRN YIIQNIPGFW MTAFRNHPQL SAMIRGQDAE
301 MLRYITNLEV KELRHPRTGC KFKFFFRRNP YFRNKLIVKE YEVRSSGRVV
351 SLSTPIIWRR GHEPQSFIRR NQDLICSFFT WFSDHSLPES DKIAEIIKED
401 LWPNPLQYYL LREGVRRARR RPLREPVEIP RPFGFQSG
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2d15, frame 3

TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds., N = 1, Score = 1202, P = 3.1e-122

TREMBL:AB018264_1 gene: "KIAA0721"; product: "KIAA0721 protein"; Homo sapiens mRNA for KIAA0721 protein, partial cds., N = 1, Score = 798, P = 2e-79

TREMBL:AB015345_1 gene: "HRIHFB2216"; Homo sapiens HRIHFB2216 mRNA, partial cds., N = 1, Score = 570, P = 2.9e-55

>TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds.
Length = 379

HSPs:

```
 Score = 1202 (180.3 bits), Expect = 3.1e-122, P = 3.1e-122
 Identities = 258/377 (68%), Positives = 283/377 (75%)

Query:    62 SPPSEEGGVPQDPAGR------GGTPQIRVVGGRGHVAIKAGQEE--GQP-P--AEGLAA 110
             SP  +EG    D  G       GTP  R + G          G+     G P P   EGL
Sbjct:     3 SPERDEGTPVPDSRGHCDADTVSGTPDRRPLLGEEKAVTGEGRAGIVGSPAPRDVEGLVP 62

Query:   111 ASVVMAADRSLKK-GVQGGEKALEICGAQRSASELTAGAEAEAEEVKTGKCATVSAAVAE 169
               V AA +        V+G   A+ +         ++ T GAE++A +VKT +  TV+AA
Sbjct:    63 QIRVAAARQGESPPSVRGPAAAVFVTPKYVEKAQETRGAESQARDVKT-EPGTVAAAA-- 119

Query:   170 RESAEVVVKEGLAEKEVMEEQMEVEEQPPEGEEIEVAEEDRLEEEAREEEGPWPLHEALR 229
              E +EV                  EE MEVE Q P GEE+E+ E        EA EE GPW L   LR
Sbjct:   120 -EKSEVATPGS-------EEVMEVE-QKPAGEEMEMLEASGGVREAPEEAGPWHLGIDLR 170

Query:   230 MDPLEAIQLELDTVNAQADRAFQQLEHKFGRMRRHYLERRNYIIQNIPGFWMTAFRNHPQ 289
              +PLEAIQLELDTVNAQADRAFQ LE KFGRMRRHYLERRNYIIQNIPGFWMTAFRNHPQ
Sbjct:   171 RNPLEAIQLELDTVNAQADRAFQHLEQKFGRMRRHYLERRNYIIQNIPGFWMTAFRNHPQ 230

Query:   290 LSAMIRGQDAEMLRYITNLEVKELRHPRTGCKFKFFFRRNPYFRNKLIVKEYEVRSSGRV 349
             LSAMIRG+DAEMLRY+T+LEVKELRHP+TGCKFKFFFRRNPYFRNKLIVKEYEVRSSGRV
Sbjct:   231 LSAMIRGRDAEMLRYVTSLEVKELRHPKTGCKFKFFFRRNPYFRNKLIVKEYEVRSSGRV 290

Query:   350 VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSDHSLPESDKIAEIIKEDLWPNPLQYY 409
             VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSDHSLPESD+IAEIIKEDLWPNPLQYY
Sbjct:   291 VSLSTPIIWRRGHEPQSFIRRNQDLICSFFTWFSDHSLPESDRIAEIIKEDLWPNPLQYY 350

Query:   410 LLREGVRRARRRPLREPVEIPRPFGFQSG 438
             L REG+RR RRRP+REPVEIPRPFGFQSG
Sbjct:   351 LCREGIRRPRRRPIREPVEIPRPFGFQSG 379
```

Pedant information for DKFZphfbr2_2d15, frame 3

Report for DKFZphfbr2_2d15.3

```
[LENGTH]        438
[MW]            49307.65
[pI]            5.36
[HOMOL]         TREMBL:AF042180_1 gene: "Tspyl1"; product: "testis-specific Y-encoded-like
protein"; Mus musculus testis-specific Y-encoded-like protein (Tspyl1) mRNA, complete cds. 1e-
107
[FUNCAT]        06.10 assembly of protein complexes  [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]        03.22 cell cycle control and mitosis  [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]        03.04 budding, cell polarity and filament formation  [S. cerevisiae, YKR048c]
1e-07
[FUNCAT]        09.13 biogenesis of chromosome structure     [S. cerevisiae, YKR048c] 1e-07
[FUNCAT]        30.10 nuclear organization     [S. cerevisiae, YKR048c] 1e-07
[BLOCKS]        BL00376F
[PIRKW]         nucleus 6e-39
[PIRKW]         DNA binding 3e-06
[PIRKW]         phosphoprotein 6e-39
[PIRKW]         alternative splicing 6e-39
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY     22.83 %
```

```
SEQ    MSGLDGVKRTTPLQTHSIIISDQVPSDQDAHQYLRLRDQSEATQVMAEPGEGGSETVALP
SEG    ...........................................................x
PRD    ccccccccccccccceeeeecccccccccchhhhhhhchhhhhccccccccccceeeecc

SEQ    PSPPSEEGGVPQDPAGRGGTPQIRVVGGRGHVAIKAGQEEGQPPAEGLAAASVVMAADRS
SEG    xxxxxxxxx...................................................
PRD    ccccccccccccccccccccceeeeeccccceeeeeccccccccccchhhhhhhhhhhhcc

SEQ    LKKGVQGGEKALEICGAQRSASELTAGAEAEAEEVKTGKCATVSAAVAERESAEVVVKEG
SEG    ....................xxxxxxxxxxxxxx......xxxxxxxxxxxxxxxxxx.
PRD    cccccccccccceeecchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ    LAEKEVMEEQMEVEEQPPEGEEIEVAEEDRLEEEAREEEGPWPLHEALRMDPLEAIQLEL
SEG    .xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....................
PRD    hhhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhcccccccchhhhhhhhhhhhhhh

SEQ    DTVNAQADRAFQQLEHKFGRMRRHYLERRNYIIQNIPGFWMTAFRNHPQLSAMIRGQDAE
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccceeeeeccccccccccccchhh

SEQ    MLRYITNLEVKELRHPRTGCKFKFFFRRNPYFRNKLIVKEYEVRSSGRVVSLSTPIIWRR
```

```
SEG    ............................................................
PRD    hhhhhhhhhhhhhccccceeeeeeeccccccccchhhhhhcccccccccccccccceeeecc

SEQ    GHEPQSFIRRNQDLICSFFTWFSDHSLPESDKIAEIIKEDLWPNPLQYYLLREGVRRARR
SEG    .................................................xxxxxxxxxxx
PRD    ccccchhhhhhcccccceeeeeccccccccchhhhhhhhcccccccceeeecccccchhhhh

SEQ    RPLREPVEIPRPFGFQSG
SEG    xxxxxxxx..........
PRD    hccccccccccccccccc
```

(No Prosite data available for DKFZphfbr2_2d15.3)

(No Pfam data available for DKFZphfbr2_2d15.3)

DKFZphfbr2_2d17
----

group: transmembrane proteins

DKFZphfbr2_2d17 encodes a novel 292 amino acid protein with similarity to a C.elegans hypothetical protein.

One transmembrane region is predicted for the protein.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans hypothetical protein

TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 1009 bp
Poly A stretch at pos. 990, polyadenylation signal at pos. 969

```
   1 TGGGCCTGTG GCTGGGGGCA GAGCTCAGAC TGTCTTCTGA AGATTGATGT
  51 CTATTTCCTT GAGCTCTTTA ATTTTGTTGC CAATTTGGAT AAACATGGCA
 101 CAAATCCAGC AGGGAGGTCC AGATGAAAAA GAAAAGACTA CCGCACTGAA
 151 AGATTTATTA TCTAGGATAG ATTTGGATGA ACTAATGAAA AAAGATGAAC
 201 CGCCTCTTGA TTTTCCTGAT ACCCTGGAAG GATTTGAATA TGCTTTTAAT
 251 GAAAAGGGAC AGTTAAGACA CATAAAAACT GGGGAACCAT TTGTTTTTAA
 301 CTACCGGGAA GATTTACACA GATGGAACCA GAAAAGATAC GAGGCTCTAG
 351 GAGAGATCAT CACGAAGTAT GTATATGAGC TCCTGGAAAA GGATTGTAAT
 401 TTGAAAAAAG TATCTATTCC AGTAGATGCC ACTGAGAGTG AACCAAAGAG
 451 TTTTATCTTT ATGAGTGAGG ATGCTTTGAC AAATCCACAG AAACTGATGG
 501 TTTTAATTCA TGGTAGTGGT GTTGTCAGGG CAGGGCAGTG GGCTAGAAGA
 551 CTTATTATAA ATGAAGATCT GGACAGTGGC ACACAGATAC CGTTTATTAA
 601 AAGAGCTGTG GCTGAAGGAT ATGGAGTAAT AGTACTAAAT CCCAATGAAA
 651 ACTATATTGA AGTAGAAAAG CCGAAGATAC ACGTACAGTC ATCATCTGAT
 701 AGTTCAGATG AACCAGCAGA AAAACGGGAA AGAAAAGATA AAGTTTCTAA
 751 AGTAACAAAG AAGCGACGTG ATTTCTATGA GAAGTATCGT AACCCCCAAA
 801 GAGAAAAAGA AATGATGCAA TTGTATATCA GAGTGAGTGA GATCACTACT
 851 TTCCTTTACT ATTTTCTTTA CCTTGTATAT ATTTTATTAT ATGTAGATTG
 901 TTTTGTTTTT CTTCAAGAAT ATTAATTTCT TTATTTGTCA TCATTTATTT
 951 CCCATGGTCG TCTACTTGGA TTAAATGGGT TTTTAAATTC AAAAAAAAAA
1001 AAAAAAAAA
```

BLAST Results

Entry I89937 from database EMBL:
Sequence 11 from patent US 5723315.
Score = 1083, P = 2.2e-42, identities = 223/231

Entry I89938 from database EMBL:
Sequence 12 from patent US 5723315.
Score = 875, P = 7.4e-33, identities = 175/175

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 47 bp to 922 bp; peptide length: 292
Category: similarity to unknown protein
Classification: unset

```
   1 MSISLSSLIL LPIWINMAQI QQGGPDEKEK TTALKDLLSR IDLDELMKKD
```

```
 51 EPPLDFPDTL EGFEYAFNEK GQLRHIKTGE PFVFNYREDL HRWNQKRYEA
101 LGEIITKYVY ELLEKDCNLK KVSIPVDATE SEPKSFIFMS EDALTNPQKL
151 MVLIHGSGVV RAGQWARRLI INEDLDSGTQ IPFIKRAVAE GYGVIVLNPN
201 ENYIEVEKPK IHVQSSSDSS DEPAEKRERK DKVSKVTKKR RDFYEKYRNP
251 QREKEMMQLY IRVSEITTFL YYFLYLVYIL LYVDCFVFLQ EY
```

BLASTP hits

Entry S67436 from database PIR:
hypothetical protein - fission yeast (Schizosaccharomyces pombe)
Length = 266
Score = 112 (39.4 bits), Expect = 0.00037, P = 0.00037
Identities = 33/147 (22%), Positives = 69/147 (46%)

Entry CEY75B8A_12 from database TREMBLNEW:
gene: "Y75B8A.31"; Caenorhabditis elegans cosmid Y75B8A
Score = 327, P = 1.5e-29, identities = 72/140, positives = 93/140

Alert BLASTP hits for DKFZphfbr2_2d17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2d17, frame 2

Report for DKFZphfbr2_2d17.2

```
[LENGTH]    292
[MW]        34260.50
[pI]        5.50
[HOMOL]     TREMBLNEW:AF064782_1 product: "unknown"; Mus musculus clone pEN87 unknown mRNA,
partial cds. 1e-119
[KW]        SIGNAL_PEPTIDE 19
[KW]        TRANSMEMBRANE  1
[KW]        LOW_COMPLEXITY    10.96 %

SEQ   MSISLSSLILLPIWINMAQIQQGGPDEKEKTTALKDLLSRIDLDELMKKDEPPLDFPDTL
SEG   .xxxxxxxxxxxxxx.............................................
PRD   ccchhhhhhchhhhhhhccccccccccchhhhhhhhhhhhcchhhhhhcccccccccccc
MEM   ............................................................

SEQ   EGFEYAFNEKGQLRHIKTGEPFVFNYREDLHRWNQKRYEALGEIITKYVYELLEKDCNLK
SEG   ............................................................
PRD   hhhhhhcccccceeeeccccccceeecccccccchhhhhhhhhhhhhhhhhhhhhhhhhe
MEM   ............................................................

SEQ   KVSIPVDATESEPKSFIFMSEDALTNPQKLMVLIHGSGVVRAGQWARRLIINEDLDSGTQ
SEG   ............................................................
PRD   eeeccccccccccceeeeeecccccccccceeeeeeccccchhhhhccccccccccccccc
MEM   ............................................................

SEQ   IPFIKRAVAEGYGVIVLNPNENYIEVEKPKIHVQSSSDSSDEPAEKRERKDKVSKVTKKR
SEG   ............................................................
PRD   chhhhhhhhccceeeeeccccceeeeeecccceeeeccccccccchhhhhhhhhhhhhhh
MEM   ............................................................

SEQ   RDFYEKYRNPQREKEMMQLYIRVSEITTFLYYFLYLVYILLYVDCFVFLQEY
SEG   .........................xxxxxxxxxxxxxxxxxx.........
PRD   hhhhhhhccccchhhhhhhhhhhhheeeeehhhhhhhhhhhhheeeeeeeeccc
MEM   .............................MMMMMMMMMMMMMMMMMMMMMMM
```

(No Prosite data available for DKFZphfbr2_2d17.2)

(No Pfam data available for DKFZphfbr2_2d17.2)

DKFZphfbr2_2d20
----

group: brain derived

DKFZphfbr2_2d20 encodes a novel 197 amino acid protein with similarity to Synechocystis sp. P74594 hypothetical32.8 kD protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to Synechocystis sp. (PCC 6803)

complete cDNA, complete cds, EST hits
potential start at bp 67 matches kozak consensus ANCatgG

Sequenced by Qiagen

Locus: unknown

Insert length: 1787 bp
Poly A stretch at pos. 1768, polyadenylation signal at pos. 1743

```
   1 TGGGGCGGCC GCGGCGGGAA CATGGAGGAG CTGCTGAGGC GCGAGCTGGG
  51 CTGCAGCTCT GTCAGGGCCA CGGGCCACTC GGGGGGCGGG TGCATCAGCC
 101 AGGGCCGGAG CTACGACACG GATCAAGGAC GAGTGTTCGT GAAAGTGAAC
 151 CCCAAGGCGG AGGCCAGAAG AATGTTTGAA GGTGAGATGG CAAGTTTAAC
 201 TGCCATCCTG AAAACAAACA CGGTGAAAGT GCCCAAGCCC ATCAAGGTTC
 251 TGGATGCCCC AGGCGGCGGG AGCGTGCTGG TGATGGAGCA CATGGACATG
 301 AGGCATCTGA GCAGTCATGC TGCAAAGCTT GGAGCCCAGC TGGCCGATTT
 351 ACACCTTGAT AACAAGAAGC TTGGAGAGAT GCGCCTGAAG GAGGCGGGCA
 401 CAGTGTGGAG AGGAGGTGGG CAGGAGGAAC GGCCCTTTGT GGCCCGGTTT
 451 GGATTTGACG TGGTGACGTG CTGTGGATAC CTCCCCCAGG TGAATGACTG
 501 GCAGGAGGAC TGGGTCGTGT TCTATGCCCG GCAGCGCATT CAGCCCCAGA
 551 TGGACATGGT GGAGAAGGAG TCTGGGGACA GGGAGGCCCT CCAGCTTTGG
 601 TCTGCTCTGC AGTAAAAGAT CCCTGACCTG TTCCGTGACC TGGAGATCAT
 651 CCCAGCCTTA CTCCACGGGG ACCTCTGGGG TGGAAACGTA GCAGAGGATT
 701 CCTCTGGGCC GGTGATTTTT GACCCAGCTT CTTTCTACGG CCACTCGGAA
 751 TATGAGCTGG CAATAGCTGG CATGTTTGGG GGCTTTAGCA GCTCCTTTTA
 801 CTCCGCCTAC CACGGCAAAA TCCCCAAGGC CCCAGGATTC GAGAAGCGCC
 851 TTCAGTTGTA TCAGCTCTTT CACTACTTGA ACCACTGGAA TCATTTTGGA
 901 TCGGGGTACA GAGGATCCTC CCTGAACATC ATGAGGAATC TGGTCAAGTG
 951 AGCGGGGCCTT ACTCTGGAAG GAGGTCTCAG AGGTTTCTCC ACAGTCCTCT
1001 TCTGGGCAAA TTCTTGTTTC TTCACATGCC GGACTAGCTT AAGACCAATG
1051 CAGTAGCTTA TTTCCAAGCC TTGCAAAGTA TATAATATCT AAGAGGAAAG
1101 GTTTTGTCAT CCCAGCGTTG TCCACTTTGT GGGGCTTTGT AGGTAGACGG
1151 AGCCACACTA CAGGCAGGGT ATGAGCAGAG GGATGTATGG AGTGTGGGCG
1201 ACTCTGAGCC TCACTGCTGC TGCAAGGTGG GGAAACTGTA AGTGAACCCC
1251 TGTGGGTGCG GGGGAGGGTA TCCGGTGCGC AGGGAGGTGG CCAGCGCCCC
1301 CGGGCACTGC TGCTCATAGG TACCTTTCCG CTGCCTCCTC CCTGCTCTCC
1351 TGTGCAGGAA TGTCTCTGAG CTGTTCACGT TGATGCTTCT TGGTTGGCAA
1401 GACTTGGGTG TAGACATGAA ACCACCTTAC TAAAAGCGTC TTAAAATGAC
1451 CAATTCCAGA ATCAAGCGTA TTCCGTTTTC CTCCTGCATG ATCCCTGGGC
1501 CCTCCCGCAG GCTGAGCAAG TCTGTAAACT GATTCTGGGA GAAACCAAGC
1551 TGCTGGCCGT AGGATGTCCT TGGGTACATC CAGGAGTCTT CATTGCTTCT
1601 GTTATTACCC CGTCTCCTCT GCCATTTTCT ACAGCTTGCT GAGTTGTCAT
1651 TCCTTTGCAA CATTAAAATA CATGCTGAAC TCATATTTTT CCTTCCTTCA
1701 CTGTTGTAGT AAAGAGACAT ATTTCATGAA TGGCATTGAT GCTAATAAAC
1751 CCTTTGCCCA AAAATTTGAA AAAAAAAAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 22 bp to 612 bp; peptide length: 197
Category: similarity to unknown protein
Prosite motifs: LEUCINE_ZIPPER (117-139)

```
  1 MEELLRRELG CSSVRATGHS GGGCISQGRS YDTDQGRVFV KVNPKAEARR
 51 MFEGEMASLT AILKTNTVKV PKPIKVLDAP GGGSVLVMEH MDMRHLSSHA
101 AKLGAQLADL HLDNKKLGEM RLKEAGTVWR GGGQEERPFV ARFGFDVVTC
151 CGYLPQVNDW QEDWVVFYAR QRIQPQMDMV EKESGDREAL QLWSALQ
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2d20, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2d20, frame 1

Report for DKFZphfbr2_2d20.1

[LENGTH]	197
[MW]	21963.25
[pI]	6.96
[HOMOL]	PIR:S76790 hypothetical protein - Synechocystis sp. (strain PCC 6803) 9e-12
[SUPFAM]	hypothetical protein b1725 1e-06
[PROSITE]	LEUCINE_ZIPPER 1
[PROSITE]	MYRISTYL 2
[PROSITE]	GLYCOSAMINOGLYCAN 1
[PROSITE]	PKC_PHOSPHO_SITE 2
[KW]	Alpha_Beta

```
SEQ  MEELLRRELGCSSVRATGHSGGGCISQGRSYDTDQGRVFVKVNPKAEARRMFEGEMASLT
PRD  ccchhhhhcccccceeeeccccccccceeeccccccccccceeeeeecchhhhhhhhhhhhhh

SEQ  AILKTNTVKVPKPIKVLDAPGGGSVLVMEHMDMRHLSSHAAKLGAQLADLHLDNKKLGEM
PRD  hhhhhheeeecccceeeeccccccceeeeecccccccchhhhhhhhhhhhhhcccccchhh

SEQ  RLKEAGTVWRGGGQEERPFVARFGFDVVTCCGYLPQVNDWQEDWVVFYARQRIQPQMDMV
PRD  hhhhhcccccccccccceeecccccceeeccccccccccccchhhhhhhhhhhhhhhh

SEQ  EKESGDREALQLWSALQ
PRD  hhhccchhhhhhhccc
```

Prosite for DKFZphfbr2_2d20.1

PS00002	20->24	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	13->16	PKC_PHOSPHO_SITE	PDOC00005
PS00005	67->70	PKC_PHOSPHO_SITE	PDOC00005
PS00008	22->28	MYRISTYL	PDOC00008
PS00008	104->110	MYRISTYL	PDOC00008
PS00029	96->118	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2_2d20.1)

DKFZphfbr2_2g18
----

group: brain derived

DKFZphfbr2_2g18 encodes a novel 229 amino acid protein with partial similarity to the humane dJ30M3.2 gene product.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

J30M3.2 extension of genmodel

complete cDNA, complete cds, EST hits
(mouse ESTs with >90% Identities)

Sequenced by Qiagen

Locus: /map="6p22.1-22"

Insert length: 2444 bp
Poly A stretch at pos. 2425, no polyadenylation signal found

```
   1 TGGTCGAGGG TCGACGGTAT CGATAAGTTT TTTTTTTTTT TTTTTTTTTT
  51 TGGAAAGCAA GGATCACACT TCCCCCTCCC TGTTCCTTAA TCCCTTTTCT
 101 AAAAAGGGGG GAAAATCCGG ATGGATTTTA GGGATTGGTC TGGTGTCAGC
 151 TGTGTCTTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG
 201 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTTCC AGAAAGTTAG
 251 TTATTTTCTC CTCTTTCTTT CCTTTCTTTC CTCCCTTTTT CCCGTCTGAC
 301 CCCAAACGTT ATTGTCCAAA CATGACTGGA CAGCAGCTTT TGTTTCTTGA
 351 CCCTGTAATA TGACAGTCTG CTAATATTGA CAGAAGGTGC AGTTTTTGGG
 401 TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA AAAAAAATGA
 451 CTTGTTTCTG TTGTACTTGA GTCTTAAGAA AAAGTGCCCA TAGTTTAGTG
 501 ACAATTTCCA AAGGCTTTAG TACCACCTGT ATTTCAAAAT GGGGGACCCA
 551 AACTCCCGGA AGAAACAAGC TCTGAACAGA CTACGTGCTC AGCTTAGAAA
 601 GAAAAAAGAA TCTCTAGCTG ACCAGTTTGA CTTCAAGATG TATATTGCCT
 651 TTGTATTCAA GGAGAAGAAG AAAAAGTCAG CACTTTTTGA AGTGTCTGAG
 701 GTTATACCAG TCATGACAAA TAATTATGAA GAAAATATCC TGAAAGGTGT
 751 GCGAGATTCC AGCTATTCCT TGGAAAGTTC CCTAGAGCTT TTACAGAAGG
 801 ATGTGGTACA GCTCCATGCT CCTCGATATC AGTCTATGAG AAGGGATGTA
 851 ATTGGCTGTA CTCAGGAGAT GGATTTCATT CTTTGGCCTC GGAATGATAT
 901 TGAAAAAATC GTCTGTCTCC TGTTTTCTAG GTGGAAAGAA TCTGATGAGC
 951 CTTTTAGGCC TGTTCAGGCC AAATTTGAGT TTCATCATGG TGACTATGAA
1001 AAACAGTTTC TGCATGTACT GAGCCGCAAG GACAAGACTG GAATCGTTGT
1051 CAACAATCCT AACCAGTCAG TGTTTCTCTT CATTGACAGA CAGCACTTGC
1101 AGACTCCAAA AAACAAAGCT ACAATCTTCA AGTTATGCAG CATCTGCCTC
1151 TACCTGCCAC AGGAACAGCT CACCCACTGG GCAGTTGGCA CCATAGAGGA
1201 TCACCTCCGT CCTTATATGC CAGAGTAGAG TACTGACCAG CAAAATGGAG
1251 AAGATCAGAG AATGCAGCAG CAGTTTTTTT TCTTGTTTTC TTACCACTTT
1301 ATTCTTTCAG AGTTTAAAGA AAATGGACTC ATGCACAGAA CACTATGCAT
1351 TTTGAAACTT GTTCATCCTG GATTTTTTTA AATCATTTTT ATCTCAGAAC
1401 TTAAACAAAA ATTAGATGTC GTGCACGGAC TGTGTGAAAG AAGATGCTTT
1451 GCATATTTGC TGCACTGCAT CAGTATCTTA CTAAAAATGT GAAATGAAAG
1501 GACTATTGTA CACTGAAATG CTTAAATGTA TCTGAAAGCA CAAGGTGATA
1551 CTCATTTTTA TGGTCTTCCC ATTTGTGCTG GTTTTTGCCT CTTTGACATC
1601 TGTCATCAGT ATTTAGAGGG TGAGAAGTGA ATGTAACAGG TATAAATAAC
1651 ATTTTTAAAA ACAATAACTT TGCTATAATC ACAGTTGTTC CAGAGCACTG
1701 TCAGATACAT TCTAATGACC AGAACTGGTT TAAAAAAAGA AAATACAACC
1751 ATGGGAAAGA AATCTTAAAT GAAAAACGCA TCTCATTGTA GGCATTTTTG
1801 CCTCATATTT TACTGGGCCA TGTTTGTTTC CTGGTACTCA TGTATTTTTT
1851 TTTTTTCCAG ATCTCTTTCC CCAAGTTGCT ATTGTAAGAG TATTCTGCTG
1901 CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT CTGAAGTAGC
1951 TATAAAGCAG CTATAAAACA GAAATACATG CATAGCTGCA GAAACCATGA
2001 TAGGTAGAGG ACTTTTCTTT TGGTTTTGTT TTGTTTTGTT TTGTTTTGTT
2051 TTTGGTTTTA CAGAGAAGAG ATTTTTATTA CAAAGAAAAA AATTCCAGTG
2101 AATTGTGCAG AAATGCTGGT TTTTACACCA TCCTAAAGAA AAACTTTACA
2151 AGGGTGTTTT GGAGTAGAAA AAAGGTTATA AAGTTGGAAT CTTAAATTGT
2201 AAAATTAACC ATTGAGTGTC AAAGTTCTAA AAGCAGAACT CATTTCGTGC
2251 AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TCTCCTTTTA
2301 AATGAAGAAA AGCTTTGCTT AAGGGTTGCA TACTTTTATT GGAGTAAATC
2351 TGAATGATCC TACTCCTTTG GAGTAAGACT AGTGCTTACC AGTTTCCAAT
2401 TGTATTTAGC TTCTGTTGGA ATTTGAAAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry HS338352 from database EMBL:
human STS EST171398.
Score = 1747, P = 3.0e-74, identities = 359/365

Entry HS447255 from database EMBL:
human STS SHGC-10143.
Score = 1717, P = 6.5e-73, identities = 365/383

Entry HS30M3 from database EMBLNEW:
Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands.
Score = 6646, P = 0.0e+00, identities = 1344/1355

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 539 bp to 1225 bp; peptide length: 229
Category: putative protein

```
  1 MGDPNSRKKQ ALNRLRAQLR KKKESLADQF DFKMYIAFVF KEKKKKSALF
 51 EVSEVIPVMT NNYEENILKG VRDSSYSLES SLELLQKDVV QLHAPRYQSM
101 RRDVIGCTQE MDFILWPRND IEKIVCLLFS RWKESDEPFR PVQAKFEFHH
151 GDYEKQFLHV LSRKDKTGIV VNNPNQSVFL FIDRQHLQTP KNKATIFKLC
201 SICLYLPQEQ LTHWAVGTIE DHLRPYMPE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2g18, frame 2

TREMBLNEW:HS30M3_2 gene: "dJ30M3.2"; product: "dJ30M3.2 (novel protein)"; Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands., N = 1, Score = 470, P = 1.1e-44

>TREMBLNEW:HS30M3_2 gene: "dJ30M3.2"; product: "dJ30M3.2 (novel protein)"; Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands.
Length = 86

HSPs:

Score = 470 (70.5 bits), Expect = 1.1e-44, P = 1.1e-44
Identities = 86/86 (100%), Positives = 86/86 (100%)

```
Query:   144 AKFEFHHGDYEKQFLHVLSRKDKTGIVVNNPNQSVFLFIDRQHLQTPKNKATIFKLCSIC 203
             AKFEFHHGDYEKQFLHVLSRKDKTGIVVNNPNQSVFLFIDRQHLQTPKNKATIFKLCSIC
Sbjct:     1 AKFEFHHGDYEKQFLHVLSRKDKTGIVVNNPNQSVFLFIDRQHLQTPKNKATIFKLCSIC 60

Query:   204 LYLPQEQLTHWAVGTIEDHLRPYMPE 229
             LYLPQEQLTHWAVGTIEDHLRPYMPE
Sbjct:    61 LYLPQEQLTHWAVGTIEDHLRPYMPE 86
```

Pedant information for DKFZphfbr2_2g18, frame 2

Report for DKFZphfbr2_2g18.2

[LENGTH] 229
[MW] 27083.42
[pI] 9.04
[HOMOL] TREMBL:HS30M3_2 gene: "dJ30M3.2"; product: "dJ30M3.2 (novel protein)"; Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands. 6e-47
[PROSITE] MYRISTYL 2
[PROSITE] CAMP_PHOSPHO_SITE 2
[PROSITE] CK2_PHOSPHO_SITE 4
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] PKC_PHOSPHO_SITE 4
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 5.24 %

```
SEQ  MGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAFVFKEKKKKSALFEVSEVIPVMT
SEG  ............................................................
PRD  ccccchhhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhheeeeec

SEQ  NNYEENILKGVRDSSYSLESSLELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRND
SEG  ............xxxxxxxxxxxx....................................
PRD  cchhhhhhhccccccccccchhhhhhhhhhhhhcccccccccceeeccccccceeeeccch

SEQ  IEKIVCLLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIVVNNPNQSVFL
SEG  ............................................................
PRD  hhhhhhhhhhhcccccccccccccccccccchhhhhhhhhhhccccceeeeccccceeee

SEQ  FIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHWAVGTIEDHLRPYMPE
SEG  .................................................
PRD  eeccccccccccceeeeeeeeeeeecccccccccceeeecccccccccc
```

Prosite for DKFZphfbr2_2g18.2

PS00001	175->179	ASN_GLYCOSYLATION	PDOC00001
PS00004	22->26	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	44->48	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	99->102	PKC_PHOSPHO_SITE	PDOC00005
PS00005	162->165	PKC_PHOSPHO_SITE	PDOC00005
PS00005	189->192	PKC_PHOSPHO_SITE	PDOC00005
PS00006	25->29	CK2_PHOSPHO_SITE	PDOC00006
PS00006	80->84	CK2_PHOSPHO_SITE	PDOC00006
PS00006	162->166	CK2_PHOSPHO_SITE	PDOC00006
PS00006	218->222	CK2_PHOSPHO_SITE	PDOC00006
PS00007	69->77	TYR_PHOSPHO_SITE	PDOC00007
PS00008	70->76	MYRISTYL	PDOC00008
PS00008	168->174	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_2g18.2)

DKFZphfbr2_2h1

group: brain derived

DKFZphfbr2_2h1 encodes a novel 180 amino acid protein with weak similarity to C.elegans D2007.4 protein

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to C.elegans D2007.4 protein

CpG island in 5' region, complete cDNA

Sequenced by Qiagen

Locus: unknown

Insert length: 957 bp
Poly A stretch at pos. 939, polyadenylation signal at pos. 916

```
  1 GGGGGTCCCT GACTTTATAT GGCTGCTCCT GGCGAGCGAC TGAGTCGTCC
 51 GTGAGGAAAA AGAGGCGAGG CTTTTCCGAG ATCGTCTCAG CGATGGCGCT
101 TCGGTCGCGG TTTTGGGGGT TGTTCTCGGT TTGCAGGAAC CCTGGGTGCA
151 GGTTCGCAGC CCTGTCAACC AGCTCCGAGC CGGCAGCGAA ACCTGAAGTG
201 GACCCTGTGG AAAATGAAGC TGTCGCCCCA GAATTCACCA ACCGGAACCC
251 CCGGAACCTG GAGCTTTTGT CTGTAGCCAG GAAAGAGCGG GGCTGGCGGA
301 CGGTGTTTCC CTCCCGTGAG TTCTGGCACA GGTTGCGAGT TATAAGGACT
351 CAGCATCATG TAGAAGCACT TGTGGAGCAT CAGAATGGCA AGGTTGTGGT
401 TTCGGCCTCC ACTCGTGAGT GGGCTATTAA AAAGCACCTT TATAGTACCA
451 GAAATGTGGT GGCTTGTGAG AGTATAGGAC GAGTGCTGGC ACAGAGATGC
501 TTAGAGGCGG GAATCAACTT CATGGTCTAC CAACCAACCC CGTGGGAGGC
551 AGCCTCAGAC TCGATGAAAC GACTACAAAG TGCCATGACA GAAGGTGGTG
601 TGGTTCTACG GGAACCTCAG AGAATCTATG AATAAATGGA AGCATTAATT
651 GTTTTGAACA TGTAAATATA AATCTGTCAG CCACTACAGC CATCAAAAGA
701 GAGCATCTGG AAGAACAGCC AGCTTGGAAG TTTTACAGCA ATAATGTTGC
751 AGTGGAATAT TATTTGTAGT TAAGGTCATC CTCCTCCCCT TTCTGTTTTT
801 TTAAATCAAG AACTACGTTC TGCCCCTCTC TTGGGCTTCA GAAGCATCTA
851 AGAAAAGCAG TCATCAATTA TAATTAACTT TCAAAGGGCA AGTCAGAAGT
901 TGTTTATAAA TTACAAAATA AAGGCATATT ATGAACTCTA AAAAAAAAAA
951 AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 93 bp to 632 bp; peptide length: 180
Category: similarity to known protein
Classification: unset

```
  1 MALRSRFWGL FSVCRNPGCR FAALSTSSEP AAKPEVDPVE NEAVAPEFTN
 51 RNPRNLELLS VARKERGWRT VFPSREFWHR LRVIRTQHHV EALVEHQNGK
101 VVVSASTREW AIKKHLYSTR NVVACESIGR VLAQRCLEAG INFMVYQPTP
151 WEAASDSMKR LQSAMTEGGV VLREPQRIYE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2h1, frame 3

PIR:S44789 D2007.4 protein - Caenorhabditis elegans, N = 1, Score = 194, P = 2e-15

PIR:JC5753 ribosomal protein L18 - Vibrio proteolyticus, N = 1, Score = 121, P = 1.1e-07

```
>PIR:S44789 D2007.4 protein - Caenorhabditis elegans
           Length = 170

  HSPs:

 Score = 194 (29.1 bits), Expect = 2.0e-15, P = 2.0e-15
 Identities = 51/134 (38%), Positives = 78/134 (58%)

Query:    48 FTNRNPRNLELLSVARKERGWRTVFP--SREFWHRLRVIRTQHHVEA-LVEHQNGKVVVS 104
             F NRNPRN EL+       G++       +R + +++ ++  + H E  LV +Q+G VV+S
Sbjct:     9 FVNRNPRNNELMGRQAPNTGYQFEKDRAARSYIYKVELVEGKSHREGRLVHYQDG-VVIS 67

Query:   105 ASTREWAIKKHLYSTRNVVACESIGRVLAQRCLEAGINFMVYQPTPWEAASDSMKRLQ-- 162
             AST+E +I    LYS  +  A  +IGRVLA RCL++GI+F +    T  EA    S  +
Sbjct:    68 ASTKEPSIASQLYSKTDTSAALNIGRVLALRCLQSGIHFAMPGATK-EAIEKSQHQTHFF 126

Query:   163 SAMTEGGVVLREPQRI 178
              A+ E G+ L+EP  +
Sbjct:   127 KALEEEGLTLKEPAHV 142
```

Pedant information for DKFZphfbr2_2h1, frame 3

Report for DKFZphfbr2_2h1.3

```
[LENGTH]      180
[MW]          20576.57
[pI]          9.63
[HOMOL]       PIR:S44789 D2007.4 protein - Caenorhabditis elegans 2e-13
[FUNCAT]      j mrna translation and ribosome biogenesis   [H. influenzae, HI0794] 2e-04
[SUPFAM]      Escherichia coli ribosomal protein L18 8e-06
[KW]          Alpha_Beta

SEQ    MALRSRFWGLFSVCRNPGCRFAALSTSSEPAAKPEVDPVENEAVAPEFTNRNPRNLELLS
PRD    cccccccceeeeeeeecccccceeeecccccccccccccccccceeeecccccccccchhhhh

SEQ    VARKERGWRTVFPSREFWHRLRVIRTQHHVEALVEHQNGKVVVSASTREWAIKKHLYSTR
PRD    hhhhcccccccccchhhhhhhhhhcccccchhhhhhhhhccccceeeeechhhhhhhhhhhhcc

SEQ    NVVACESIGRVLAQRCLEAGINFMVYQPTPWEAASDSMKRLQSAMTEGGVVLREPQRIYE
PRD    ccceeehhhhhhhhhhhhhcceeeeeccccchhhhhhhhhhhhhhccceeeccccccccc
```

(No Prosite data available for DKFZphfbr2_2h1.3)

(No Pfam data available for DKFZphfbr2_2h1.3)

DKFZphfbr2_2h10
----

group: brain derived

DKFZphfbr2_2h10 encodes a novel 220 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 2176 bp
Poly A stretch at pos. 2161, polyadenylation signal at pos. 2143

```
   1 TGGGGAGTAT TCTAATTATA TTTTATATTT AATAAATTAT TTTTCTATTT
  51 CTTTGTTATA TTAAGTTGCA CACTTGTTTC TTTTATCCAG AAAGTTTAGT
 101 ATAATAAAAA TAGTTTTAAG ATTAACTGTG AATGTAAAGG AAAAGTATTA
 151 TTAATTATTT CAGGAAATTG CAAGACCTAA CATGGCTGAA AGAGAAACAG
 201 AAACATCAAA TTCTGAAAGT AAACAAGATA AAGCTGCTTC TTCAAAAGAA
 251 AAAAATGGAT GTAATGCAAA TTCATTTGAA GGCTCATCAA CAACAAAAAG
 301 TGAAGAAAGC ATAACAGTTT CAGATAAGGA AAATGAAACC TGTCTTGCAG
 351 ACCAGGAAAC TGGCTCAAAA AACATCGTCA GTTGTGATTC AAATATTGGT
 401 GCAGATAAAG TGGAAAAGAA AAAACAAATA CAACACGTTT GTCAGGAAAT
 451 GGAGTTGAAG ATGTGCCAGA GTTCAGAAAA CATAATCTTA TCTGATCAGA
 501 TTAAAGATCA CAACTCCAGT GAAGCCAGAT TTTCTTCAAA GAATATTAAG
 551 GATTTGCGAT TAGCATCAGA TAATGTAAGC ATTGATCAGT TTTTGAGAAA
 601 AAGACATGAA CCTGAATCTG TTAGTTCTGA TGTTAGCGAG CAAGGCAGTA
 651 TTCATTTGGA ACCTCTGACT CCATCCGAGG TACTTGAGTA TGAAGCCACA
 701 GAGATTCTTC AGAAAGGTAG TGGTGATCCT TCAGCCAAGA CTGATGAAGT
 751 AGTGTCTGAT CAAACAGATG ACATTCCTGG AGGAAATAAC CCTAGCACAA
 801 CAGAGGCAAC AGTAGACCTG GAAGATGAAA AAGAAAGAAG TTGAAATTAG
 851 TCATTTTAAG TTTCAGTGTA CCAACGATAA GGGCATTTGG AACAGTGCTA
 901 TCAGGTGAGC TCAGTGGTGC TGTTGTAGGT TCAGAAATGG AAATATGTAA
 951 GGGAGGTCAC ACATACACTT TACCTGTATG TTCAACCTAT GTTATCAAAC
1001 AAACCAATTC ACCAATAATA GCATGATTAG TAGGGATTCC CAAAAAGTTT
1051 TTAAAAACAC GAACAGGATT TTAATGATAA TTAAATTTGC AGTGGAAAGG
1101 TCTCATTTAA TGGTTTTCAA GGAAATGGGA TTTGGTTGCT GACATGAATT
1151 GATGATATTA GTAATATTTA TAAAGCCTTT CAAACTTCCA TCAATCCTAA
1201 GCTAAAAATC TTTATTACCT GTATATCCTT TTCAGTTAAC TGAGAGGAAG
1251 GGATTTGGAA ACCATGTACT TTTGGGGAGT AATTGATTAA AAACAATGGC
1301 TGATTGGCAT TGTTAATGAA GGCTTTATTT GTGAGGATGA TGCTGGTAAA
1351 TGGAGCATGC TTAGAGTACT AAATTGATCT AATGAGAATT TGGATGAACA
1401 TAAACTTAAT TTTGGATTTA ATATAACATT CCAGTCAGAC GCATGTAAAC
1451 AGAATATTTG AATCTTTGTA CCTCCATACA AGTGTTAGCC TGCCAGGCTG
1501 TAAGCTTACC TTAATTAAAC TTTCAGTGAA AGTGGAATTA TTAAGATATA
1551 AATTTATATT TGTGCTTTTT GTCAGTGTGT AAGCTGTGTA GAAATTCTTT
1601 GATGTATTAG TTGTATTAAT GTAAAGTAGA AACCCATTGT TGAAACTCCT
1651 GTAGCTATTA TGCTTTTAAT ATTGTTTTAA TGTTCTTCCT TAGAAATAGG
1701 CCCATAAAAA TGGTCTGGAA GCCAAACCAA AGTATGGTAT AATGTAGATA
1751 TTGTAAAGCA GTAAACTGAA AACATGTCCT GGCATGTATT CAGCCATGTT
1801 TAAGTGACTT TTCTGTAATT GTAAAATAAA AACTTCAAAT GGGACCTAAA
1851 ACAGTGATGT AAAAGAACTG GTTTTGGAAA TTTAGCCTAA TTTATCTATA
1901 AGATGGCTGC TAAATTGATT TTTCAGTTCT TTTTATCATC TAAAATATAA
1951 TAGATATAGA AATGAATAAT ATGAAGAACA GTAGTTTGCT TTGAAATACT
2001 AATAAACTTT TATTTAAGAT GCTTCATTTT TACTTCTTAA AACGTGCTTT
2051 GGATTCTTAA ATTTTGTTTC ACTGAATGTT CAATGTTTTA AATGGCGATT
2101 AAAATACTCT GCTGTATATA GTAGTTTTTG AGTAAATATT TGCAATAAAA
2151 ATCTGCCCCC GAAAAAAAAA AAAAAA
```

BLAST Results

Entry G35287 from database EMBL:
human STS SHGC-37375.
Score = 2163, P = 2.8e-91, identities = 437/441

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 182 bp to 841 bp; peptide length: 220
Category: putative protein

```
  1 MAERETETSN SESKQDKAAS SKEKNGCNAN SFEGSSTTKS EESITVSDKE
 51 NETCLADQET GSKNIVSCDS NIGADKVEKK KQIQHVCQEM ELKMCQSSEN
101 IILSDQIKDH NSSEARFSSK NIKDLRLASD NVSIDQFLRK RHEPESVSSD
151 VSEQGSIHLE PLTPSEVLEY EATEILQKGS GDPSAKTDEV VSDQTDDIPG
201 GNNPSTTEAT VDLEDEKERS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2h10, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_2h10, frame 2

Report for DKFZphfbr2_2h10.2

```
[LENGTH]      220
[MW]          24109.02
[pI]          4.51
[FUNCAT]      04.99 other transcription activities  [S. cerevisiae, YKR092c] 4e-05
[FUNCAT]      30.10 nuclear organization   [S. cerevisiae, YKR092c] 4e-05
[PROSITE]     MYRISTYL         3
[PROSITE]     CK2_PHOSPHO_SITE      8
[PROSITE]     PKC_PHOSPHO_SITE      5
[PROSITE]     ASN_GLYCOSYLATION     3
[PFAM]        TNFR/NGFR cysteine-rich region
[KW]          Alpha_Beta
```

```
SEQ   MAERETETSNSESKQDKAASSKEKNGCNANSFEGSSTTKSEESITVSDKENETCLADQET
PRD   cccccccccccccchhhhhhhcccccccccccccccccceeeeeeeeccccccccccccc

SEQ   GSKNIVSCDSNIGADKVEKKKQIQHVCQEMELKMCQSSENIILSDQIKDHNSSEARFSSK
PRD   cccceeeecccccchhhhhhhhhhhhhhhhhhhhhhcceeeeccccccccccccccccc

SEQ   NIKDLRLASDNVSIDQFLRKRHEPESVSSDVSEQGSIHLEPLTPSEVLEYEATEILQKGS
PRD   cchhhhhhccccchhhhhhhcccccccccccccccceeecccccccchhhhhhhcccccc

SEQ   GDPSAKTDEVVSDQTDDIPGGNNPSTTEATVDLEDEKERS
PRD   ccccccccccccccccccccccccccceeeehhhhhhccc
```

Prosite for DKFZphfbr2_2h10.2

PS00001	51->55	ASN_GLYCOSYLATION	PDOC00001
PS00001	111->115	ASN_GLYCOSYLATION	PDOC00001
PS00001	131->135	ASN_GLYCOSYLATION	PDOC00001
PS00005	20->23	PKC_PHOSPHO_SITE	PDOC00005
PS00005	37->40	PKC_PHOSPHO_SITE	PDOC00005
PS00005	47->50	PKC_PHOSPHO_SITE	PDOC00005
PS00005	118->121	PKC_PHOSPHO_SITE	PDOC00005
PS00005	184->187	PKC_PHOSPHO_SITE	PDOC00005
PS00006	9->13	CK2_PHOSPHO_SITE	PDOC00006
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00006	20->24	CK2_PHOSPHO_SITE	PDOC00006
PS00006	38->42	CK2_PHOSPHO_SITE	PDOC00006
PS00006	45->49	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	163->167	CK2_PHOSPHO_SITE	PDOC00006
PS00006	205->209	CK2_PHOSPHO_SITE	PDOC00006
PS00008	26->32	MYRISTYL	PDOC00008

PS00008	34->40	MYRISTYL	PDOC00008
PS00008	201->207	MYRISTYL	PDOC00008

Pfam for DKFZphfbr2_2h10.2

```
HMM_NAME     TNFR/NGFR cysteine-rich region

HMM             *CpeG.tYtD.WNHvpqClpCtrCePEMGQYMvqPCTwTQNTVC*
                 +E+ T +D +N  ++C      E   G+  + +C+++  +
Query        40  SEESITVSDKEN--ETC--LADQET--GSKNIVSCDSNIGADK      76
```

DKFZphfbr2_2i17
----

group: intracellular transport and trafficking

DKFZphfbr2_2i17.3 encodes a novel 201 amino acid putative GTP-binding protein related to Rab1B.

Rab proteins are members of the Ras superfamily of GTPases. Rab proteins are localised to the cytoplasmic side of organelles and vesicles involved in the secretory(biosynthetic) and endocytotic pathways in eukaryotic cells. Rab proteins direct the targeting and fusion of transport vesicles to their acceptor membranes. Rab1B is essential for the intracellular transport of nascent low density lipoprotein (LDL) receptor. It is discussed as a universal mediator of endoplasmatic reticulum to Golgi transport of membrane glycoproteins in mammalian cells.

The new protein can find clinical application in modulating the transport of glycoproteins inside cells, especially of the LDL receptor.

Medline
96245776: Intracellular transport and maturation of nascent low density lipoprotein receptor is blocked by mutation in the Ras-related GTP-binding protein, RAB1B

strong similarity to rab1

complete cDNA, complete cds, start at 47, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1985 bp
Poly A stretch at pos. 1901, polyadenylation signal at pos. 1859

```
   1 GGGAGCAGAG TCGACTGGGA GCGACCGAGC GGGCCGCCGC CGCCGCCATG
  51 AACCCCGAAT ATGACTACCT GTTTAAGCTG CTTTTGATTG GCGACTCAGG
 101 CGTGGGCAAG TCATGCCTGC TCCTGCGGTT TGCTGATGAC ACGTACACAG
 151 AGAGCTACAT CAGCACCATC GGGGTGGACT TCAAGATCCG AACCATCGAG
 201 CTGGATGGCA AAACTATCAA ACTTCAGATC TGGGACACAG CGGGCCAGGA
 251 ACGGTTCCGG ACCATCACTT CCAGCTACTA CCGGGGGGCT CATGGCATCA
 301 TCGTGGTGTA TGACGTCACT GACCAGGAAT CCTACGCCAA CGTGAAGCAG
 351 TGGCTGCAGG AGATTGACCG CTATGCCAGC GAGAACGTCA ATAAGCTCCT
 401 GGTGGGCAAC AAGAGCGACC TCACCACCAA GAAGGTGGTG GACAACACCA
 451 CAGCCAAGGA GTTTGCAGAC TCTCTGGGCA TCCCCTTCTT GGAGACGAGC
 501 GCCAAGAATG CCACCAATGT CGAGCAGGCG TTCATGACCA TGGCTGCTGA
 551 AATCAAAAAG CGGATGGGGC CTGGAGCAGC CTCTGGGGGC GAGCGGCCCA
 601 ATCTCAAGAT CGACAGCACC CCTGTAAAGC CGGCTGGCGG TGGCTGTTGC
 651 TAGGAGGGGC ACATGGAGTG GGACAGGAGG GGGCACCTTC TCCAGATGAT
 701 GTCCCTGGAG GGGGGAGGAG GTACCTCCCT CTCCCTCTCC TGGGGCATTT
 751 GAGTCTGTGG CTTTGGGGTG TCCTGGGCTC CCCATCTCCT TCTGGCCCAT
 801 CTGCCTGCTG CCCTGAGCCC CGGTTCTGTC AGGGTCCCTA AGGGAGGACA
 851 CTCAGGGCCT GTGGCCAGGC AGGGCGGAGG CCTGCTGTGC AGTTGCCTCT
 901 AGGTGACTTT CCAAGATGCC CCCCTACACA CCTTTCTTTG GAACGAGGGC
 951 TCTTCTGTCG GTGTCCCTCC CACCCCCATG TATGCTGCAC TGGGTTCTCT
1001 CCTTCTTCTT CCTGCTGTCC TGCCCAAGAA CTGAGGGTCT CCCCGGCCTC
1051 TACTGCCCTG GCTGCAGTCA GTGCCCAGGG CGAGGAATGT GGCCAGGGGA
1101 TCCAGGACCT GGGATCCAGG GCCCTGGGCT GGACCTCAGG ACAGGCATGG
1151 AGGCCACAGG GGCCCAGCAG CCCACCCTTT CCTCTCCCCA CTGCCTCCTC
1201 TCCCTTCCTA CACTCCCAGC TCGAGCCGTC CAGCTGCGGT GGGATCTGAG
1251 TATATCTAGG GCGGGTGGGC GGGTAGCAGT GCTGGGCCTG TGTCTTGAGC
1301 CTGGAGGGAG ACTGCTCCTG CCGCCCTCTG CCCTGCCGGA GACAGACCCA
1351 TGCGCTGCCT GCCCACCGTG CCCCTTTGTC CCCATGTCAG GCGGAGGCGG
1401 AAGGCCCACC GTGCCAGAGG CTGGGCACCA GCCTTAACCC TCACTCTGCT
1451 AGCACCTCCT CCCTTTCCCC AAGGTAGCAC ATCTGGCTCA CTCCCCACTC
1501 CGTCTCTGGA GCCCACCAGG GAAGGCCCTC ATCCCCTGCC GCTACTTCTC
1551 TGGGGAATGT GGGTTCCATC CAGGATTGGG GGCCTCTCTG CTCACCCACT
1601 CTGCACCCAG GATCCTAGTC CCCTGCCCTC TGGCACAGCT GCTTCCTGCA
1651 AGAAAGCAAG TCTTTGGTCT CCCTGAGAAG CCATGTCCCT CGTGCTGTCT
1701 CTTGCCTGTC CCACCTGTGC CCTGCCCTCC AGCTTGTATT TAAGTCCCTG
1751 GGCTGCCCCC TTGGGGTGCC CCCCGCTCCC AGGTTCCCCT CTGGTGTCAT
1801 GTCAGGCATT TTGCAAGGAA AAGCCACTTG GGGAAAGATG GAAAAGGACA
1851 AAAAAAATTA ATAAATTTCC ATTGGCCCTC GGGTGAGCTG AGGGTTTTTG
1901 CAAGGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
1951 AAAAAAAAAA AAAAGAAAAA AAAAAAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

91115900:
A family of ras-like GTP-binding proteins expressed in electromotor neurons.

Peptide information for frame 3

ORF from 48 bp to 650 bp; peptide length: 201
Category: strong similarity to known protein

```
  1 MNPEYDYLFK LLLIGDSGVG KSCLLLRFAD DTYTESYIST IGVDFKIRTI
 51 ELDGKTIKLQ IWDTAGQERF RTITSSYYRG AHGIIVVYDV TDQESYANVK
101 QWLQEIDRYA SENVNKLLVG NKSDLTTKKV VDNTTAKEFA DSLGIPFLET
151 SAKNATNVEQ AFMTMAAEIK KRMGPGAASG GERPNLKIDS TPVKPAGGGC
201 C
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2i17, frame 3

SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B., N = 1, Score = 1023, P = 2.7e-103

PIR:S06147 GTP-binding protein rab1B - rat, N = 1, Score = 1013, P = 3.2e-102

SWISSPROT:RAB1_DISOM RAS-RELATED PROTEIN ORAB-1., N = 1, Score = 967, P = 2.4e-97

PIR:TVHUYP GTP-binding protein Rab1 - human, N = 1, Score = 966, P = 3e-97

>SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B.
Length = 201

HSPs:

Score = 1023 (153.5 bits), Expect = 2.7e-103, P = 2.7e-103
Identities = 197/201 (98%), Positives = 199/201 (99%)

```
Query:    1 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 60
            MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
Sbjct:    1 MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ 60

Query:   61 IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG 120
            IWDTAGQERFRT+TSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG
Sbjct:   61 IWDTAGQERFRTVTSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG 120

Query:  121 NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG 180
            NKSDLTTKKVVDNTTAKEFADSLG+PFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
Sbjct:  121 NKSDLTTKKVVDNTTAKEFADSLGVPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG 180

Query:  181 GERPNLKIDSTPVKPAGGGCC 201
            GERPNLKIDSTPVK A GGCC
Sbjct:  181 GERPNLKIDSTPVKSASGGCC 201
```

Pedant information for DKFZphfbr2_2i17, frame 3

Report for DKFZphfbr2_2i17.3

[LENGTH] 201

[MW] 22171.25
[pI] 5.56
[HOMOL] SWISSPROT:RB1B_RAT RAS-RELATED PROTEIN RAB-1B. 1e-112
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YFL038c] 2e-77
[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YFL038c] 2e-77
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YFL005w] 4e-57
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YFL005w] 4e-57
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL005w] 4e-57
[FUNCAT] 08.19 cellular import [S. cerevisiae, YER031c] 8e-46
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YER031c] 8e-46
[FUNCAT] 09.09 biogenesis of intracellular transport vesicles [S. cerevisiae, YGL210w] 1e-44
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YOR089c] 1e-30
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 11.01 stress response [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 03.99 other cell growth, cell division and dna synthesis activities [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 01.03.13 regulation of nucleotide metabolism [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 10.04.07 g-proteins [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 3e-25
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR101w] 9e-24
[FUNCAT] 11.10 cell death [S. cerevisiae, YOR101w] 9e-24
[FUNCAT] 04.07 rna transport [S. cerevisiae, YOR185c] 4e-23
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YOR185c] 4e-23
[FUNCAT] 08.01 nuclear transport [S. cerevisiae, YOR185c] 4e-23
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YPR165w] 7e-17
[FUNCAT] 10.02.07 g-proteins [S. cerevisiae, YPR165w] 7e-17
[FUNCAT] 10.99 other signal-transduction activities [S. cerevisiae, YCR027c] 1e-16
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR229c] 1e-11
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YLR229c] 1e-11
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YDL192w] 4e-10
[FUNCAT] 03.01 cell growth [S. cerevisiae, YNL180c] 9e-09
[FUNCAT] 06.07 protein modification (glycolsylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YPL051w] 3e-08
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YAL048c] 5e-05
[BLOCKS] BL01019A ADP-ribosylation factors family proteins
[BLOCKS] BL01115A GTP-binding nuclear protein ran proteins
[SCOP] d1plk__ 3.25.1.3.1 cH-p21 Ras protein [human (Homo sapiens) 2e-41
[SCOP] d1guaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens) 5e-60
[SCOP] d1rrga_ 3.25.1.3.5 ADP-ribosylation factor 1 (ARF1) [rat (Rattu 2e-30
[SCOP] d1hura_ 3.25.1.3.4 ADP-ribosylation factor 1 (ARF1) [human (Hom 2e-33
[PIRKW] nucleus 1e-21
[PIRKW] membrane trafficking 1e-110
[PIRKW] oncogene 1e-25
[PIRKW] endoplasmic reticulum 1e-105
[PIRKW] phosphoprotein 1e-105
[PIRKW] glycoprotein 3e-25
[PIRKW] prenylated cysteine 1e-110
[PIRKW] signal transduction 4e-23
[PIRKW] transforming protein 1e-105
[PIRKW] purine nucleotide binding 2e-24
[PIRKW] alternative splicing 5e-26
[PIRKW] P-loop 1e-110
[PIRKW] lipoprotein 1e-110
[PIRKW] proto-oncogene 3e-27
[PIRKW] methylated carboxyl end 3e-27
[PIRKW] hydrolase 7e-25
[PIRKW] membrane protein 1e-105
[PIRKW] GTP binding 1e-110
[PIRKW] thiolester bond 5e-76
[PIRKW] Golgi apparatus 1e-105
[SUPFAM] ras transforming protein 1e-110
[PROSITE] ATP_GTP_A 1
[PROSITE] MYRISTYL 2
[PROSITE] CK2_PHOSPHO_SITE 5
[PROSITE] SIGMA54_INTERACT_1 1
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] GLYCOSAMINOGLYCAN 1
[PROSITE] PKC_PHOSPHO_SITE 4
[PROSITE] ASN_GLYCOSYLATION 3
[PFAM] Ras family (contains ATP/GTP binding P-loop)
[KW] Alpha_Beta
[KW] 3D

```
SEQ    MNPEYDYLFKLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIKLQ
221p-  ........EEEEEEETTTTCHHHHHHHHHHCCCCCCCCCTTTEEEE-EEEEETTEEEEEE

SEQ    IWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDRYASENVNKLLVG
221p-  EEECTTTTTTCGGGHHHHHHCCEEEEEEETTBHHHHHHHHHHHHHHHHHHHTTTTCEEEEE

SEQ    NKSDLTTKKVVDNTTAKEFADSLGIPFLETSAKNATNVEQAFMTMAAEIKKRMGPGAASG
221p-  ETTTTCCC-CCCHHHHHHHHHHHCCCCEEEETTTTTTTHHHHHHHHHHHHHH.........

SEQ    GERPNLKIDSTPVKPAGGGCC
221p-  .....................
```

Prosite for DKFZphfbr2_2i17.3

PS00001	121->125	ASN_GLYCOSYLATION	PDOC00001
PS00001	133->137	ASN_GLYCOSYLATION	PDOC00001
PS00001	154->158	ASN_GLYCOSYLATION	PDOC00001
PS00002	17->21	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	56->59	PKC_PHOSPHO_SITE	PDOC00005
PS00005	126->129	PKC_PHOSPHO_SITE	PDOC00005
PS00005	135->138	PKC_PHOSPHO_SITE	PDOC00005
PS00005	151->154	PKC_PHOSPHO_SITE	PDOC00005
PS00006	32->36	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	135->139	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	179->183	CK2_PHOSPHO_SITE	PDOC00006
PS00007	27->34	TYR_PHOSPHO_SITE	PDOC00007
PS00008	18->24	MYRISTYL	PDOC00008
PS00008	176->182	MYRISTYL	PDOC00008
PS00017	15->23	ATP_GTP_A	PDOC00017
PS00675	11->25	SIGMA54_INTERACT_1	PDOC00579

Pfam for DKFZphfbr2_2i17.3

```
HMM_NAME      Ras family (contains ATP/GTP binding P-loop)

HMM               *KLVLIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIEIDGKtIK
                   KL+LIGDSGVGKSCLL+RF +++++E+YI+TIGVDF+++TIE+DGKTIK
Query          10  KLLLIGDSGVGKSCLLLRFADDTYTESYISTIGVDFKIRTIELDGKTIK    58

HMM               LQIWDTAGQERYRsMRPMYYRGAMGFMLVYDITNRqSFENIrNWweEIrR
                  LQIWDTAGQER+R+++++YYRGA+G+++VYD+T+++S+ N+++W++EI+R
Query          59 LQIWDTAGQERFRTITSSYYRGAHGIIVVYDVTDQESYANVKQWLQEIDR   108

HMM               HCDrDENVPIMLVGNKCDLEDQRQVStEEGQeFAREWGAIPFMETSAKTN
                  +++  ENV ++LVGNK+DL  +++V+  +++EFA+++G IPF+ETSAK++
Query         109 YAS--ENVNKLLVGNKSDLTTKKVVDNTTAKEFADSLG-IPFLETSAKNA   155

HMM               iNVEEAFMEIvReIlqrMqe.q.NqteNinidQpsrnrk...rCCCIM*
                  +NVE+AFM+++ EI++RM+     +++E +N++ +S++ K     +CC
Query         156 TNVEQAFMTMAAEIKKRMGPGAASGGERPNLKIDSTPVKPAGGGCC--   201
```

DKFZphfbr2_2k19
----

group: brain derived

DKFZphfbr2_2k19 encodes a novel 303 amino acid protein with similarity to human KIAA0378 product.

The protein contains a leucine zipper, which can mediate protein-protein-interaction.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to KIAA0378

encoded by the genomic clones HS147M19/HS608E8

Sequenced by Qiagen

Locus: unknown

Insert length: 1931 bp
Poly A stretch at pos. 1866, no polyadenylation signal found

```
   1 GGGGGGGGCG CGCGGTGACA GCGCGGGGTT GGCGGCGTGG GACCCAGGGG
  51 GCGACAGAGG CAGCAGCAGC CCGAGGCCTG AGGAGAGGAG ACCGGCGGCG
 101 GCGGCAATGC TGGAGACCCT TCGCGAGCGG CTGCTGAGCG TGCAGCAGGA
 151 TTTCACCTCC GGGCTGAAGA CTTTAAGTGA CAAGTCAAGA GAAGCAAAAG
 201 TGAAAAGCAA ACCCAGGACT GTTCCATTTT TGCCAAAGTA CTCTGCTGGA
 251 TTAGAATTAC TTAGCAGGTA TGAGGATACA TGGGCTGCAC TTCACAGAAG
 301 AGCCAAAGAC TGTGCAAGTG CTGGAGAGCT GGTGGATAGC GAGGTGGTCA
 351 TGCTTTCTGC GCACTGGGAG AAGAAAAAGA CAAGCCTCGT GGAGCTGCAA
 401 GAGCAGCTCC AGCAGCTCCC AGCTTTAATC GCAGACTTAG AATCCATGAC
 451 AGCAAATCTG ACTCATTTAG AGGCGAGTTT TGAGGAGGTA GAGAACAACC
 501 TGCTGCATCT GGAAGACTTA TGTGGGCAGT GTGAATTAGA AAGATGCAAA
 551 CATATGCAGT CCCAGCAACT GGAGAATTAC AAGAAAAATA AGAGGAAGGA
 601 ACTTGAAACC TTCAAAGCTG AACTAGATGC AGAGCACGCC CAGAAGGTCC
 651 TGGAAATGGA GCACACCCAG CAAATGAAGC TGAAGGAGCG GCAGAAGTTT
 701 TTTGAGGAAG CCTTCCAGCA GGACATGGAG CAGTACCTGT CCACTGGCTA
 751 CCTGCAGATT GCAGAGCGGC GAGAGCCCAT AGGCAGCATG TCATCCATGG
 801 AAGTGAACGT GGACATGCTG GAGCAGATGG TCCTGATGGA CATATCGGAC
 851 CAGGAGGCCC TGGACGTCTT CCTGAACTCT GGAGGAGAAG AGAACACTGT
 901 GCTGTCCCCC GCCTTAGGTA GGGTTGACAA ACTTGCATTA GCTGAACCAG
 951 GGCAGTATCG ATGCCACTCC CCTCCAAAGG TGAGACGTGA GAACCATCTG
1001 CCAGTCACTT ACGCATAAAC CCCCAAGCTC ACAGCCAGCT CCTGGCTCCC
1051 TAACCCCACG GTTCCACACG GCTGTGTGGC AGCTGCAACA GTGGTGTGGT
1101 TCCGTCATGA ATTCTTCTCA AAGATTTGAC ATGCTCCACT CCGGTAACTT
1151 TGGTGAGTTG AGAGCTTCTT TGTTTGTTTT CCCTCCTTTA CCATCCAGAA
1201 ATCCATTTGA GTCTGCTCCT TGTGGTTAAG GACTGGCGTT TGCAGGGAGG
1251 TGCGGACTCT CCTGCGGGGC TCACGGGAAA CTCTTCCCTC TTCGTGCGAC
1301 AGGCATTTAG GGGCGTGCCT GCCATGGGCA AAGCCATGGT GTGTGTTCAG
1351 CTCTTGGCCT GTGTTGTAAA CTTAGTTGCA CTTCAGTTCC TTTCATCCCT
1401 TCACAAAATT TTGTTTCACA TTCATGCAGC AAATATGGGC TGAGGTGCCA
1451 GACCTGTACC TGGGCTTGGT GCGTTTCAAA TTTCAGACCA GTTCTTTGGG
1501 CTGGGTCAAG GCAAAGCTCA GTCGTCCCAG CAGCACCTCA GCCATCTGTA
1551 GAAGGTTCTA CCATTACCAC GGTTTCAGCT TCCTCTAAAC TTCTCACCCG
1601 CTTCTCCTGG CAATCTGTCA GAACGGTGTC ATCCTGGGGA AGAGAAGGAG
1651 CTTGGGTGCA TTTGCCCTCA TCCTGAGAAG GCCAGAATAC TGGAGACCAG
1701 CGTGAACCCT CACCCAGAGT CAGGGGAAGA TTTAGAAACA GTGACACCTG
1751 CATATAGAAT TTTGATTCCT TGAAGAGCCT ATTTAGTTCC ATAAAATTGG
1801 AGAACTGCTG AAGGTCAGTA ATTCCGACTT TCTCAGCAGT GGTGTCTCTG
1851 AATTACTGCA AAGGGTAAAA AAAAAAAAAA AAAAAACTTA TCGATACCGT
1901 CGACCTCGAT GATGATGATG ATGATGTCGA C
```

BLAST Results

Entry HS147M19 from database EMBL:
Homo sapiens DNA sequence from PAC 147M19 on chromosome 6p22.1-22.3.
Contains an unknown gene, ESTs and GSSs.
Score = 5540, P = 4.1e-275, identities = 1114/1120
3 exons 592-1884

Entry HS608E8 from database EMBL:
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E8
Score = 797, P = 1.2e-78, identities = 161/163

6 exons 1-592

Medline entries

90294724:
The involucrin gene of the gibbon: The middle region shared by the hominoids

Peptide information for frame 2

ORF from 107 bp to 1015 bp; peptide length: 303
Category: similarity to known protein
Classification: unset
Prosite motifs: LEUCINE_ZIPPER (97-119)

```
  1 MLETLRERLL SVQQDFTSGL KTLSDKSREA KVKSKPRTVP FLPKYSAGLE
 51 LLSRYEDTWA ALHRRAKDCA SAGELVDSEV VMLSAHWEKK KTSLVELQEQ
101 LQQLPALIAD LESMTANLTH LEASFEEVEN NLLHLEDLCG QCELERCKHM
151 QSQQLENYKK NKRKELETFK AELDAEHAQK VLEMEHTQQM KLKERQKFFE
201 EAFQQDMEQY LSTGYLQIAE RREPIGSMSS MEVNVDMLEQ MVLMDISDQE
251 ALDVFLNSGG EENTVLSPAL GRVDKLALAE PGQYRCHSPP KVRRENHLPV
301 TYA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2k19, frame 2

TREMBL:HSAB2376_1 gene: "KIAA0378"; Human mRNA for KIAA0378 gene, partial cds., N = 1, Score = 137, P = 4.8e-06

PIR:I37037 involucrin - common gibbon, N = 1, Score = 124, P = 7.4e-05

PIR:A57013 early endosome antigen 1 - human, N = 1, Score = 128, P = 9.5e-05

>TREMBL:HSAB2376_1 gene: "KIAA0378"; Human mRNA for KIAA0378 gene, partial cds.
Length = 808

HSPs:

```
 Score = 137 (20.6 bits), Expect = 4.8e-06, P = 4.8e-06
 Identities = 59/222 (26%), Positives = 103/222 (46%)

Query:     2 LETLRERLLSVQQDFTSGLKTL---SDKSREAKVKS-KPRTVPFLPKYSAGLELLSRYED 57
             L TL E L S ++     LK      D+ R  +++S +        K +A    L+  E
Sbjct:   434 LATLEEAL-SEKERIIERLKEQRERDDRERLEEIESFRKENKDLKEKVNALQAELTEKES 492

Query:    58 TWAALHRRAKDCASAGELVDSEVVMLSAHWEKKKTSLVELQEQLQQLPALIADLESMTAN 117
             +   L   A   ASAG   DS++  L    E+KK    +L+ QL++    I D   M
Sbjct:   493 SLIDLKEHASSLASAGLKRDSKLKSLEIAIEQKKEECSKLEAQLKKAHN-IEDDSRMNPE 551

Query:   118 LTHLEASFEEVENNLLHLEDLCG--QCELERCKHMQSQQLENYKKNKRK---ELETFKAE 172
                     ++++    +  D CG  Q E++R   +  +++EN K +K K   ELE+
Sbjct:   552 FAD---QIKQLDKEASYYRDECGKAQAEVDRLLEIL-KEVENEKNDKDKKIAELESLTLR 607

Query:   173 LDAEHAQKVLEMEHTQQMKLKERQKFFEEAFQQDMEQYLSTGYLQIAE 220
                +  +KV  ++H QQ++ K+  +  EE  +++     ++ +LQI E
Sbjct:   608 HMKDQNKKVANLKHNQQLEKKKNAQLLEEVRRREDSMADNSQHLQIEE 655

 Score = 100 (15.0 bits), Expect = 6.2e-02, P = 6.0e-02
 Identities = 44/156 (28%), Positives = 76/156 (48%)

Query:    57 DTWAALHRRAKDCASAGELVDSEVVMLSAHWEKKKTSLVELQEQLQQLPAL-IADLESMT 115
             D  A+ +R   +C  A   VD  + +L    E +K    +   +L+ L    + D
Sbjct:   560 DKEASYYR--DECGKAQAEVDRLLEILK-EVENEKNDKDKKIAELESLTLRHMKDQNKKV 616

Query:   116 ANLTHLEASFEEVENNLLHLEDLCGQCE--LERCKHMQSQQLENYKKNKRKELETFKAEL 173
```

```
                 ANL H +    E+ +N  L LE++  + +    +  +H+Q ++L N  +  R+EL+  KA L
Sbjct:    617 ANLKHNQ-QLEKKKNAQL-LEEVRRREDSMADNSQHLQIEELMNALEKTRQELDATKARL 674

Query:    174 DAEHAQKVLEME-HTQQMKLKERQKFFEEAFQQDMEQYLS 212
                 A   Q + E E H   +++ ER+K  EE  +    E  L+
Sbjct:    675 -ASTQQSLAEKEAHLANLRI-ERRKQLEEILEMKQEALLA 712
```

Pedant information for DKFZphfbr2_2k19, frame 2

Report for DKFZphfbr2_2k19.2

```
[LENGTH]        303
[MW]            34814.78
[pI]            5.23
[PROSITE]       LEUCINE_ZIPPER 1
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY     3.63 %
[KW]            COILED_COIL       14.52 %

SEQ     MLETLRERLLSVQQDFTSGLKTLSDKSREAKVKSKPRTVPFLPKYSAGLELLSRYEDTWA
SEG     ............................................................
PRD     ccchhhhhhhhhhhcccccchhhhhhhhhhhhccccccccccchhhhhhhhhhhhhchhh
COILS   ............................................................

SEQ     ALHRRAKDCASAGELVDSEVVMLSAHWEKKKTSLVELQEQLQQLPALIADLESMTANLTH
SEG     ................................xxxxxxxxxxx.................
PRD     hhhhhhhhchhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   ..................................cccccccccccccccccccccccccc

SEQ     LEASFEEVENNLLHLEDLCGQCELERCKHMQSQQLENYKKNKRKELETFKAELDAEHAQK
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   cccccccccccccccccccc........................................

SEQ     VLEMEHTQQMKLKERQKFFEEAFQQDMEQYLSTGYLQIAERREPIGSMSSMEVNVDMLEQ
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcchhhhhhhccccccccccchhhhhhhhh
COILS   ............................................................

SEQ     MVLMDISDQEALDVFLNSGGEENTVLSPALGRVDKLALAEPGQYRCHSPPKVRRENHLPV
SEG     ............................................................
PRD     hhhhhhchhhhhhhhhhccccccceeeccccccccccceeecccccccccccccccceeecccccc
COILS   ............................................................

SEQ     TYA
SEG     ...
PRD     ccc
COILS   ...
```

Prosite for DKFZphfbr2_2k19.2

```
PS00029      97->119    LEUCINE_ZIPPER        PDOC00029
```

(No Pfam data available for DKFZphfbr2_2k19.2)

DKFZphfbr2_2k14
----

group: cell cycle

DKFZphfbr2_2k14 encodes a novel 335 amino acid protein with strong similarity to rattus rattus IAG2 "implantation-associated protein" and the human N33 tumour-suppressor gene.

Tumour-suppressor genes are known to be involved in the control of cell growth and division, interacting with proteins which control the cell cycle. The N33 gene is significantly methylated in tumour cells, a mechanism by which tumor-suppressor genes are inactivated in cancer. In addition, the novel protein contains a RGD cell attachment site. Therefore the novel protein is a new putative tumour-suppressor gene.

The new protein can find application in modulating/blocking the cell cycle and in the therapy of tumours.

strong similarity to human N33 tumor suppressor gene

complete cDNA, complete cds, EST hits,
potential start at Bp 30 matches kozak consensus ANCatgG
potential transmembran protein (4 TM)
similarity to yeast OST3p (oligosaccharyltransferase gamma chain)

Sequenced by Qiagen

Locus: unknown

Insert length: 2241 bp
Poly A stretch at pos. 2221, no polyadenylation signal found

```
   1 TGGGACTTAT AGAAGGGAGA GGAGCGAACA TGGCAGCGCG TTGGCGGTTT
  51 TGGTGTGTCT CTGTGACCAT GGTGGTGGCG CTGCTCATCG TTTGCGACGT
 101 TCCCTCAGCC TCTGCCCAAA GAAAGAAGGA GATGGTGTTA TCAGAAAAGG
 151 TTAGTCAGCT GATGGAATGG ACTAACAAAA GACCTGTAAT AAGAATGAAT
 201 GGAGACAAGT TCCGTCGCCT TGTGAAAGCC CCACCGAGAA ATTACTCCGT
 251 TATCGTCATG TTCACTGCTC TCCAACTGCA TAGACAGTGT GTCGTTTGCA
 301 AGCAAGCTGA TGAAGAATTC CAGATCCTGG CAAACTCCTG GCGATACTCC
 351 AGTGCATTCA CCAACAGGAT ATTTTTTGCC ATGGTGGATT TTGATGAAGG
 401 CTCTGATGTA TTTCAGATGC TAAACATGAA TTCAGCTCCA ACTTTCATCA
 451 ACTTTCCTGC AAAAGGGAAA CCCAAACGGG GTGATACATA TGAGTTACAG
 501 GTGCGGGGTT TTTCAGCTGA GCAGATTGCC CGGTGGATCG CCGACAGAAC
 551 TGATGTCAAT ATTAGAGTGA TTAGACCCCC AAATTATGCT GGTCCCCTTA
 601 TGTTGGGATT GCTTTTGGCT GTTATTGGTG GACTTGTGTA TCTTCGAAGA
 651 AGTAATATGG AATTTCTCTT TAATAAAACT GGATGGGCTT TTGCAGCTTT
 701 GTGTTTTGTG CTTGCTATGA CATCTGGTCA AATGTGGAAC CATATAAGAG
 751 GACCACCATA TGCCCATAAG AATCCCCACA CGGGACATGT GAATTATATC
 801 CATGGAAGCA GTCAAGCCCA GTTTGTAGCT GAAACACACA TTGTTCTTCT
 851 GTTTAATGGT GGAGTTACCT TAGGAATGGT GCTTTTGTGT GAAGCTGCTA
 901 CCTCTGACAT GGATATTGGA AAGCGAAAGA TAATGTGTGT GGCTGGTATT
 951 GGACTTGTTG TATTATTCTT CAGTTGGATG CTCTCTATTT TTAGATCTAA
1001 ATATCATGGC TACCCATACA GCTTTCTGAT GAGTTAAAAA GGTCCCAGAG
1051 ATATATAGAC ACTGGAGTAC TGGAAATTGA AAAACGAAAA TCGTGTGTGT
1101 TTGAAAAGAA GAATGCAACT TGTATATTCT GTATTACCTC TTTTTTTCAA
1151 GTGATTTAAA TAGTTAATCA TTTAACCAAA GAAGATGTGT AGTGCCTTAA
1201 CAAGCAATCC TCTGTCAAAA TCTGAGGTAT TTGAAAATAA TTATCCTCTT
1251 AACCTTCTCT TCCCAGTGAA CTTTATGGAA CATTTAATTT AGTACAATTA
1301 AGTATATTAT AAAAATTGTA AAACTACTAC TTTGTTTTAG TTAGAACAAA
1351 GCTCAAAACT ACTTTAGTTA ACTTGGTCAT CTGATCTTAT ATTGCCTTAT
1401 CCAAAGATGG GGAAAGTAAG TCCTGACCAG GTGTTCCCAC ATATGCCTGT
1451 TACAGATAAC TACATTAGGA ATTCATTCTT AGCTTCTTCA TCTTTGTGTG
1501 GATGTGTATA CTTTACGCAT CTTTCCTTTT GAGTAGAGAA ATTATGTGTG
1551 TCATGTGGTC TTCTGAAAAT GGAACACCAT TCTTCAGAGC ACACGTCTAG
1601 CCCTCAGCAA GACAGTTGTT TCTCCTCCTC CTTGCATATT TCCTACTGCG
1651 CTCCAGCCTG AGTGATAGAG TGAGACTCTG TCTCAAAAAA AAAGTATCTC
1701 TAAATACAGG ATTATAATTT CTGCTTGAGT ATGGTGTTAA CTACCTTGTA
1751 TTTAGAAAGA TTTCAGATTC ATTCCATCTC CTTAGTTTTC TTTTAAGGTG
1801 ACCCATCTGT GATAAAAATA TAGCTTAGTG CTAAAATCAG TGTAACTTAT
1851 ACATGGCCTA AAATGTTTCT ACAAATTAGA GTTTGTCACT TATTCCATTT
1901 GTACCTAAGA GAAAAATAGG CTCAGTTAGA AAAGGACTCC CTGGCCAGGC
1951 GCAGTGACTT ACGCCTGTAA TCTCAGCACT TTGGGAGGCC AAGGCAGGCA
2001 GATCACGAGG TCAGGAGTTC GAGACCATCC TGGCCAACAT GGTGAAACCC
2051 CGTCTCTACT AAAAATATAA AAATTAGCTG GGTGTGGTGG CAGGAGCCTG
2101 TAATCCCAGC TGCACAGGAG GCTGAGGCAC GAGAATCACT TGAACTCAGG
2151 AGATGGAGGT TTCAGTGAGC CGAGATCACG CCACTGCACT CCAGCCTGGC
2201 AACAGAGCGA GACTCCATCT CAAAAAAAAA AAAAAAAAAA A
```

BLAST Results

No BLAST result

Medline entries

96299740:
Structure and methylation-associated silencing of a gene within a homozygously deleted region of human chromosome band 8p22.

97243398:
Tumour-suppressor genes in prostatic oncogenesis: a positional approach.

98334474:
Concordant methylation of the ER and N33 genes in glioblastoma multiforme.

Peptide information for frame 3

ORF from 30 bp to 1034 bp; peptide length: 335
Category: strong similarity to known protein

```
  1 MAARWRFWCV SVTMVVALLI VCDVPSASAQ RKKEMVLSEK VSQLMEWTNK
 51 RPVIRMNGDK FRRLVKAPPR NYSVIVMFTA LQLHRQCVVC KQADEEFQIL
101 ANSWRYSSAF TNRIFFAMVD FDEGSDVFQM LNMNSAPTFI NFPAKGKPKR
151 GDTYELQVRG FSAEQIARWI ADRTDVNIRV IRPPNYAGPL MLGLLLAVIG
201 GLVYLRRSNM EFLFNKTGWA FAALCFVLAM TSGQMWNHIR GPPYAHKNPH
251 TGHVNYIHGS SQAQFVAETH IVLLFNGGVT LGMVLLCEAA TSDMDIGKRK
301 IMCVAGIGLV VLFFSWMLSI FRSKYHGYPY SFLMS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_2k14, frame 3

TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein"; Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds., N = 1, Score = 1560, P = 3.4e-160

PIR:G02297 gene N33 protein - human, N = 1, Score = 1256, P = 5.6e-128

TREMBL:HSN33S11_1 gene: "N33"; product: "N33 protein form 2"; Human N33 protein form 2 (N33) gene, exon 11 and complete cds., N = 1, Score = 1252, P = 1.5e-127

```
>TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein";
     Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds.
            Length = 308

  HSPs:

 Score = 1560 (234.1 bits), Expect = 3.4e-160, P = 3.4e-160
 Identities = 295/307 (96%), Positives = 299/307 (97%)

Query:    29 AQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDKFRRLVKAPPRNYSVIVMFTALQLHRQCV 88
             AQRKKE VL EKV QLMEWTN+RPVIRMNGDKFR LVKAPPRNYSVIVMFTALQLHRQCV
Sbjct:     2 AQRKKEKVLVEKVIQLMEWTNQRPVIRMNGDKFRPLVKAPPRNYSVIVMFTALQLHRQCV 61

Query:    89 VCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFPAKGKP 148
             VCKQADEEFQILAN WRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFP KGKP
Sbjct:    62 VCKQADEEFQILANFWRYSSAFTNRIFFAMVDFDEGSDVFQMLNMNSAPTFINFPPKGKP 121

Query:   149 KRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAVIGGLVYLRRS 208
             KR DTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAVIGGLVYLRRS
Sbjct:   122 KRADTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNYAGPLMLGLLLAVIGGLVYLRRS 181

Query:   209 NMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE 268
             NMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE
```

```
Sbjct:  182 NMEFLFNKTGWAFAALCFVLAMTSGQMWNHIRGPPYAHKNPHTGHVNYIHGSSQAQFVAE 241

Query:  269 THIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLVVLFFSWMLSIFRSKYHGY 328
            THIVLLFNGGVTLGMVLLCEAA SDMDIGKR++MC+AGIGLVVLFFSWMLSIFRSKYHGY
Sbjct:  242 THIVLLFNGGVTLGMVLLCEAAASDMDIGKRRMMCIAGIGLVVLFFSWMLSIFRSKYHGY 301

Query:  329 PYSFLMS 335
            PYSFLMS
Sbjct:  302 PYSFLMS 308
```

Pedant information for DKFZphfbr2_2k14, frame 3

Report for DKFZphfbr2_2k14.3

```
[LENGTH]        335
[MW]            38036.83
[pI]            9.68
[HOMOL]         TREMBL:RNAF8554_1 gene: "IAG2"; product: "implantation-associated protein";
Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds. 1e-161
[FUNCAT]        30.07 organization of endoplasmatic reticulum      [S. cerevisiae, YOR085w]
4e-14
[FUNCAT]        06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)       [S. cerevisiae, YOR085w] 4e-14
[FUNCAT]        01.05.01 carbohydrate utilization    [S. cerevisiae, YOR085w] 4e-14
[EC]            2.4.1.119 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 1e-12

[PIRKW]         glycosyltransferase 1e-12
[PIRKW]         transmembrane protein 6e-69
[PIRKW]         hexosyltransferase 1e-12
[PROSITE]       RGD     1
[PROSITE]       MYRISTYL        4
[PROSITE]       AMIDATION       1
[PROSITE]       CK2_PHOSPHO_SITE        2
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       2
[KW]            SIGNAL_PEPTIDE 30
[KW]            TRANSMEMBRANE  4
[KW]            LOW_COMPLEXITY      5.97 %

SEQ     MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMEWTNKRPVIRMNGDK
SEG     ............................................................
PRD     ccccceeeeeehhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhccceeeeecccc
MEM     ............................................................

SEQ     FRRLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVD
SEG     ............................................................
PRD     ceeeeeccccccceeeehhhhhhccceeeehhhhhhhhhhhhcccccccccceeeeeec
MEM     ............................................................

SEQ     FDEGSDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRV
SEG     ............................................................
PRD     cccccceeeecccccccceeecccccccccccceeeeeeecchhhhhhhhhhhheeeee
MEM     ...........................................................M

SEQ     IRPPNYAGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVLAMTSGQMWNHIR
SEG     .....xxxxxxxxxxxxxxxxxxx....................................
PRD     eccccccchhhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccceeec
MEM     MMMMMMMMMMMMMMMMMMMMMMMMMMM.....MMMMMMMMMMMMMMMMMMMMMMMM...

SEQ     GPPYAHKNPHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRK
SEG     ............................................................
PRD     cccccccccccceeeeccccchhhhhhhheeeeeecccchhhhhhhhhhhcccccccccc
MEM     .....................MMMMMMMMMMMMMMMMMMMMMMMMMMMMMM.........

SEQ     IMCVAGIGLVVLFFSWMLSIFRSKYHGYPYSFLMS
SEG     ...................................
PRD     eeeeccccceeeeeehhhhhhhhhccccccccccc
MEM     MMMMMMMMMMMMMMMMMMMMMMMMMM.........
```

Prosite for DKFZphfbr2_2k14.3

PS00001	71->75	ASN_GLYCOSYLATION	PDOC00001
PS00001	215->219	ASN_GLYCOSYLATION	PDOC00001
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	48->51	PKC_PHOSPHO_SITE	PDOC00005

PS00005	103->106	PKC_PHOSPHO_SITE	PDOC00005
PS00005	111->114	PKC_PHOSPHO_SITE	PDOC00005
PS00006	208->212	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00008	193->199	MYRISTYL	PDOC00008
PS00008	233->239	MYRISTYL	PDOC00008
PS00008	259->265	MYRISTYL	PDOC00008
PS00008	278->284	MYRISTYL	PDOC00008
PS00009	296->300	AMIDATION	PDOC00009
PS00016	150->153	RGD	PDOC00016

(No Pfam data available for DKFZphfbr2_2k14.3)

DKFZphfbr2_3c18
----

group: nucleic acid management

DKFZphfbr2_3c18 encodes a novel 448 amino acid protein with strong similarity to mus musculus RNA helicase and several RNA-dependent ATPases from the DEAD box family.

RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis. The novel protein contains a DEAD-box and is a new member of this subgroup.

The new protein can find application in modulating RNA metabolism and gene expression.

strong similarity to RNA helicase and RNA-dependent ATPase
from the DEAD box family
group helicases
Summary DKFZphfbr2_3c18 encodes a novel 448 amino acid protein with
similarity to DEAD-box subfamily ATP-dependent RNA helicases.
Deletion of the yeast homolouge DBP5 is lethal.

strong similarity to RNA helicase and RNA-dependent ATPase from the
DEAD box family

complete cDNA, EST hits
complete cds ATG at Bp 109

Sequenced by AGOWA

Locus: /map="87.50 cR from top of Chr16 linkage group"

Insert length: 1713 bp
Poly A stretch at pos. 1696, no polyadenylation signal found

```
   1 TGGGGTAGTG GGGCTGGAGC AGAGCCTGCC GCGAACCCCC GGAGCCCACG
  51 ATCCCTCGTG CCATCCCTCG AATCCACCAG CACGAGCGTC CCACCCGCGC
 101 CTGGGACCAT GGCCACTGAC TCATGGGCCC TGGCGGTGGA CGAGCAGGAA
 151 GCTGCGGCTG AGTCGTTGAG CAACTTGCAT CTTAAGGAAG AGAAAATCAA
 201 ACCAGATACC AATGGTGCTG TTGTCAAGAC CAATGCCAAT GCAGAGAAGA
 251 CAGATGAAGA AGAGAAAGAG GACAGAGCTG CCCAGTCCTT ACTCAACAAG
 301 CTGATCAGAA GCAACCTTGT TGATAACACA AACCAAGTGG AAGTCCTGCA
 351 GCGGGATCCA AACTCCCCTC TGTACTCGGT GAAGTCTTTT GAAGAGCTTC
 401 GGCTCCCACA GAACTTAATT GCCCAATCTC AGTCTGGTAC TGGTAAAACA
 451 GCTGCCTTCG TGCTGGCCAT GCTTAGCCAA GTAGAACCTG CAAACAAATA
 501 CCCCCAGTGT CTATGTCTCT CCCCAACGTA TGAGCTCGCC CTCCAAACAG
 551 GAAAAGTGAT TGAACAAATG GGCAAATTTT ACCCTGAACT GAAGCTAGCT
 601 TATGCTGTTC GAGGCAATAA ATTGGAAAGA GGCCAGAAGA TCAGTGAGCA
 651 GATTGTCATT GGCACCCCTG GGACTGTGCT GGACTGGTGC TCCAAGCTCA
 701 AGTTCATTGA TCCCAAGAAA ATCAAGGTGT TTGTTCTGGA TGAGGCTGAT
 751 GTCATGATAG CCACTCAGGG CCACCAAGAT CAGAGCATCC GCATCCAGAG
 801 GATGCTGCCC AGGAACTGCC AGATGCTGCT TTTCTCCGCC ACCTTTGAAG
 851 ACTCTGTGTG GAAGTTTGCC CAGAAAGTGG TCCCAGACCC AAACGTTATC
 901 AAACTGAAGC GTGAGGAAGA GACCCTGGAC ACCATCAAGC AGTACTATGT
 951 CCTGTGCAGC AGCAGAGACG AGAAGTTCCA GGCCTTGTGT AACCTCTACG
1001 GGGCCATCAC CATTGCTCAA GCCATGATCT TCTGCCATAC TCGCAAAAACA
1051 GCTAGTTGGC TGGCAGCAGA GCTCTCAAAA GAAGGCCACC AGGTGGCTCT
1101 GCTGAGTGGG GAGATGATGG TGGAACAGAG GGCTGCAGTG ATTGAGCGCT
1151 TCCGAGAGGG CAAAGAGAAG GTTTTGGTGA CCACCAACGT GTGTGCCCGC
1201 GGCATTGATG TTGAACAAGT GTCTGTCGTC ATCAACTTTG ATCTTCCCGT
1251 GGACAAGGAC GGGAATCCTG ACAATGAGAC CTACCTGCAC CGGATCGGGC
1301 GCACGGGCCG CTTTGGCAAG AGGGGCCTGG CAGTGAACAT GGTGGACAGC
1351 AAGCACAGCA TGAACATCCT GAACAGAATC CAGGAGCATT TTAATAAGAA
1401 GATAGAAAGA TTGGACACAG ATGATTTGGA CGAGATTGAG AAAATAGCCA
1451 ACTGAGAAGC TCCACCAGCC ACTGATGCCA GCCCTGGCAC TGCCCCTGCA
1501 CAGGAGACAA GTGCGTTCAG GGCACAGGCC CCGACATCAC CCCAAGGACA
1551 ACGGCACAAG TAGAGAGAAA CTACCTACCT CACTTCAAAT TATGTTTGGA
1601 CTTGACAAAA ATGTATGCAA ATGATGGGGG ATGGTAGAAA AAAATTATTT
1651 ACACAACCTT GGAAGATTAG GCATGAATAC ACAGAGATTT ACCTTTAAAA
1701 AAAAAAAAAA AAA
```

BLAST Results

Entry G36496 from database EMBL:
SHGC-53094 Human Homo sapiens STS cDNA.
Length = 459
Minus Strand HSPs:
Score = 1693 (254.0 bits), Expect = 2.8e-70, P = 2.8e-70
Identities = 369/387 (95%), Positives = 369/387 (95%)

Entry G44014 from database EMBLNEW:
WIAF-3643-STS Human THudson SANGER Homo sapiens STS genomic, sequence tagged site.
Score = 901, P = 2.3e-35, identities = 183/185

Medline entries

94192995:
Gene 1994 Mar 25;140(2):171-177
Mouse erythroid cells express multiple putative RNA helicase genes exhibiting
high sequence conservation from yeast to mammals.

Peptide information for frame 1

ORF from 109 bp to 1452 bp; peptide length: 448
Category: strong similarity to known protein

```
  1 MATDSWALAV DEQEAAAESL SNLHLKEEKI KPDTNGAVVK TNANAEKTDE
 51 EEKEDRAAQS LLNKLIRSNL VDNTNQVEVL QRDPNSPLYS VKSFEELRLP
101 QNLIAQSQSG TGKTAAFVLA MLSQVEPANK YPQCLCLSPT YELALQTGKV
151 IEQMGKFYPE LKLAYAVRGN KLERGQKISE QIVIGTPGTV LDWCSKLKFI
201 DPKKIKVFVL DEADVMIATQ GHQDQSIRIQ RMLPRNCQML LFSATFEDSV
251 WKFAQKVVPD PNVIKLKREE ETLDTIKQYY VLCSSRDEKF QALCNLYGAI
301 TIAQAMIFCH TRKTASWLAA ELSKEGHQVA LLSGEMMVEQ RAAVIERFRE
351 GKEKVLVTTN VCARGIDVEQ VSVVINFDLP VDKDGNPDNE TYLHRIGRTG
401 RFGKRGLAVN MVDSKHSMNI LNRIQEHFNK KIERLDTDDL DEIEKIAN
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3c18, frame 1

PIR:I49731 RNA helicase - mouse, N = 2, Score = 1758, P = 3.8e-223

TREMBL:AF005239_1 gene: "Dbp80"; product: "DEAD-box helicase"; Drosophila melanogaster DEAD-box helicase (Dbp80) mRNA, complete cds., N = 2, Score = 1142, P = 1.8e-125

SWISSPROT:YB66_SCHPO PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06., N = 2, Score = 911, P = 5.5e-103

PIR:S66920 probable RNA helicase CA5/6 - yeast (Saccharomyces cerevisiae), N = 2, Score = 887, P = 1.9e-98

```
>PIR:I49731 RNA helicase - mouse
           Length = 478

  HSPs:

 Score = 1758 (263.8 bits), Expect = 3.8e-223, Sum P(2) = 3.8e-223
 Identities = 338/349 (96%), Positives = 349/349 (100%)

Query:   100 PQNLIAQSQSGTGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQMGKFYP 159
             PQNLIAQSQSGTGKTAAFVLAMLS+VEPA++YPQCLCLSPTYELALQTGKVIEQMGKF+P
Sbjct:   130 PQNLIAQSQSGTGKTAAFVLAMLSRVEPADRYPQCLCLSPTYELALQTGKVIEQMGKFHP 189

Query:   160 ELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLKFIDPKKIKVFVLDEADVMIAT 219
             ELKLAYAVRGNKLERGQK+SEQIVIGTPGTVLDWCSKLKFIDPKKIKVFVLDEADVMIAT
Sbjct:   190 ELKLAYAVRGNKLERGQKVSEQIVIGTPGTVLDWCSKLKFIDPKKIKVFVLDEADVMIAT 249

Query:   220 QGHQDQSIRIQRMLPRNCQMLLFSATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQY 279
```

```
              QGHQDQSIRIQR++PRNCQMLLFSATFEDSVWKFAQKVVPDPN+IKLKREEETLDTIKQY
Sbjct:   250 QGHQDQSIRIQRIVPRNCQMLLFSATFEDSVWKFAQKVVPDPNIIKLKREEETLDTIKQY 309

Query:   280 YVLCSSRDEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVALLSGEMMVE 339
             YVLC++R+EKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVALLSGEMMVE
Sbjct:   310 YVLCNNREEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVALLSGEMMVE 369

Query:   340 QRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVVINFDLPVDKDGNPDNETYLHRIGRT 399
             QRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVVINFDLPVDKDGNPDNETYLHRIGRT
Sbjct:   370 QRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVVINFDLPVDKDGNPDNETYLHRIGRT 429

Query:   400 GRFGKRGLAVNMVDSKHSMNILNRIQEHFNKKIERLDTDDLDEIEKIAN 448
             GRFGKRGLAVNMVDSKHSMNILNRIQEHFNKKIERLDTDDLDEIEKIAN
Sbjct:   430 GRFGKRGLAVNMVDSKHSMNILNRIQEHFNKKIERLDTDDLDEIEKIAN 478

 Score = 419 (62.9 bits), Expect = 3.8e-223, Sum P(2) = 3.8e-223
 Identities = 94/136 (69%), Positives = 104/136 (76%)

Query:     1 MATDSWALAVDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEKEDRAAQS 60
             MATDSWALAVDEQEAA +S+S+L +KEEK K DTNG V+KT+  AEKT+EEEKEDRAAQS
Sbjct:     1 MATDSWALAVDEQEAAVKSMSSLQIKEEKAKSDTNG-VIKTSTTAEKTEEEEKEDRAAQS 59

Query:    61 LLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEELRL-PQNL---IAQSQSGTGKTAA 116
             LLNKLIRSNLVDNTNQVEVLQRDP+SPLYSVKSFEELRL PQ L    A   +   K
Sbjct:    60 LLNKLIRSNLVDNTNQVEVLQRDPSSPLYSVKSFEELRLKPQLLQGVYAMGFNRPSKIQE 119

Query:   117 FVLAMLSQVEPANKYPQ 133
             L M+    P N  Q
Sbjct:   120 NALPMMLAEPPQNLIAQ 136
```

Pedant information for DKFZphfbr2_3c18, frame 1

Report for DKFZphfbr2_3c18.1

```
[LENGTH]     448
[MW]         50490.07
[pI]         5.83
[HOMOL]      PIR:I49731 RNA helicase - mouse 0.0
[FUNCAT]     98 classification not yet clear-cut  [S. cerevisiae, YOR046c] 1e-102
[FUNCAT]     04.01.04 rrna processing     [S. cerevisiae, YDR021w] 2e-65
[FUNCAT]     30.10 nuclear organization   [S. cerevisiae, YDR021w] 2e-65
[FUNCAT]     30.03 organization of cytoplasm      [S. cerevisiae, YJL138c] 1e-63
[FUNCAT]     05.04 translation (initiation, elongation and termination)  [S. cerevisiae,
YJL138c] 1e-63
[FUNCAT]     04.99 other transcription activities [S. cerevisiae, YDL160c] 2e-49
[FUNCAT]     j mrna translation and ribosome biogenesis   [H. influenzae, HI0231 RNA] 9e-48
[FUNCAT]     04.05.03 mrna processing (splicing)   [S. cerevisiae, YDL084w] 1e-43
[FUNCAT]     l genome replication, transcription, recombination and repair      [H.
influenzae, HI0892] 3e-39
[FUNCAT]     06.10 assembly of protein complexes   [S. cerevisiae, YLL008w] 1e-35
[FUNCAT]     09.01 biogenesis of cell wall         [S. cerevisiae, YJL033w] 9e-27
[FUNCAT]     04.05.01.07 chromatin modification    [S. cerevisiae, YMR290c] 8e-26
[FUNCAT]     30.16 mitochondrial organization      [S. cerevisiae, YDR194c] 1e-23
[FUNCAT]     r general function prediction         [M. jannaschii, MJ1401] 9e-08
[FUNCAT]     11.10 cell death       [S. cerevisiae, YMR190c] 1e-05
[FUNCAT]     03.19 recombination and dna repair    [S. cerevisiae, YMR190c] 1e-05
[FUNCAT]     99 unclassified proteins        [S. cerevisiae, YIR002c] 7e-04
[BLOCKS]     BL00039D DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]     BL00039C DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]     BL00039B DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]     BL00039A DEAD-box subfamily ATP-dependent helicases proteins
[PIRKW]      nucleus 4e-64
[PIRKW]      RNA binding 1e-64
[PIRKW]      DEAD box 4e-64
[PIRKW]      transmembrane protein 3e-22
[PIRKW]      DNA binding 2e-32
[PIRKW]      ATP 1e-101
[PIRKW]      purine nucleotide binding 4e-64
[PIRKW]      P-loop 1e-101
[PIRKW]      hydrolase 4e-43
[PIRKW]      protein biosynthesis 1e-64
[PIRKW]      ATP binding 2e-35
[SUPFAM]     WW repeat homology 3e-29
[SUPFAM]     translation initiation factor eIF-4A 1e-64
[SUPFAM]     DEAD/H box helicase homology 1e-101
[SUPFAM]     DNA helicase recG 2e-06
[SUPFAM]     unassigned DEAD/H box helicases 1e-101
[SUPFAM]     ATP-dependent RNA helicase DBP1 9e-33
```

```
[SUPFAM]        ATP-dependent RNA helicase DHH1 4e-48
[SUPFAM]        tobacco ATP-dependent RNA helicase DB10 3e-29
[PROSITE]       MYRISTYL        5
[PROSITE]       AMIDATION       1
[PROSITE]       CK2_PHOSPHO_SITE        6
[PROSITE]       GLYCOSAMINOGLYCAN       1
[PROSITE]       PKC_PHOSPHO_SITE        8
[PROSITE]       ASN_GLYCOSYLATION       1
[PFAM]          Helicases conserved C-terminal domain
[PFAM]          DEAD and DEAH box helicases
[KW]            Alpha_Beta

SEQ     MATDSWALAVDEQEAAAESLSNLHLKEEKIKPDTNGAVVKTNANAEKTDEEEKEDRAAQS
PRD     ccchhhhhhhhhhhhhhhhhccccchhhhhhhcccccceeeeeehhhhhhhhhhhhhhhh

SEQ     LLNKLIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEELRLPQNLIAQSQSGTGKTAAFVLA
PRD     hhhhhhhhhcccccceeeeeeccccccceeehhhhhhhhccceeeeecccccchhhhhh

SEQ     MLSQVEPANKYPQCLCLSPTYELALQTGKVIEQMGKFYPELKLAYAVRGNKLERGQKISE
PRD     hhhhhhhhhccceeeeecccchhhhhhhhhhhhhhcccccccccceeeccccchhhhhhhe

SEQ     QIVIGTPGTVLDWCSKLKFIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQML
PRD     eeeeccccchhhhhhhhhhccccceeeeeecchhhhhhhcchhhhhhhhhhhcccccceee

SEQ     LFSATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSRDEKFQALCNLYGAI
PRD     eeecccccchhhhhhhhhhccccceeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhch

SEQ     TIAQAMIFCHTRKTASWLAAELSKEGHQVALLSGEMMVEQRAAVIERFREGKEKVLVTTN
PRD     hhhhhheeecchhhhhhhhhhhhhcccceeeeeccccchhhhhhhhhhhcccccceeeeeec

SEQ     VCARGIDVEQVSVVINFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSMNI
PRD     cccccceeeeeeeeeccccccccccccccceeeeeeccccccccccceeeeeeeccchhhh

SEQ     LNRIQEHFNKKIERLDTDDLDEIEKIAN
PRD     hhhhhhhhhhhccccccccchhhhhccc
```

Prosite for DKFZphfbr2_3c18.1

PS00001	389->393	ASN_GLYCOSYLATION	PDOC00001
PS00002	109->113	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	90->93	PKC_PHOSPHO_SITE	PDOC00005
PS00005	111->114	PKC_PHOSPHO_SITE	PDOC00005
PS00005	147->150	PKC_PHOSPHO_SITE	PDOC00005
PS00005	226->229	PKC_PHOSPHO_SITE	PDOC00005
PS00005	275->278	PKC_PHOSPHO_SITE	PDOC00005
PS00005	284->287	PKC_PHOSPHO_SITE	PDOC00005
PS00005	311->314	PKC_PHOSPHO_SITE	PDOC00005
PS00005	399->402	PKC_PHOSPHO_SITE	PDOC00005
PS00006	48->52	CK2_PHOSPHO_SITE	PDOC00006
PS00006	93->97	CK2_PHOSPHO_SITE	PDOC00006
PS00006	123->127	CK2_PHOSPHO_SITE	PDOC00006
PS00006	189->193	CK2_PHOSPHO_SITE	PDOC00006
PS00006	245->249	CK2_PHOSPHO_SITE	PDOC00006
PS00006	284->288	CK2_PHOSPHO_SITE	PDOC00006
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	175->181	MYRISTYL	PDOC00008
PS00008	185->191	MYRISTYL	PDOC00008
PS00008	385->391	MYRISTYL	PDOC00008
PS00008	406->412	MYRISTYL	PDOC00008
PS00009	402->406	AMIDATION	PDOC00009

Pfam for DKFZphfbr2_3c18.1

```
HMM_NAME        DEAD and DEAH box helicases

HMM                 *gLpPWILRnIyeMGFEkPTPIQQqAIPiILeG....RDVMACAQTGSGK
                     ++ ++ +N ++          P         E+     +++A++Q+G+GK
Query           65   LIRSNLVDNTNQVEVLQRDPNSPLYSVKSFEELRLPQNLIAQSQSGTGK     113

HMM                 TAAFlIPMLQHIDwdPWpqpPQdPrALILAPTRELAMQIQEEcRkFgkHM
                    TAAF++ ML+++ +      + PQ     +L L+PT ELA+Q+ ++++++GK++
Query          114  TAAFVLAMLSQVEPAN--KYPQ---CLCLSPTYELALQTGKVIEQMGKFY     158

HMM                 ngIRImcIYGGtnMRdQMRmLeRGpPHIVIATPGRLIDHIER.gtldLDr
                    + ++ + ++       ++ +++ +++  +IVI+TPG ++D   +    +D ++
```

```
Query          159 PELKLAYAVR----GNKLERGQKISEQIVIGTPGTVLDWCSKLKFIDPKK   204

HMM                IeMLVMDEADRMLD.MGFIDQIRrIMrqIPMpwNRQTMMFSATMPdeIqE
                   I+++V+DEAD M+  +G +DQ  RI R++P  +N Q ++FSAT+ D++ +
Query          205 IKVFVLDEADVMIATQGHQDQSIRIQRMLP--RNCQMLLFSATFEDSVWK   252

HMM                LARrFMRNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdcLcrLIe*
                   +A ++   +P  I ++++E T++ +IKQ+Y+ + + ++KF +LC+L++
Query          253 FAQKVVPDPNVIKLKREEETLD-TIKQYYVLCSSRDEKFQALCNLYG    298


HMM_NAME       Helicases conserved C-terminal domain

HMM                *EileeWLknlGIrvmYIHGdMpQeERdeIMddFNnGEynVLIcTDVggR
                    +L+ +L+++G +V+ + G M+ E+R   ++++F++G+ +VL++T+V +R
Query          316  SWLAAELSKEGHQVALLSGEMMVEQRAAVIERFREGKEKVLVTTNVCAR   364

HMM                GIDIPdVNHVINYDM....PWNPEq..YIQRIGRTgRIG*
                   GID+++V++VIN+D+    + NP++  Y++RIGRTGR+G
Query          365 GIDVEQVSVVINFDLPVDKDGNPDNETYLHRIGRTGRFG    403
```

Medline
PMID: 10322435
"Unwinding RNA in : DEAD-box proteins and related families." de la Cruz J, Kressler D, Linder P

DKFZphfbr2_3f16
----

group: brain derived

DKFZphfbr2_3f16 encodes a novel 127 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 1514 bp
Poly A stretch at pos. 1454, polyadenylation signal at pos. 1434

```
   1 GGGGGGACTG GAGAAGGGAG GCGGCGGGCG AAGCGCACGT CGAGCGGGGG
  51 AGCGGCGCTG CCTGTGGAGA TCCGCGGAGG CCGACAGGAT TCGTTGGCTG
 101 CCGTCCCCGC TGCTGTGCAT TGGGTTAAAA ACGACAACCA ACATCAGCCA
 151 TGAAAGATCC AAGTCGCAGC AGTACTAGCC CAAGCATCAT CAATGAAGAT
 201 GTGATTATTA ACGGTCATTC TCATGAAGAT GACAATCCAT TTGCAGAGTA
 251 CATGTGGATG GAAAATGAAG AAGAATTCAA CAGACAAATA GAAGAGGAGT
 301 TATGGGAAGA AGAATTTATT GAACGCTGTT TCCAAGAAAT GCTGGAAGAG
 351 GAAGAAGAGC ATGAATGGTT TATTCCAGCT CGAGATCTCC CACAAACTAT
 401 GGACCAAATC CAAGACCAGT TTAATGACCT TGTTATCAGT GAAGGCTCTT
 451 CTCTGGAAGA TCTTGTGGTC AAGAGCAATC TGAATCCAAA TGCAAAGGAG
 501 TTTGTTCCTG GGGTGAAGTA CGGAAATATT TGAGTAGACG GGGCCCTCTT
 551 TTGGTGGATG TAGCACAATT TCCACACTGT GAAGGCAGTA TTAGAAGACT
 601 TAATTGTAAA AGCACTCTTG TCACTGTGTT ACACTTATGC ATTGCCAAAG
 651 TTTTTGTTAG TCTTGCATGC TTAATAAAAG TGCTGAGACT GTTACTAAGT
 701 AAAAAGCTGT CAAACATTTA CTGAAAATAG AATTGGCCCC ATGGCTTGAT
 751 GTGAAGACAG CAAGGAAAGA AGCACCAGTC AAGTTGTGAA CAAGCACCAA
 801 ATTAAAAGAC CTAAACCTTA CCAAATTGTC TTTTTTTGAG GCTAATCTAT
 851 CACTTGTTAA TGTCTAAACT TTAAAATCAG TACATTTAAT TTGAGTTCCA
 901 ACTGTTAAGC ATATTTCTCA GACTTAAATT TGATTATGTC CCCATCAAAA
 951 AGAATCTCCA TTTTCTGAAG GTCTGTTAGT TAATTTGAGA TAATTTGTTA
1001 AAGGCAAGTA TGTCATATTA CTGAGGCTAC AAGTTAGTCA GCAGATGAGT
1051 GCCAGTCCAG CCTTTTCCGG TATGTTATTG TTAGAAATAT TGAGTTCTAA
1101 TGTTACATCT GAGGAAGTAT GTAATTTGAG AATTGTAACT TCTAAGGGAT
1151 TCACTGCATC ATAGCTATGC CTGTATGGAG TCTAACATAT GACCAATACC
1201 AACCCATAAT CCAGCTGAAC AAAGATACTG TAACATTATG ATTTGAGTGG
1251 TGCTTTTCCT TGCTTTGTTA ACCATCACGA GAGTCTGCAG CACAACTTTT
1301 AACAAAGCTA GAACAGTTTT GGCTTCTTAA ACTTCATATT TGGGTAGGTT
1351 AAGCTGCCAT ACGTGTTCAG TGTGAATAGT GTTTAAGTTG AAAATATTGT
1401 AAAAAAATTA TATTTTTTCA AAAATATTTA AAAAAATAAA TAATAGTAGA
1451 ACTGAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAAAAA
1501 AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 150 bp to 530 bp; peptide length: 127
Category: putative protein

```
   1 MKDPSRSSTS PSIINEDVII NGHSHEDDNP FAEYMWMENE EEFNRQIEEE
```

```
 51 LWEEEFIERC FQEMLEEEEE HEWFIPARDL PQTMDQIQDQ FNDLVISEGS
101 SLEDLVVKSN LNPNAKEFVP GVKYGNI
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3f16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_3f16, frame 3

Report for DKFZphfbr2_3f16.3

```
[LENGTH]     127
[MW]         14998.41
[pI]         4.04
[BLOCKS]     BL01269D
[PROSITE]    MYRISTYL         1
[PROSITE]    CK2_PHOSPHO_SITE     2
[KW]         Alpha_Beta
[KW]         LOW_COMPLEXITY   27.56 %
```

```
SEQ    MKDPSRSSTSPSIINEDVIINGHSHEDDNPFAEYMWMENEEEFNRQIEEELWEEEFIERC
SEG    ......................................xxxxxxxxxxxxxxxxxxxxxx
PRD    cccccccccccccccceeeeccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ    FQEMLEEEEEHEWFIPARDLPQTMDQIQDQFNDLVISEGSSLEDLVVKSNLNPNAKEFVP
SEG    xxxxxxxxxxxx................................................
PRD    hhhhhhhhhhhhhcccccccccchhhhhhhhhcceeeeccccccceeeeeccccccccccccc

SEQ    GVKYGNI
SEG    .......
PRD    ccccccc
```

Prosite for DKFZphfbr2_3f16.3

```
PS00006     24->28    CK2_PHOSPHO_SITE     PDOC00006
PS00006    100->104   CK2_PHOSPHO_SITE     PDOC00006
PS00008    121->127   MYRISTYL             PDOC00008
```

(No Pfam data available for DKFZphfbr2_3f16.3)

DKFZphfbr2_3g8
----

group: metabolism

DKFZphfbr2_3g8.1 encodes a novel 178 amino acid protein with similarity to yeast ARD1 protein.

In yeast, ARD1 and NAT1, are required for the expression of an N-terminal protein acetyltransferase 1. NAT1 controls full repression of the silent mating type locus HML, sporulation and entry into G0. ARD1 is involved in the assembly of the NAT 1-complex. The new protein could be part of this or an other NAT complex.

The new protein can find application modulating NAT assembly and action and therefore be important in metabolism of drugs and environmental mutagens.

strong similarity to N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 homolog

complete cDNA, complete cds? start at Bp 40, EST hits

Sequenced by AGOWA

Locus: /map="20"

Insert length: 1030 bp
Poly A stretch at pos. 1013, no polyadenylation signal found

```
   1 TGGGCTTGGC GAACGGTCTT CGGAAGCGGC GGCGGCGCGA TGACCACGCT
  51 ACGGGCCTTT ACCTGCGACG ACCTGTTCCG CTTCAACAAC ATTAACTTGG
 101 ATCCACTTAC AGAAACTTAT GGGATTCCTT TCTACCTACA ATACCTCGCC
 151 CACTGGCCAG AGTATTTCAT TGTTGCAGTG GCACCTGGTG GAGAATTAAT
 201 GGGTTATATT ATGGGTAAAG CAGAAGGCTC AGTAGCTAGG GAAGAATGGC
 251 ACGGGCACGT CACAGCTCTG TCTGTTGCCC CAGAATTTCG ACGCCTTGGT
 301 TTGGCTGCTA AACTTATGGA GTTACTAGAG GAGATTTCAG AAAGAAAGGG
 351 TGGGTTTTTT GTGGATCTCT TTGTAAGAGT ATCTAACCAA GTTGCAGTTA
 401 ACATGTACAA GCAGTTGGGC TACAGTGTAT ATAGGACGGT CATAGAGTAC
 451 TATTCGGCCA GCAACGGGGA GCCTGATGAG GACGCTTATG ATATGAGGAA
 501 AGCACTTTCC AGGGATACTG AGAAGAAATC CATCATACCA TTACCTCATC
 551 CTGTGAGGCC TGAAGACATT GAATAACCCT GGGCAGTGGT TCTTAGGCAG
 601 ATACTCTAGA TGCTTTATGG ACAATATTAT TTTCATTGGA TGATTCTGGA
 651 GCTCTATTAG GAGAAAAGTA ATCATTTTAG GTCTTAAAGA CTTCAAGAAA
 701 ATACAGGTTA TCAATTTATT TTAAATCTCA TTGTTTCCAG TTAGCAATAT
 751 CATACCTATT AAAGCTGTTC ATTGTAACAA AATTCAATCA AAAAGGCAGC
 801 TAGGTCAGAA GGAAACATAC CACTCTCATG GTTCATAGTA TTCACTGTAT
 851 GTATGCTAGG GAAAAGACTT GCTCCAGTCT CCTCCTCAGT TCTGTGCCTG
 901 AGAACCACTG CTGCATATAT TTGTTTTTAA ATTTTGTATT GAACTGTTAA
 951 TTGAAGCTTT AAAAGCATAT ATGAAATGTA TAAATCTAAG ATGTATAATA
1001 CATTATTGAC TCCAAAAAAA AAAAAAAAAA
```

BLAST Results

Entry HSG0101 from database EMBL:
human STS SHGC-35956.
Length = 401
Minus Strand HSPs:
Score = 1417 (212.6 bits), Expect = 9.3e-58, P = 9.3e-58
Identities = 301/311 (96%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 40 bp to 573 bp; peptide length: 178
Category: strong similarity to known protein

```
  1 MTTLRAFTCD DLFRFNNINL DPLTETYGIP FYLQYLAHWP EYFIVAVAPG
 51 GELMGYIMGK AEGSVAREEW HGHVTALSVA PEFRRLGLAA KLMELLEEIS
```

```
101 ERKGGFFVDL FVRVSNQVAV NMYKQLGYSV YRTVIEYYSA SNGEPDEDAY
151 DMRKALSRDT EKKSIIPLPH PVRPEDIE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_3g8, frame 1

TREMBL:SPCC16C4_12 gene: "SPCC16C4.12"; product: "putative n-terminal acetyltransferase complex subunit"; S.pombe chromosome III cosmid c16C4., N = 1, Score = 475, P = 3.2e-45

SWISSPROT:ARDH_LEIDO N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG., N = 1, Score = 451, P = 1.1e-42

PIR:S69021 hypothetical protein YPR131c - yeast (Saccharomyces cerevisiae), N = 1, Score = 382, P = 2.3e-35

```
>TREMBL:SPCC16C4_12 gene: "SPCC16C4.12"; product: "putative n-terminal
     acetyltransferase complex subunit"; S.pombe chromosome III cosmid c16C4.
            Length = 180

  HSPs:

 Score = 475 (71.3 bits), Expect = 3.2e-45, P = 3.2e-45
 Identities = 96/165 (58%), Positives = 118/165 (71%)

Query:     1 MTTLRAFTCDDLFRFNNINLDPLTETYGIPFYLQYLAHWPEYFIVAVAPGGE--LMGYIM 58
             MT  R F    DLF FNNINLDPLTET+ I FYL YL  WP    +V  +    + LMGYIM
Sbjct:     1 MTDTRKFKATDLFSFNNINLDPLTETFNISFYLSYLNKWPSLCVVQESDLSDPTLMGYIM 60

Query:    59 GKAEGSVAREEWHGHVTALSVAPEFRRLGLAAKLMELLEEISERKGGFFVDLFVRVSNQV 118
             GK+EG+    +EWH HVTA++VAP  RRLGLA  +M+ LE +   +  FFVDLFVR SN +
Sbjct:    61 GKSEGT--GKEWHTHVTAITVAPNSRRLGLARTMMDYLETVGNSENAFFVDLFVRASNAL 118

Query:   119 AVNMYKQLGYSVYRTVIEYYSASNGEPDEDAYDMRKALSRDTEKKSI 165
             A++ YK LGYSVYR VI YYS  +G+ DED++DMRK LSRD  ++SI
Sbjct:   119 AIDFYKGLGYSVYRRVIGYYSNPHGK-DEDSFDMRKPLSRDVNRESI 164
```

Pedant information for DKFZphfbr2_3g8, frame 1

Report for DKFZphfbr2_3g8.1

```
[LENGTH]        178
[MW]            20338.24
[pI]            5.06
[HOMOL]         TREMBL:SPCC16C4_12 gene: "SPCC16C4.12"; product: "putative n-terminal
acetyltransferase complex subunit"; S.pombe chromosome III cosmid c16C4. 7e-47
[FUNCAT]        06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)        [S. cerevisiae, YPR131c] 6e-37
[FUNCAT]        01.06.07 lipid, fatty-acid and sterol utilization    [S. cerevisiae, YHR013c]
4e-14
[FUNCAT]        30.03 organization of cytoplasm        [S. cerevisiae, YHR013c] 4e-14
[FUNCAT]        03.22 cell cycle control and mitosis  [S. cerevisiae, YHR013c] 4e-14
[FUNCAT]        r general function prediction          [M. jannaschii, MJ1530] 6e-09
[PIRKW]         acyltransferase 1e-12
[SUPFAM]        arrest-defective protein 1 1e-12
[SUPFAM]        Escherichia coli peptide N-acetyltransferase rimI 1e-07
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        3
[KW]            Alpha_Beta

SEQ     MTTLRAFTCDDLFRFNNINLDPLTETYGIPFYLQYLAHWPEYFIVAVAPGGELMGYIMGK
PRD     cccccccccchhhhhhccccccccccchhhhhhcccccceeeeeecccccceeeehhhh

SEQ     AEGSVAREEWHGHVTALSVAPEFRRLGLAAKLMELLEEISERKGGFFVDLFVRVSNQVAV
PRD     hcccccccccccceeeeehhhhhhhhcchhhhhhhhhhhhhhccceeeeeeeeecchhhhh

SEQ     NMYKQLGYSVYRTVIEYYSASNGEPDEDAYDMRKALSRDTEKKSIIPLPHPVRPEDIE
PRD     hhhhhhccccchhhhhhcccccccccccchhhhhhhhhhhhhhhhccccccccccccc
```

Prosite for DKFZphfbr2_3g8.1

PS00005	3->6	PKC_PHOSPHO_SITE	PDOC00005
PS00005	100->103	PKC_PHOSPHO_SITE	PDOC00005
PS00005	160->163	PKC_PHOSPHO_SITE	PDOC00005
PS00006	8->12	CK2_PHOSPHO_SITE	PDOC00006
PS00006	133->137	CK2_PHOSPHO_SITE	PDOC00006
PS00006	141->145	CK2_PHOSPHO_SITE	PDOC00006

(No Pfam data available for DKFZphfbr2_3g8.1)

DKFZphfbr2_312
----

group: brain derived

DKFZphfbr2_312 encodes a novel 589 amino acid protein with weak similarity to S. cerevisiae ubiquitin-like protein DSK2.

Pfam predicts for this protein similarity to the ubiquitin family; No informative BLAST results; No predictive prosite or SCOP motive

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to ubiquitin-like protein DSK2 yeast

complete cDNA, complete cds, EST hits
Dsk2p is involved in spindel pole body SPB duplication, SPB = centomer
strong similarity to HRIHFB2157 human mRNA

Sequenced by AGOWA

Locus: unknown

Insert length: 2978 bp
Poly A stretch at pos. 2958, polyadenylation signal at pos. 2924

```
   1 GGGGGGAGGA AGCGGTGGCT GCTGCGGATG TCGGTGTGAG CGAGCGGCGC
  51 CTGAACACAC GGCGGCTGCC GAGCGCCTGA CCCGGGCCTG CGCCAGAGCC
 101 TGCACCGAGC TCCGGGGCCC CACACCCGCT ACGGTGGCCC TGCGCCCGTT
 151 GCTACTGAGG CGGCGTGCTC TGCATTCTTC GCTGTCCAGG CCTGCCGGCT
 201 CTGGTGTCTG CTGGCTCCTC CTTGCTCGCC TGCTCCCTCC TGCTTGCCTG
 251 AGTCACCGCC GCCGCCGCCG CCACAGCCAT GGCCGAGAGT GGTGAAAGCG
 301 GCGGTCCTCC GGGCTCCCAG GATAGCGCCG CCGGAGCCGA AGGTGCTGGC
 351 GCCCCCGCGG CCGCTGCCTC CGCGGAGCCC AAAATCATGA AAGTCACCGT
 401 GAAGACCCCG AAGGAAAAGG AGGAATTCGC CGTGCCCGAG AATAGCTCCG
 451 TCCAGCAGTT TAAGGAAGAA ATCTCTAAAC GTTTTAAATC ACATACTGAC
 501 CAACTTGTGT TGATATTTGC TGGAAAAATT TTGAAAGATC AAGATACCTT
 551 GAGTCAGCAT GGAATTCATG ATGGACTTAC TGTTCACCTT GTCATTAAAA
 601 CACAAAACAG GCCTCAGGAT CATTCAGCTC AGCAAACAAA TACAGCTGGA
 651 GGCAATGTTA CTACATCATC AACTCCTAAT AGTAACTCTA CATCTGGTTC
 701 TGCTACTAGC AACCCTTTTG GTTTAGGTGG CCTTGGGGGA CTTGCAGGTC
 751 TGAGTAGCTT GGGTTTGAAT ACTACCAACT TCTCTGAACT ACAGAGTCAG
 801 ATGCAGCGAC AACTTTTGTC TAACCCTGAA ATGATGGTCC AGATCATGGA
 851 AAATCCCTTT GTTCAGAGCA TGCTCTCAAA TCCTGACCTG ATGAGACAGT
 901 TAATTATGGC CAATCCACAA ATGCAGCAGT TGATACAGAG AAATCCAGAA
 951 ATTAGTCATA TGTTGAATAA TCCAGATATA ATGAGACAAA CGTTGGAACT
1001 TGCCAGGAAT CCAGCAATGA TGCAGGAGAT GATGAGGAAC CAGGACCGAG
1051 CTTTGAGCAA CCTAGAAAGC ATCCCAGGGG GATATAATGC TTTAAGGCGC
1101 ATGTACACAG ATATTCAGGA ACCAATGCTG AGTGCTGCAC AAGAGCAGTT
1151 TGGTGGTAAT CCATTTGCTT CCTTGGTGAG CAATACATCC TCTGGTGAAG
1201 GTAGTCAACC TTCCCGTACA GAAAATAGAG ATCCACTACC CAATCCATGG
1251 GCTCCACAGA CTTCCCAGAG TTCATCAGCT TCCAGCGGCA CTGCCAGCAC
1301 TGTGGGTGGC ACTACTGGTA GTACTGCCAG TGGCACTTCT GGGCAGAGTA
1351 CTACTGCGCC AAATTTGGTG CCTGGAGTAG GAGCTAGTAT GTTCAACACA
1401 CCAGGAATGC AGAGCTTGTT GCAACAAATA ACTGAAAACC CACAACTGAT
1451 GCAAAACATG TTGTCTGCCC CCTACATGAG AAGCATGATG CAGTCACTAA
1501 GCCAGAATCC TGACCTTGCT GCACAGATGA TGCTGAATAA TCCCCTATTT
1551 GCTGGAAATC CTCAGCTTCA AGAACAAATG AGACAACAGC TCCCAACTTT
1601 CCTCCAACAA ATGCAGAATC CTGATACACT ATCAGCAATG TCAAACCCTA
1651 GAGCAATGCA GGCCTTGTTA CAGATTCAGC AGGGTTTACA GACATTAGCA
1701 ACGGAAGCCC CGGGCCTCAT CCCAGGGTTT ACTCCTGGCT TGGGGGCATT
1751 AGGAAGCACT GGAGGCTCTT CGGGAACTAA TGGATCTAAC GCCACACCTA
1801 GTGAAAACAC AAGTCCCACA GCAGGAACCA CTGAACCTGG ACATCAGCAG
1851 TTTATTCAGC AGATGCTGCA GGCTCTTGCT GGAGTAAATC CTCAGCTACA
1901 GAATCCAGAA GTCAGATTTC AGCAACAACT GGAACAACTC AGTGCAATGG
1951 GATTTTTGAA CCGTGAAGCA AACTTGCAAG CTCTAATAGC AACAGGAGGT
2001 GATATCAATG CAGCTATTGA AAGGTTACTG GGCTCCCAGC CATCATAGCA
2051 GCATTTCTGT ATCTTGAAAA AATGTAATTT ATTTTTGATA ACGGCTCTTA
2101 AACTTTAAAA TACCTGCTTT ATTTCATTTT GACTCTTGGA ATTCTGTGCT
2151 GTTATAAACA AACCCAATAT GATGCATTTT AAGGTGGAGT ACAGTAAGAT
2201 GTGTGGGTTT TTCTGTATTT TTCTTTTCTG GAACAGTGGG AATTAAGGCT
2251 ACTGCATGCA TCACTTCTGC ATTTATTGTA ATTTTTTAAA AACATCACCT
2301 TTTATAGTTG GGTGACCAGA TTTTGTCCTG CATCTGTCCA GTTTATTTGC
2351 TTTTTAAACA TTAGCCTATG GTAGTAATTT ATGTAGAATA AAAGCATTAA
2401 AAAGAAGCAA ATCATTTGCA CTCTATAATT TGTGGTACAG TATTGCTTAT
2451 TGTGACTTTG GCATGCATTT TTGCAAACAA TGCTGTAAGA TTTATACTAC
2501 TGATAATTTT GTTTTATTTG TATACAATAT AGAGTATGCA CATTTGGGAC
```

```
2551 TGCATTTCTG GAAACATACT GCAATAGGCT CTCTGAGCAA AACACCTGTA
2601 ACTAAAAAAG TGAAGATAAG AAAATACTCT TAAAGCTGAG TATTTCCTAA
2651 TTGTATAGAA TCTTACAGCA TCTTTGACAA ACATCTCCCA GCAAAAGTGC
2701 CGGTTAGTCA GGTTTGTTGA AAATACAGTA GAAAAGCTGA TTCTGGTTAT
2751 CTCTTTAAGG ACAATTAATT GTACAGACAC ATAATGTAAC ATTGTCTCAA
2801 CATTCATTCA CAGATTGACT GTAAATTACC TTAATCTTTG TGCAGACTGA
2851 AGGAACACTG TAGTATACCC CAAAGTGCAT TTGCCTAGGA CTTCTCAGCT
2901 TCTCCCATAG GTAGTTTAAC AGGCATTAAA ATTTGTAATT GAAATGTTGC
2951 TTTCACTCAA AAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 279 bp to 2045 bp; peptide length: 589
Category: similarity to known protein

```
  1 MAESGESGGP PGSQDSAAGA EGAGAPAAAA SAEPKIMKVT VKTPKEKEEF
 51 AVPENSSVQQ FKEEISKRFK SHTDQLVLIF AGKILKDQDT LSQHGIHDGL
101 TVHLVIKTQN RPQDHSAQQT NTAGGNVTTS STPNSNSTSG SATSNPFGLG
151 GLGGLAGLSS LGLNTTNFSE LQSQMQRQLL SNPEMMVQIM ENPFVQSMLS
201 NPDLMRQLIM ANPQMQQLIQ RNPEISHMLN NPDIMRQTLE LARNPAMMQE
251 MMRNQDRALS NLESIPGGYN ALRRMYTDIQ EPMLSAAQEQ FGGNPFASLV
301 SNTSSGEGSQ PSRTENRDPL PNPWAPQTSQ SSSASSGTAS TVGGTTGSTA
351 SGTSGQSTTA PNLVPGVGAS MFNTPGMQSL LQQITENPQL MQNMLSAPYM
401 RSMMQSLSQN PDLAAQMMLN NPLFAGNPQL QEQMRQQLPT FLQQMQNPDT
451 LSAMSNPRAM QALLQIQQGL QTLATEAPGL IPGFTPGLGA LGSTGGSSGT
501 NGSNATPSEN TSPTAGTTEP GHQQFIQQML QALAGVNPQL QNPEVRFQQQ
551 LEQLSAMGFL NREANLQALI ATGGDINAAI ERLLGSQPS
```

BLASTP hits

Entry CE1_1 from database TREMBL:
"F15C11.2"; Caenorhabditis elegans cosmid VF15C11L
Length = 293
Score = 454 (159.8 bits), Expect = 4.4e-43, P = 4.4e-43
Identities = 81/162 (50%), Positives = 113/162 (69%)

Entry S54583 from database PIR:
ubiquitin-like protein DSK2 - yeast (Saccharomyces cerevisiae)
Length = 373
Score = 278 (97.9 bits), Expect = 1.2e-23, P = 1.2e-23
Identities = 100/307 (32%), Positives = 155/307 (50%)

Entry AB015344_1 from database TREMBLNEW:
gene: "HRIHFB2157"; Homo sapiens HRIHFB2157 mRNA, partial cds.
Score = 1135, P = 3.6e-115, identities = 227/301, positives = 253/301

Alert BLASTP hits for DKFZphfbr2_312, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_312, frame 3

Report for DKFZphfbr2_312.3

```
[LENGTH]      589
[MW]          62489.22
[pI]          5.02
[HOMOL]       TREMBL:AB015344_1 gene: "HRIHFB2157"; Homo sapiens HRIHFB2157 mRNA, partial
cds. 1e-121
[FUNCAT]      03.22 cell cycle control and mitosis [S. cerevisiae, YMR276w] 2e-17
```

```
[FUNCAT]       30.10 nuclear organization    [S. cerevisiae, YMR276w] 2e-17
[BLOCKS]       BL00299 Ubiquitin family proteins
[SUPFAM]       unassigned ubiquitin-related proteins 5e-16
[SUPFAM]       ubiquitin homology 5e-16
[PROSITE]      MYRISTYL        24
[PROSITE]      CK2_PHOSPHO_SITE       9
[PROSITE]      GLYCOSAMINOGLYCAN      1
[PROSITE]      PKC_PHOSPHO_SITE       3
[PROSITE]      ASN_GLYCOSYLATION      7
[PFAM]         Ubiquitin family
[KW]           Irregular
[KW]           3D
[KW]           LOW_COMPLEXITY    23.43 %
```

```
SEQ    MAESGESGGPPGSQDSAAGAEGAGAPAAAASAEPKIMKVTVKTPKEKEEFAVPENSSVQQ
SEG    ..xxxxxxxxxxx..xxxxxxxxxxxxxxxxxx...xxxxxxxxxxxx..........
1aarA  ..................................CEEEEEETTTCEEEECTTTTBHHH

SEQ    FKEEISKRFKSHTDQLVLIFAGKILKDQDTLSQHGIHDGLTVHLVIKTQNRPQDHSAQQT
SEG    ............................................................
1aarA  HHHHHHHHHCCCGGGEEEEETTEECTTTTBGGGGCCTTTTEEEEEBC.............

SEQ    NTAGGNVTTSSTPNSNSTSGSATSNPFGLGGLGGLAGLSSLGLNTTNFSELQSQMQRQLL
SEG    ...xxxxxxxxxxxxxxxxxxxxx..xxxxxxxxxxxxxxxx................
1aarA  ............................................................

SEQ    SNPEMMVQIMENPFVQSMLSNPDLMRQLIMANPQMQQLIQRNPEISHMLNNPDIMRQTLE
SEG    ............................................................
1aarA  ............................................................

SEQ    LARNPAMMQEMMRNQDRALSNLESIPGGYNALRRMYTDIQEPMLSAAQEQFGGNPFASLV
SEG    ............................................................
1aarA  ............................................................

SEQ    SNTSSGEGSQPSRTENRDPLPNPWAPQTSQSSSASSGTASTVGGTTGSTASGTSGQSTTA
SEG    ..........................xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
1aarA  ............................................................

SEQ    PNLVPGVGASMFNTPGMQSLLQQITENPQLMQNMLSAPYMRSMMQSLSQNPDLAAQMMLN
SEG    ............................................................
1aarA  ............................................................

SEQ    NPLFAGNPQLQEQMRQQLPTFLQQMQNPDTLSAMSNPRAMQALLQIQQGLQTLATEAPGL
SEG    ............................................................
1aarA  ............................................................

SEQ    IPGFTPGLGALGSTGGSSGTNGSNATPSENTSPTAGTTEPGHQQFIQQMLQALAGVNPQL
SEG    ....xxxxxxxxxxxxxxxxxxxxxxxx................................
1aarA  ............................................................

SEQ    QNPEVRFQQQLEQLSAMGFLNREANLQALIATGGDINAAIERLLGSQPS
SEG    .................................................
1aarA  .................................................
```

Prosite for DKFZphfbr2_312.3

PS00001	55->59	ASN_GLYCOSYLATION	PDOC00001
PS00001	126->130	ASN_GLYCOSYLATION	PDOC00001
PS00001	136->140	ASN_GLYCOSYLATION	PDOC00001
PS00001	164->168	ASN_GLYCOSYLATION	PDOC00001
PS00001	167->171	ASN_GLYCOSYLATION	PDOC00001
PS00001	302->306	ASN_GLYCOSYLATION	PDOC00001
PS00001	501->505	ASN_GLYCOSYLATION	PDOC00001
PS00002	305->309	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	40->43	PKC_PHOSPHO_SITE	PDOC00005
PS00005	43->46	PKC_PHOSPHO_SITE	PDOC00005
PS00005	66->69	PKC_PHOSPHO_SITE	PDOC00005
PS00006	43->47	CK2_PHOSPHO_SITE	PDOC00006
PS00006	71->75	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	200->204	CK2_PHOSPHO_SITE	PDOC00006
PS00006	260->264	CK2_PHOSPHO_SITE	PDOC00006
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00006	312->316	CK2_PHOSPHO_SITE	PDOC00006
PS00006	506->510	CK2_PHOSPHO_SITE	PDOC00006
PS00006	572->576	CK2_PHOSPHO_SITE	PDOC00006
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	12->18	MYRISTYL	PDOC00008

PS00008	19->25	MYRISTYL	PDOC00008
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	95->101	MYRISTYL	PDOC00008
PS00008	124->130	MYRISTYL	PDOC00008
PS00008	140->146	MYRISTYL	PDOC00008
PS00008	150->156	MYRISTYL	PDOC00008
PS00008	153->159	MYRISTYL	PDOC00008
PS00008	162->168	MYRISTYL	PDOC00008
PS00008	267->273	MYRISTYL	PDOC00008
PS00008	293->299	MYRISTYL	PDOC00008
PS00008	308->314	MYRISTYL	PDOC00008
PS00008	337->343	MYRISTYL	PDOC00008
PS00008	343->349	MYRISTYL	PDOC00008
PS00008	347->353	MYRISTYL	PDOC00008
PS00008	355->361	MYRISTYL	PDOC00008
PS00008	366->372	MYRISTYL	PDOC00008
PS00008	479->485	MYRISTYL	PDOC00008
PS00008	489->495	MYRISTYL	PDOC00008
PS00008	492->498	MYRISTYL	PDOC00008
PS00008	495->501	MYRISTYL	PDOC00008
PS00008	499->505	MYRISTYL	PDOC00008
PS00008	573->579	MYRISTYL	PDOC00008

Pfam for DKFZphfbr2_312.3

```
HMM_NAME         Ubiquitin family

HMM                 *MQIFVKTLtGRTcTFEVepQEtVeqIKQHIeekEGIPPeQQRLIFaGRQ
                     M ++VKT   +  +F V+++  V Q+K+ I+       +Q +LIFAG+
Query             37 MKVTVKTPK-EKEEFAVPENSSVQQFKEEISKRFKSHTDQLVLIFAGKI      84

HMM                 LEDeKTLsDYNIggeSTLHLVlR*
                    L D  TLS+++I  + T+HLV++
Query            85 LKDQDTLSQHGIHDGLTVHLVIK     107
```

DKFZphfbr2_62b11
----

group: signal transduction

DKFZphfbr2_62b11.encodes a novel 655 amino acid putative GTPase-activating protein, related to human chimaerins.

The rac small GTPase is associated with type-I phosphatidylinositol 4-phosphate 5-kinase and regulating the production of phosphatidylinositol 4,5-bisphosphate. The new protein is expected to activate p21rac-related small GTPases.

The new protein can find clinical application in modulating/blocking the response to a cellular receptor.

similarity to CHIMAERIN

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="4"

Insert length: 4593 bp
Poly A stretch at pos. 4571, polyadenylation signal at pos. 4553

```
   1 GGGGGAGTTT GAAGACAGAA AGGAAAGGGG AGAAACCTGC AGAGAGCATC
  51 AAAGGATGGG GGGTGCTATA AAAGAAGCAG GGGGGTCCTT TGAAAGAAAT
 101 CTATCATGCA CTGAAATGCT TTCTGGAGAA GGTGCCGTTA TTTTCCTCCC
 151 CTCTTGCTCA GATGAAAGGA GCCAGCAAGG ACAGTCCTGA AATATTCCTC
 201 AGGGGACTTT TTGTCATTGT TCCTCTTTCC TCTTGCACAG AGCTATTTGC
 251 TGACCTTTCC AGAGGAATCT CAGTCCAGCT GAGAAGACAG TTCTTAATAA
 301 AAACAAAAAA ATGCAAAAAC CAATTCCTGC TGTTTGAATG GGAATGGTAG
 351 CTTGCTTGCT GCAGTTCTTT TCCTGTGACA TTTTGGAATG TCTGCAGAAA
 401 CTTAAAAAAA AGAAAAAAAA AACCTTAAAA ACTCCCTGGA TTAGGCAAGA
 451 GAAAAGGAAG TTTTTTTTTG CTAAACAGGA GTAAATGAGA GGTGGTAACT
 501 TATCCCTAAG CCAGGACCTG GATGATCAAA ACCTTCAAAT TCTAGGGATC
 551 AGCACTTCAA AAATAACAAG TAAACAAGCA TGAGGAGTGG CTGTTGGGTT
 601 TCGCTCAGAG GCAGGTTTTA AAGGAAGCCA AAACCGGGTT CAGAACTTCA
 651 GGCCTGTACG ATGCCTGAAG ACCGGAATTC TGGGGGGTGC CCGGCTGGTG
 701 CCTTAGCCTC AACTCCTTTC ATCCCTAAAA CTACATACAG AAGAATCAAA
 751 CGGTGTTTTA GTTTTCGGAA AGGCATTTTT GGACAGAAAC TGGAGGATAC
 801 TGTTCGTTAT GAGAAGAGAT ATGGGAACCG TCTGGCTCCG ATGTTGGTGG
 851 AGCAGTGCGT GGACTTTATC CGACAAAGGG GGCTGAAAGA AGAGGGTCTC
 901 TTTCGACTGC CAGGCCAGGC TAATCTTGTT AAGGAGCTCC AAGATGCCTT
 951 TGACTGTGGG GAGAAGCCAT CATTTGACAG CAACACAGAT GTACACACGG
1001 TGGCATCACT TCTTAAGCTG TACCTCCGAG AACTTCCAGA ACCAGTTATT
1051 CCTTATGCGA AGTATGAAGA TTTTTTGTCA TGTGCCAAAC TGCTCAGCAA
1101 GGAAGAGGAA GCAGGTGTTA AGGAATTAGC AAAGCAGGTG AAGAGTTTGC
1151 CAGTGGTAAA TTACAACCTC CTCAAGTATA TTTGCAGATT CTTGGATGAA
1201 GTACAGTCCT ACTCGGGAGT TAACAAAATG AGTGTGCAGA ACTTGGCAAC
1251 GGTCTTTGGT CCTAATATCC TGCGCCCCAA AGTGGAAGAT CCTTTGACTA
1301 TCATGGAGGG CACTGTGGTG GTCCAGCAGT TGATGTCAGT GATGATTAGC
1351 AAACATGATT GCCTCTTTCC CAAAGATGCA GAACTACAAA GCAAGCCCCA
1401 AGATGGAGTG AGCAACAACA ATGAAATTCA GAAGAAAGCC ACCATGGGGC
1451 TGTTACAGAA CAAGGAGAAC AATAACACCA AGGACAGCCC TAGTAGGCAG
1501 TGCTCCTGGG ACAAGTCTGA GTCACCCCAG AGAAGCAGCA TGAACAATGG
1551 ATCCCCCACA GCTCTATCAG GCAGCAAAAC CAACAGCCCA AAGAACAGTG
1601 TTCACAAGCT AGATGTGTCT AGAAGCCCCC CTCTCATGGT CAAAAAGAAC
1651 CCAGCCTTTA ATAAGGGTAG TGGGATAGTT ACCAATGGGT CCTTCAGCAG
1701 CAGTAATGCA GAAGGTCTTG AGAAAACCCA AACCACCCCC AATGGGAGCC
1751 TACAGGCCAG AAGGAGCTCT TCACTGAAGG TATCTGGTAC CAAAATGGGC
1801 ACGCACAGTG TACAGAATGG AACGGTGCGC ATGGGCATTT TGAACAGCGA
1851 CACACTCGGG AACCCCACAA ATGTTCGAAA CATGAGCTGG CTGCCAAATG
1901 GCTATGTGAC CCTGAGGGAT AACAAGCAGA AAGAACAAGC TGGAGAGTTA
1951 GGCCAGCACA ACAGACTGTC CACCTATGAT AATGTCCATC AACAGTTCTC
2001 CATGATGAAC CTTGATGACA AGCAGAGCAT TGACAGTGCT ACCTGGTCCA
2051 CTTCCTCCTG TGAAATCTCC CTCCCTGAGA ACTCCAACTC CTGTCGCTCT
2101 TCTACCACCA CCTGCCCAGA GCAAGACTTT TTTGGGGGGA ACTTTGAGGA
2151 CCCTGTTTTG GATGGGCCCC CGCAGGACGA CCTTTCCCAC CCCAGGGACT
2201 ATGAAAGCAA AAGTGACCAC AGGAGTGTGG GAGGTCGAAG TAGTCGTGCC
2251 ACCAGTAGCA GTGACAACAG TGAGACATTT GTGGGCAACA GCAGCAGCAA
2301 CCACAGTGCA CTGCACAGTT TAGTTTCCAG CCTGAAACAG GAAATGACCA
2351 AACAGAAGAT AGAGTATGAG TCCAGGATAA AGAGCTTAGA ACAGCGAAAC
2401 TTGACTTTGG AAACAGAAAT GATGAGCCTC CATGATGAAC TGGATCAGGA
2451 GAGGAAAAAG TTCACAATGA TAGAAATAAA AATGCGAAAT GCCGAGCGAG
2501 CAAAAGAAGA TGCCGAGAAA AGAAATGACA TGCTACAGAA AGAAATGGAG
2551 CAGTTTTTTT CCACGTTTGG AGAACTGACA GTGGAACCCA GGAGAACCGA
```

```
2601 GAGAGGAAAC ACAATATGGA TTCAGTGAGC CTGCTTTCGC CTGCTGTCTC
2651 TGATGGCTCT GGCAAGGACT CCAGGGATTC TGGTGGGATA TGACTTAGAA
2701 CCAGGTGGCT GGTCACCTGG ATGTACAGAA GTCTAACTGG TGAAGGAATA
2751 TCATTTACAG ACATTAAACA TCCATATCTG CAATGTGTAC CAAAGTTATA
2801 TCATGCCCCA TAATGCTACT GTCAAGTGTT ACAACTGGAT ATGTGTATAT
2851 AGAGTAGTTT TTCAAAAGTA AACTAAAAAT GAGAAGCATA TTTCAAGAAT
2901 TATTTTATTG CAAGTCTTGT ATTTAAATGT TAAATCAATA TGTTGTTGCA
2951 ATTTAGCTTG CTTTCAAGCT TCACCCCTTG CACTTAACAT AAGCTATTTT
3001 TGGCATTGTG TTATCATCGG CTTATTTTAT AGATCAATAT TTTTATTTCC
3051 CTTTTTTGCT GAGGAAATGA AGATAAGCAA AAATATAAAT ATATATATAA
3101 ATATATGAGT TATTAAAACC AGAAGAATAC TTTGTGGCTG TGCTGTTTGT
3151 GCCAATAGAC TTTGTCATGA CCAAAAAGAG AAATGTAAAT AGTTTTATAA
3201 AATACAGTCG AATCACCAGG AACCTTTGAG CTGCTTTTAA AATTCTTCCC
3251 CTGGCACCAC TCAGTTTTGC TTTTGCGAGG CGATTTGACA TAGGAACTTT
3301 GAGACTCCAT GAGAAAGTCC CTTTCTGAGG CCCACTGTCT ACCTTGCCAG
3351 ATCCTCAGTG CGTATCGCCA ATGCAGGATG CTCCTTAGAA AAGAAAAAAT
3401 GGTAAAGGAT GGCATTTAAC GATTCAGGCT TTGAATTACT CTGTCCCTCT
3451 GGACCGAATC TCTTTAACTG CTGGATAGTT TTAGAGGAAT TCTCCTGCTA
3501 CTTAGGTACT GGGAAACAAT GCTTGCTAAA CCATGCCCAC GTGAGCACCT
3551 GTCTCCCACT CAAACCTCTC CCATCTCCCA ACAACTGCAC TTTAGAATAC
3601 CAGCAGTGAA ATGGTATTAC TGTTTCCCTC TGAGTGAAAC TGCTAGAGTA
3651 TATGTCACGT AGTGACATTT TTTTCTCACT CAGGCTATTG CCATCTGGGA
3701 TTCTCTCCCT ACTACAGCTG GCAAAGTTGG TTTGCAGCAA GAAGATAGTG
3751 GGAGGGGGCC AGGCTGCAGG AGAAGGAGAA AAGTTTAGAA GAAACAAACC
3801 ATTTTGCTTC TAATTTTGAC AGTATCACTT TCCTGTTAAA ACATACAATA
3851 ATTTTAAAAG GTGAATGCCT AAAGTTCCAA TTTTAGCAAA TATGGGAACC
3901 TCAGCAATGC TAATTTTCTA GAAAAACCCA GGGCTCTTTG GAGCTAGAGT
3951 TTTGGGAGAA CAGTTCTTCA CAATAAGGCA ATGGTTTTGA GAGGCCAGGC
4001 AAATAATCTT TCTCACCGTA GAACAAAAAG TTACAAAAGG CATAATCGGA
4051 AATAGAGACT ACATACTTGA GTTTATGGGG TTTGTGTTGT TTGAAGGTTC
4101 AATGCTTGCA TGTGTTTATT TATTTTCAAG AGGGAAAGTG GTCTGTACTG
4151 CTTTCATCCT TGCCACTGTC TTGCTTTTAT TTTTTACTCT CCCACTGAGC
4201 AAGCGTCTGT GGTCCTATGG TATCAACCAG TATCTTTATA GCAATAATTT
4251 CTTTAATTCC CTTTTCTCTC TCTTTCCAAT TATTTAACCA GTTACTTCCA
4301 CCTGGACATA CGATAGGAAA TTCAAACTCA AAATATGAAA ATTGATCTTA
4351 ATAACTCTCC CTTCATATCT TTTCACCTAT TTCCAGTCCT TATCATAGTT
4401 GATAAAAACC TCAGACTCAT CCAGAAAGCT ATATGATGCA CTAGTAAAAA
4451 AAACAAAGAT ATTTAAACTG CTTGGGTTCA AATGGTATAC AATTTGCCAG
4501 CTGTTACTGA ACCTTCTATG CATAACTTTT TTTTTCCTCT GTGCAATTGG
4551 AATAATAAAA ATACTACTCC CATAAAAAAA AAAAAAAAAA AAC
```

BLAST Results

Entry G38474 from database EMBLNEW:
SHGC-58303 Human Homo sapiens STS genomic, sequence tagged site.
Score = 2175, P = 1.2e-92, identities = 439/441

Medline entries

97476250:
Beta2-chimaerin is a high affinity receptor for the phorbol ester tumor promoters.

Peptide information for frame 1

ORF from 661 bp to 2625 bp; peptide length: 655
Category: similarity to known protein

```
  1 MPEDRNSGGC PAGALASTPF IPKTTYRRIK RCFSFRKGIF GQKLEDTVRY
 51 EKRYGNRLAP MLVEQCVDFI RQRGLKEEGL FRLPGQANLV KELQDAFDCG
101 EKPSFDSNTD VHTVASLLKL YLRELPEPVI PYAKYEDFLS CAKLLSKEEE
151 AGVKELAKQV KSLPVVNYNL LKYICRFLDE VQSYSGVNKM SVQNLATVFG
201 PNILRPKVED PLTIMEGTVV VQQLMSVMIS KHDCLFPKDA ELQSKPQDGV
251 SNNNEIQKKA TMGLLQNKEN NNTKDSPSRQ CSWDKSESPQ RSSMNNGSPT
301 ALSGSKTNSP KNSVHKLDVS RSPPLMVKKN PAFNKGSGIV TNGSFSSSNA
351 EGLEKTQTTP NGSLQARRSS SLKVSGTKMG THSVQNGTVR MGILNSDTLG
401 NPTNVRNMSW LPNGYVTLRD NKQKEQAGEL GQHNRLSTYD NVHQQFSMMN
451 LDDKQSIDSA TWSTSSCEIS LPENSNSCRS STTTCPEQDF FGGNFEDPVL
501 DGPPQDDLSH PRDYESKSDH RSVGGRSSRA TSSSDNSETF VGNSSSNHSA
551 LHSLVSSLKQ EMTKQKIEYE SRIKSLEQRN LTLETEMMSL HDELDQERKK
```

```
  601 FTMIEIKMRN AERAKEDAEK RNDMLQKEME QFFSTFGELT VEPRRTERGN
  651 TIWIQ
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62b11, frame 1

SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053., N = 3, Score = 661, P = 2.4e-89

TREMBL:HSU90908_1 product: "unknown"; Human clones 23549 and 23762 mRNA, complete cds., N = 1, Score = 348, P = 1.1e-29

PIR:S29128 N-chimerin - rat, N = 1, Score = 286, P = 2.8e-24

PIR:S29956 beta-chimerin - rat, N = 1, Score = 279, P = 1.6e-23

TREMBL:AB014572_1 gene: "KIAA0672"; product: "KIAA0672 protein"; Homo sapiens mRNA for KIAA0672 protein, complete cds., N = 1, Score = 314, P = 1e-24

>SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053.
Length = 638

HSPs:

Score = 661 (99.2 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 122/209 (58%), Positives = 160/209 (76%)

```
Query:    38 GIFGQKLEDTVRYEKRYGNRLAPMLVEQCVDFIRQRGLKEEGLFRLPGQANLVKELQDAF 97
             G+FGQ+L++TV YE+++G  L P+LVE+C +FI + G  EEG+FRLPGQ NLVK+L+DAF
Sbjct:   148 GVFGQRLDETVAYEQKFGPHLVPILVEKCAEFILEHGRNEEGIFRLPGQDNLVKQLRDAF 207

Query:    98 DCGEKPSFDSNTDVHTVASLLKLYLRELPEPVIPYAKYEDFLSCAKLLSKEEEAGVKELA 157
             D GE+PSFD +TDVHTVASLLKLYLR+LPEPV+P+++YE FL C +L + +E    +EL
Sbjct:   208 DAGERPSFDRDTDVHTVASLLKLYLRDLPEPVVPWSQYEGFLLCGQLTNADEAKAQQELM 267

Query:   158 KQVKSLPVVNYNLLKYICRFLDEVQSYSGVNKMSVQNLATVFGPNILRPKVEDPLTIMEG 217
             KQ+   LP  NY+LL YICRFL E+Q    VNKMSV NLATV G N++R KVEDP  IM G
Sbjct:   268 KQLSILPRDNYSLLSYICRFLHEIQLNCAVNKMSVDNLATVIGVNLIRSKVEDPAVIMRG 327

Query:   218 TVVVQQLMSVMISKHDCLFPKDAELQSKP 246
             T  +Q++M++MI  H+ LFPK  ++   P
Sbjct:   328 TPQIQRVMTMMIRDHEVLFPKSKDIPLSP 356
```

Score = 210 (31.5 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 45/115 (39%), Positives = 73/115 (63%)

```
Query:   531 TSSSDNSETFVGNSSSNHSALHSL---VSSLKQEMTKQKIEYESRIKSLEQRNLTLETEM 587
             T +S NSET  G  +S    + SL    V  L++E+  QK  YE +IK+LE+ N  +  ++
Sbjct:   523 TLASPNSETGPGKKNSGEEEIDSLQRMVQELRKEIETQKQMYEEQIKNLEKENYDVWAKV 582

Query:   588 MSLHDELDQERKKFTMIEIKMRNAERAKEDAEKRNDMLQKEMEQFFSTFGELTVE 642
             + L++EL++E+KK  +EI +RN ER++ED EKRN  L++E+++F  +  E   E
Sbjct:   583 VRLNEELEKEKKKSAALEISLRNMERSREDVEKRNKALEEEVKEFVKSMKEPKTE 637
```

Score = 70 (10.5 bits), Expect = 1.2e-74, Sum P(3) = 1.2e-74
Identities = 28/121 (23%), Positives = 54/121 (44%)

```
Query:   528 SRATSSSDNSETFVGNSSSNHSALHSLVSSLKQE-MTKQKIEYESRIKSLEQRNL-TLET 585
             S+ TS+ DN  +  G+      SAL S      K + +      E      K+ +  + +L+
Sbjct:   489 SQRTSTYDNVPSLPGSPGEEASALSSQACDSKGDTLASPNSETGPGKKNSGEEEIDSLQR 548

Query:   586 EMMSLHDELDQERKKFTMIEIKMRNAERAKEDAEKRNDMLQKEMEQFFSTFGELTVEPRR 645
               +  L  E++ +++   M E +++N E+   D   +  L +E+E+          L + R
Sbjct:   549 MVQELRKEIETQKQ---MYEEQIKNLEKENYDVWAKVVRLNEELEKEKKKSAALEISLRN 605

Query:   646 TER 648
              ER
Sbjct:   606 MER 608
```

Score = 53 (8.0 bits), Expect = 2.4e-89, Sum P(3) = 2.4e-89
Identities = 31/111 (27%), Positives = 46/111 (41%)

```
Query:   344 SFSSSNAEGLEKTQTTPNGSLQARRSSSLKVSGTKMGTHSVQNG----TV--RMGILNSD 397
             SFSS  ++   + T  T       A     S KV   K G    +Q+       T+  R   L S
Sbjct:   388 SFSSMTSDS-DTTSPTGQQPSDAFPEDSSKVPREKPGDWKMQSRKRTQTLPNRKCFLTSA 446
```

```
Query:   398 TLG-NPTNV---RNMSWLPNGYVTLRDNKQKEQAGELGQ---HNRLSTYDNV 442
             G N + +    +N  W P+       +  ++  + +L Q     R STYDNV
Sbjct:   447 FQGANSSKMEIFKNEFWSPSSEAKAGEGHRRTMSQDLRQLSDSQRTSTYDNV 498

 Score = 53 (8.0 bits), Expect = 3.5e-14, Sum P(3) = 3.5e-14
 Identities = 32/125 (25%), Positives = 56/125 (44%)

Query:   242 LQSKPQDG---VSNNNEIQKKATMGLLQNKEN--NNTKD---SPSRQCSWDKSESPQRSS 293
             ++SK +D     +     +IQ+  TM ++++ E      +KD   SP  Q +  K     RSS
Sbjct:   314 IRSKVEDPAVIMRGTPQIQRVMTM-MIRDHEVLFPKSKDIPLSPPAQKNDPKKAPVARSS 372

Query:   294 MNNGSPTALSGSKTNSPKNSVHKLDVSRSPPLMVKKNPAFNKGSGIVTNGSFSSSNAEGL 353
             +   +   L  S+T+S  +     D +    P    + + AF + S   V           +
Sbjct:   373 VGWDATEDLRISRTDSFSSMTSDSDTTS--PTGQQPSDAFPEDSSKVPREKPGDWKMQSR 430

Query:   354 EKTQTTPN 361
             ++TQT PN
Sbjct:   431 KRTQTLPN 438
```

Pedant information for DKFZphfbr2_62b11, frame 1

Report for DKFZphfbr2_62b11.1

```
[LENGTH]        655
[MW]            73394.60
[pI]            8.13
[HOMOL]         SWISSPROT:Y053_HUMAN HYPOTHETICAL PROTEIN KIAA0053. 3e-71
[FUNCAT]        03.07 pheromone response, mating-type determination, sex-specific proteins
        [S. cerevisiae, YPL115c] 1e-16
[FUNCAT]        09.04 biogenesis of cytoskeleton      [S. cerevisiae, YPL115c] 1e-16
[FUNCAT]        03.04 budding, cell polarity and filament formation [S. cerevisiae, YPL115c]
1e-16
[FUNCAT]        10.02.09 regulation of g-protein activity    [S. cerevisiae, YPL115c] 1e-16
[FUNCAT]        03.22 cell cycle control and mitosis [S. cerevisiae, YER155c] 2e-16
[FUNCAT]        30.03 organization of cytoplasm      [S. cerevisiae, YER155c] 2e-16
[FUNCAT]        10.99 other signal-transduction activities   [S. cerevisiae, YDR379w] 4e-16
[FUNCAT]        03.10 sporulation and germination     [S. cerevisiae, YDL240w] 3e-15
[FUNCAT]        06.10 assembly of protein complexes   [S. cerevisiae, YOR134w] 2e-13
[FUNCAT]        30.04 organization of cytoskeleton    [S. cerevisiae, YOR134w] 2e-13
[SCOP]          d1rgp__ 1.83.1.1.1 p50 RhoGAP domain [human (Homo sapiens) 2e-46
[SCOP]          d1pbwa_ 1.83.1.1.2 p85 alpha subunit RhoGAP domain [human (Hom 6e-37
[PIRKW]         phosphotransferase 3e-13
[PIRKW]         breakpoint cluster region 2e-20
[PIRKW]         transmembrane protein 7e-14
[PIRKW]         brain 2e-20
[PIRKW]         alternative splicing 2e-20
[PIRKW]         P-loop 9e-19
[PIRKW]         cytoskeleton 1e-08
[SUPFAM]        CDC24 homology 7e-21
[SUPFAM]        bcr protein 7e-21
[SUPFAM]        myosin motor domain homology 9e-19
[SUPFAM]        pleckstrin repeat homology 2e-15
[SUPFAM]        LIM metal-binding repeat homology 9e-15
[SUPFAM]        protein kinase C zinc-binding repeat homology 5e-24
[PROSITE]       MYRISTYL        16
[PROSITE]       CAMP_PHOSPHO_SITE       3
[PROSITE]       CK2_PHOSPHO_SITE        15
[PROSITE]       TYR_PHOSPHO_SITE        2
[PROSITE]       PKC_PHOSPHO_SITE        11
[PROSITE]       ASN_GLYCOSYLATION       8
[KW]            Irregular
[KW]            3D
[KW]            LOW_COMPLEXITY     6.87 %
[KW]            COILED_COIL       12.06 %

SEQ     MPEDRNSGGCPAGALASTPFIPKTTYRRIKRCFSFRKGIFGQKLEDTVRYEKRYGNRLAP
SEG     ............................................................
COILS   ............................................................
1rgp-   ...........................................................C

SEQ     MLVEQCVDFIRQRGLKEEGLFRLPGQANLVKELQDAFDCGEKPSFDSNTDVHTVASLLKL
SEG     ............................................................
COILS   ............................................................
1rgp-   HHHHHHHHHHHHHHTTTTTTTTCCCHHHHHHHHHHHHHCCCCCGGGCCCCHHHHHHHHH

SEQ     YLRELPEPVIPYAKYEDFLSCAKLLSKEEEAGVKELAKQVKSLPVVNYNLLKYICRFLDE
SEG     ............................................................
```

```
COILS   ............................................................
1rgp-   HHHHTTTTTTTGGGHHHHHH---TTTTCGGGHHHHHHHHHHHHCCHHHHHHHHHHHHHHH

SEQ     VQSYSGVNKMSVQNLATVFGPNILRPKVEDPLTIMEGTVVVQQLMSVMISKHDCLFPKDA
SEG     ............................................................
COILS   ............................................................
1rgp-   HHHHHHHHCCCHHHHHHHHGGGCC....................................

SEQ     ELQSKPQDGVSNNNEIQKKATMGLLQNKENNNTKDSPSRQCSWDKSESPQRSSMNNGSPT
SEG     ............................................................
COILS   ............................................................
1rgp-   ............................................................

SEQ     ALSGSKTNSPKNSVHKLDVSRSPPLMVKKNPAFNKGSGIVTNGSFSSSNAEGLEKTQTTP
SEG     ............................................................
COILS   ............................................................
1rgp-   ............................................................

SEQ     NGSLQARRSSSLKVSGTKMGTHSVQNGTVRMGILNSDTLGNPTNVRNMSWLPNGYVTLRD
SEG     ............................................................
COILS   ............................................................
1rgp-   ............................................................

SEQ     NKQKEQAGELGQHNRLSTYDNVHQQFSMMNLDDKQSIDSATWSTSSCEISLPENSNSCRS
SEG     .....................................................xxxxxxx
COILS   ............................................................
1rgp-   ............................................................

SEQ     STTTCPEQDFFGGNFEDPVLDGPPQDDLSHPRDYESKSDHRSVGGRSSRATSSSDNSETF
SEG     xxxxx...................................xxxxxxxxxxxxxxxxx...
COILS   ............................................................
1rgp-   ............................................................

SEQ     VGNSSSNHSALHSLVSSLKQEMTKQKIEYESRIKSLEQRNLTLETEMMSLHDELDQERKK
SEG     ..xxxxxxxxxxxxxxxx..........................................
COILS   .................CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
1rgp-   ............................................................

SEQ     FTMIEIKMRNAERAKEDAEKRNDMLQKEMEQFFSTFGELTVEPRRTERGNTIWIQ
SEG     .......................................................
COILS   CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC....................
1rgp-   .......................................................
```

Prosite for DKFZphfbr2_62b11.1

PS00001	271->275	ASN_GLYCOSYLATION	PDOC00001
PS00001	342->346	ASN_GLYCOSYLATION	PDOC00001
PS00001	361->365	ASN_GLYCOSYLATION	PDOC00001
PS00001	386->390	ASN_GLYCOSYLATION	PDOC00001
PS00001	407->411	ASN_GLYCOSYLATION	PDOC00001
PS00001	543->547	ASN_GLYCOSYLATION	PDOC00001
PS00001	547->551	ASN_GLYCOSYLATION	PDOC00001
PS00001	580->584	ASN_GLYCOSYLATION	PDOC00001
PS00004	258->262	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	367->371	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	599->603	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	25->28	PKC_PHOSPHO_SITE	PDOC00005
PS00005	34->37	PKC_PHOSPHO_SITE	PDOC00005
PS00005	47->50	PKC_PHOSPHO_SITE	PDOC00005
PS00005	309->312	PKC_PHOSPHO_SITE	PDOC00005
PS00005	371->374	PKC_PHOSPHO_SITE	PDOC00005
PS00005	388->391	PKC_PHOSPHO_SITE	PDOC00005
PS00005	417->420	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	527->530	PKC_PHOSPHO_SITE	PDOC00005
PS00005	557->560	PKC_PHOSPHO_SITE	PDOC00005
PS00005	646->649	PKC_PHOSPHO_SITE	PDOC00005
PS00006	107->111	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	213->217	CK2_PHOSPHO_SITE	PDOC00006
PS00006	230->234	CK2_PHOSPHO_SITE	PDOC00006
PS00006	348->352	CK2_PHOSPHO_SITE	PDOC00006
PS00006	417->421	CK2_PHOSPHO_SITE	PDOC00006
PS00006	437->441	CK2_PHOSPHO_SITE	PDOC00006
PS00006	465->469	CK2_PHOSPHO_SITE	PDOC00006
PS00006	470->474	CK2_PHOSPHO_SITE	PDOC00006
PS00006	484->488	CK2_PHOSPHO_SITE	PDOC00006
PS00006	516->520	CK2_PHOSPHO_SITE	PDOC00006
PS00006	532->536	CK2_PHOSPHO_SITE	PDOC00006

PS00006	589->593	CK2_PHOSPHO_SITE	PDOC00006
PS00006	602->606	CK2_PHOSPHO_SITE	PDOC00006
PS00006	635->639	CK2_PHOSPHO_SITE	PDOC00006
PS00007	43->51	TYR_PHOSPHO_SITE	PDOC00007
PS00007	176->185	TYR_PHOSPHO_SITE	PDOC00007
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	13->19	MYRISTYL	PDOC00008
PS00008	249->255	MYRISTYL	PDOC00008
PS00008	263->269	MYRISTYL	PDOC00008
PS00008	297->303	MYRISTYL	PDOC00008
PS00008	304->310	MYRISTYL	PDOC00008
PS00008	338->344	MYRISTYL	PDOC00008
PS00008	343->349	MYRISTYL	PDOC00008
PS00008	352->358	MYRISTYL	PDOC00008
PS00008	362->368	MYRISTYL	PDOC00008
PS00008	376->382	MYRISTYL	PDOC00008
PS00008	392->398	MYRISTYL	PDOC00008
PS00008	400->406	MYRISTYL	PDOC00008
PS00008	524->530	MYRISTYL	PDOC00008
PS00008	542->548	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_62b11.1)

DKFZphfbr2_62f10
----

group: intracellular transport and trafficking

DKFZphfbr2_62f10 encodes a novel 320 amino acid protein with strong similarity to mammalian zinc transporter proteins.

The novel proteins is a membrane protein, which should be involved in the transport of Zinc across the cell membrane.

The Zn-T-transporters are membrane proteins that facilitates sequestration of zinc in endosomal vesicles. In the brain, ZnT-3 mRNA seems to be involved in the accumulation of zinc in synaptic vesicles. Zinc (Zn) is an essential element in normal development and metabolism. Recent studies show that in Alzheimer's disease, Zn functions as a double-edged sword, affording protection against Alzheimer's amyloid beta peptide (the major component of senile plaques) at low concentrations and enhancing toxicity at high concentrations by accelerated aggregation of the amyloid beta peptide.

The new protein can find application in modulation of Zinc transport in neuronal cells, thus providing means for a modulation of Alzheimer's amyloid beta peptide plaque formation.

strong similarity to zinc transporter proteins ;
membrane regions: 5
Summary DKFZphfbr2_62f10 encodes a novel 320 amino acid protein with
similarity to zinc transporter protein.
The new protein can find clinical application in modulating Zn2+
uptake.

strong similarity to zinc transporter proteins

complete cDNA, complete cds, few EST hits

Sequenced by LMU

Locus: unknown

Insert length: 5422 bp
Poly A stretch at pos. 5397, polyadenylation signal at pos. 5381

```
   1 GTCTAACTTT GGAAATATCA CCCTCATGCT GTCTTCCCAG GATGTCTCTC
  51 TCCCTAAGTA AGGGATGTTA CTTCCTGGAG GGAATGCAGT GTTGGGAATC
 101 TGAAGACCCA GCTTTGAGCT GAATTTGCTT TGTGATACCT GGAGAGAAGA
 151 CGTGTTTTCT TGACAACAGC ACAGTACCTA GTGAGTTCAA CAACAACGAC
 201 AACAACAGCC GCAGCTCATC CTGGCCGTCA TGGAGTTTCT TGAAAGAGCG
 251 TATCTTGTGA ATGATAAAGC TGCCAAGATG TATGCTTTCA CACTAGAAAG
 301 AAGGAGCTGC AAATGAACAC TTCATAGCAA TGTGGAACTC CAACAGAAAC
 351 CGGTGAATAA AGATCAGTGT CCCAGAGAGA GACCAGAGGA GCTGGAGTCA
 401 GGAGGCATGT ACCACTGCCA CAGTGGCTCC AAGCCCACAG AAAAGGGGGC
 451 GAATGAGTAC GCCTATGCCA AGTGGAAACT CTGTTCTGCT TCAGCAATAT
 501 GCTTCATTTT CATGATTGCA GAGGTCGTGG GTGGGCACAT TGCTGGGAGT
 551 CTTGCTGTTG TCACAGATGC TGCCCACCTC TTAATTGACC TGACCAGTTT
 601 CCTGCTCAGT CTCTTCTCCC TGTGGTTGTC ATCGAAGCCT CCCTCTAAGC
 651 GGCTGACATT TGGATGGCAC CGAGCAGAGA TCCTTGGTGC CCTGCTCTCC
 701 ATCCTGTGCA TCTGGGTGGT GACTGGCGTG CTAGTGTACC TGGCATGTGA
 751 GCGCCTGCTG TATCCTGATT ACCAGATCCA GGCGACTGTG ATGATCATCG
 801 TTTCCAGCTG CGCAGTGGCG GCCAACATTG TACTAACTGT GGTTTTGCAC
 851 CAGAGATGCC TTGGCCACAA TCACAAGGAA GTACAAGCCA ATGCCAGCGT
 901 CAGAGCTGCT TTTGTGCATG CCCCTGGAGA TCTATTTCAG AGTATCAGTG
 951 TGCTAATTAG TGCACTTATT ATCTACTTTA AGCCAGAGTA TAAAATAGCC
1001 GACCCAATCT GCACATTCAT CTTTTCCATC CTGGTCTTGG CCAGCACCAT
1051 CACTATCTTA AAGGACTTCT CCATCTTACT CATGGAAGGT GTGCCAAAGA
1101 GCCTGAATTA CAGTGGTGTG AAAGAGCTTA TTTTAGCAGT CGACGGGGTG
1151 CTGTCTGTGC ACTGCCTGCA CATCTGGTCT CTAACAATGA ATCAAGTAAT
1201 TCTCTCAGCT CATGTTGCTA CAGCAGCCAG CCGGGACAGC CAAGTGGTTC
1251 GGAGAGAAAT TGCTAAAGCC CTTAGCAAAA GCTTTACGAT GCACTCACTC
1301 ACCATTCAGA TGGAATCTCC AGTTGACCAG GACCCCGACT GCCTTTTCTG
1351 TGAAGACCCC TGTGACTAGC TCAGTCACAC CGTCAGTTTC CCAAATTTGA
1401 CAGGCCACCT TCAAACATGC TGCTATGCAA TTTCTGCATC ATAGAAAATA
1451 AGGAACCAAA GGAAGAAATT CATGTCATGG TGCAATGCAT ATTTTATCTA
1501 TTTATTTAGT TCCATTCACC ATGAAGGAAG AGGCACTGAG ATCCATCAAT
1551 CAATTGGATT ATATACTGAT CAGTAGCTGT GTTCAATTGC AGGAATGTGT
1601 ATATAGATTA TTCCTGAGTG GAGCCGAAGT AACAGCTGTT TGTAACTATC
1651 GGCAATACCA AATTCATCTC CCTTCCAATA ATGCATCTTG AGAACACATA
1701 GGTAAATTTG AACTCAGGAA AGTCTTACTA GAAATCAGTG GAAGGGACAA
1751 ATAGTCACAA AATTTACCA AAACATTAGA AACAAAAAAT AAGGAGAGCC
1801 AAGTCAGGAA TAAAAGTGAC TCTGTATGCT AACGCCACAT TAGAACTTGG
```

```
1851 TTCTCTCACC AAGCTGTAAT GTGATTTTTT TTTCTACTCT GAATTGGAAA
1901 TATGTATGAA TATACAGAGA AGTGCTTACA ACTAATTTTT ATTTACTTGT
1951 CACATTTTGG CAATAAATCC CTCTTATTTC TAAATTCTAA CTTGTTTATT
2001 TCAAAACTTT ATATAATCAC TGTTCAAAAG GAAATATTTT CACCTACCAG
2051 AGTGCTTAAA CACTGGCACC AGCCAAAGAA TGTGGTTGTA GAGACCCAGA
2101 AGTCTTCAAG AACAGCCGAC AAAAACATTC GAGTTGACCC CACCAAGTTG
2151 TTGCCACAGA TAATTTAGAT ATTTACCTGC AAGAAGGAAT AAAGCAGATG
2201 CAACCAATTC ATTCAGTCCA CGAGCATGAT GTGAGCACTG CTTTGTGCTA
2251 GACATTGGGC TTAGCACTGA AACTATAAAG AGGAATCAGA CGCAGCAAGT
2301 GCTTCTGTGT TCTGGTAGCA ACTCAACACT ATCTGTGGAG AGTAAACTGA
2351 AGATGTGCAG GCCAACATTC TGGAAATCCT ATGTCAGTGG GTTTGGTTTG
2401 GAACCTGGAC TTCTGCATTT TTAAAAGTTA CCCAGAGATG CTTCTAAAGA
2451 TGAGCCATAG TCTAGAAGAT TGTCAACCAC AGGAGTTCAT TGAGTGGGAC
2501 AGCTAGACAC ATACATTGGC AGTTACAATA GTATCATGAA TTGCAATGAT
2551 GTAGTGGGGT ATAAAAGGAA AGCGATGGAT ATTGCCGGAT GGGCATGGCC
2601 AGTGATGTTT CACGTCATTG AGGTGACAGC TCTGCTGGAC TTTGAATTAC
2651 ATATGGAGGC TCTCCAGGAA GACGAAGAAG AGAAGGACAT TCTAGGCAAA
2701 AAGAAGACTA GGCACAAGGC ACACTTATGT TTGTCTGTTA GCTTTTAGTT
2751 GAAAAAGCAA AATACATGAT GCAAAGAAAC CTCTCCACGC TGTGATTTTT
2801 AAAACTACAT ACTTTTTGCA ACTTTATGGT TATGAGTATT GTAGAGAACA
2851 GGAGATAGGT CTTAGATGAT TTTTATGTTG TTGTCAGACT CTAGCAAGGT
2901 ACTAGAAACC TAGCAGGCAT TAATAATTGT TGAGGCAATG ACTCTGAGGC
2951 TATATCTGGG CCTTGTCATT ATTTATCATT TATATTTGTA TTTTTTTCTG
3001 AAATTTGAGG GCCAAGAAAA CATTGACTTT GACTGAGGAG GTCACATCTG
3051 TGCCATCTCT GCAAATCAAT CAGCACCACT GAAATAACTA CTTAGCATTC
3101 TGCTGAGCTT TCCCTGCTCA GTAGAGACAA ATATACTCAT CCCCCACCTC
3151 AGTGAGCTTG TTTAGGCAAC CAGGATTAGA GCTGCTCAGG TTCCCAACGT
3201 CTCCTGCCAC ATCGGGTTCT CAAAATGGAA AGAATGGTTT ATGCCAAATC
3251 ACTTTTCCTG TCTGAAGGAC CACTGAATGG TTTTGTTTTT CCATATTTTG
3301 CATAGGACGC CCTAAAGACT AGGTGACTTG GCAAACACAC AAGTGTTAGT
3351 ATAATTCTTT GCTTCTGCTT CTTTTTGAAA ATCATGTTTA GATTTGATTT
3401 TAAGTCAGAA ATTCACTGAA TGTCAGGTAA TCATTATGGA GGGAGATTTG
3451 TGTGTCAACC AAAGTAATTG TCCCATGGCC CCAGGGTATT TCTGTTGTTT
3501 CCCTGAAATT CTGCTTTTTT AGTCAGCTAG ATTGAAAACT CTGAACAGTA
3551 GATGTTTATA TGGCAAAATG CAAGACAATC TATAAGGGAG ATTTTAAGGA
3601 TTTTGAGATG AAAAAACAGA TGCTACTCAG GGGCTTTATG GACCATCCAT
3651 CAATTCTGAA GTTCTGACTC TCCCATTACC CTTTCCCTGG TGTGGTCAGA
3701 ACTCCAGGTC ACTGGAAGTT AGTGGAATCA TGTAGTTGAA TTCTTTACTT
3751 CAAGACATTG TATTCTCTCC AGCTATCAAA ACATTAATGA TCTTTTATGT
3801 CTTTTTTTTG TTATTGTTAT ACTTTAAGTT CTGGGGTACA TGTGCGGAAC
3851 ATGTAGGTTT GTTACATAGG TATACATGTG CCATGGTGGT TTGCTGCACT
3901 CATCAACCTG TCATCTACAT TCTTTTATGT CTGTCTTTCA AAGCAACACT
3951 CTGTTCTTCT GAGTAGTGAA ATCAGGTCAA CTTTACCACC AGCCTCCATT
4001 TTTAATATGC TTCACCATCA TCCAGCACCT ACTTAAGATT TATCTAGGGC
4051 TCTGTGGTGA TGTTAGGACC CATAAAAGAA ATTTATGCCT TCCATATGTT
4101 TGGTTACAGA TGGGAAATGG GAATGTTGAA GGACATGAAA GAAAGGATGT
4151 TTACACATTA AGCATCAGTT CTGAAGCTAG ATTGTCTGAG TTTGAATCTT
4201 AGCTCTTCCC TTTATTAGCT CTGTGACCTC GAGCTAGTTA CTTAAATGCT
4251 CTGATCCTCT ATTTCCTGAT CAGTGAAACC TCCCTATTCA AATGTGTGAG
4301 AGTTTAATAA ATTAGGACAC TTAAAAATGT TGGAGCAGTG CATAGCATGT
4351 AGTGTTCAGT ACATGTTAAA TGTTGTTTTT TATTATGTAC AAACATGTGT
4401 GGGCACAGAA TTTTAAATCA TCTCAACTTT TGAGAAATTT TGAGTTATCA
4451 ACACCGTTCC CACAAGACAG TGGCAAAATT ATTGGTGAGA ATTAAACAGC
4501 TGTTTCTCAG AGGAAGCAAT GGAGGCTTGC TGGGATAAAG GCATTTACTG
4551 AGAGGCTGTT ACCTAGTGAG AGTGATGAAT TAATTAAAAT AGTCGAATCC
4601 CTTTCTGACT GTCTCTGAAA GCTTCCGCTT TTATCTTTGA AGAGCAGAAT
4651 TGTCACCCCA AGGACATTTA TTAATAAAAA GAACAACTGT CCAGTGCAAT
4701 GAAGGCAAAG TCATAGGTCT CCCAAGTCTT ACCCCATTCC TGTGAAATAT
4751 CAAGTTCTTG GCTTTTCTCT GTCATGTAGC CTCAACTTTC TCCGACCGGG
4801 TGCATTTCTT TCTCTGGTTT CTAAATTGCC AGTGGCAAAT TTGGATCACT
4851 TACTTAATAT CTGTTAAATT TTGTGACCCA ACAAAGTCTT TTAGCACTGT
4901 GGTGTCAAAA AGAAAAACAC CTCCCAGGCA TATACATTTT ATAGATTCCT
4951 GGAGAATGTT GCTCTCCAGC TCCATCCCCA CCCAATGAAA TATGATCCAG
5001 AGAGTCTTGC AAAGAGACAA GCCTCATTTT CCACAATTAG CTCTAAAGTG
5051 CCTCCAGGAA ATGATTTTCT CAGCTCATCT CTCTGTATTC CCTGTTTTGG
5101 ATCACAGGGC AATCTGTTTA AATGACTAAT TACAGAAATC ATTAAAGGCA
5151 CCAAGCAAAT GTCATCTCTG AATACACACA TCCCAAGCTT TACAAATCCT
5201 GCCTGGCTTG ACAGTGATGA GGCCACTTAA CAGTCCAGCG CAGGCGGATG
5251 TTAAAAAAAA TAAAAAGGTG ACCATCTGCG GTTTAGTTTT TTAACTTTCT
5301 GATTTCACAC TTAACGTCTG TCATTCTGTT ACTGGGCACC TGTTTAAATT
5351 CTATTTTAAA ATGTTAATGA GTGTTGTTTA AAATAAAATC AGGAAAGAGA
5401 GAAAAAAAAA AAAAAAAAAA AC
```

BLAST Results

No BLAST result

Medline entries

97121493:
ZnT-3, a putative transporter of zinc into synaptic vesicles.

96203098:
ZnT-2, a mammalian protein that confers resistance to zinc by facilitating vesicular sequestration.

Peptide information for frame 2

ORF from 407 bp to 1366 bp; peptide length: 320
Category: strong similarity to known protein

```
  1 MYHCHSGSKP TEKGANEYAY AKWKLCSASA ICFIFMIAEV VGGHIAGSLA
 51 VVTDAAHLLI DLTSFLLSLF SLWLSSKPPS KRLTFGWHRA EILGALLSIL
101 CIWVVTGVLV YLACERLLYP DYQIQATVMI IVSSCAVAAN IVLTVVLHQR
151 CLGHNHKEVQ ANASVRAAFV HAPGDLFQSI SVLISALIIY FKPEYKIADP
201 ICTFIFSILV LASTITILKD FSILLMEGVP KSLNYSGVKE LILAVDGVLS
251 VHCLHIWSLT MNQVILSAHV ATAASRDSQV VRREIAKALS KSFTMHSLTI
301 QMESPVDQDP DCLFCEDPCD
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62f10, frame 2

PIR:S70632 zinc transporter ZnT-2 - rat, N = 1, Score = 884, P = 1.5e-88

TREMBL:MMU76007_1 gene: "ZnT-3"; product: "ZnT-3"; Mus musculus zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds., N = 1, Score = 772, P = 1.1e-76

TREMBL:HSU76010_1 gene: "ZnT-3"; product: "ZnT-3"; Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds., N = 1, Score = 742, P = 1.6e-73

TREMBL:MMUZNT02_1 gene: "ZnT-3"; product: "zinc transporter"; Mus musculus zinc transporter (ZnT-3) gene, complete cds., N = 1, Score = 715, P = 1.2e-70

TREMBL:CET18D3_3 gene: "T18D3.3"; Caenorhabditis elegans cosmid T18D3, N = 1, Score = 699, P = 5.9e-69

```
>PIR:S70632 zinc transporter ZnT-2 - rat
           Length = 359

  HSPs:

 Score = 884 (132.6 bits), Expect = 1.5e-88, P = 1.5e-88
 Identities = 171/326 (52%), Positives = 230/326 (70%)

Query:     2 YHCHSGSKPTEKGANEYAYAKWKLCSASAICFIFMIAEVVGGHIAGSLAVVTDAAHLLID 61
             ++CH+          +E   A+ KL  ASAIC +FMI E++GG++A SLA++TDAAHLL D
Sbjct:    34 HYCHAQKDSGSHPNSEKQRARRKLYVASAICLVFMIGEIIGGYLAQSLAIMTDAAHLLTD 93

Query:    62 LTSFLLSLFSLWLSSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYPD 121
               S L+SLFSLW+SS+P +K + FGW RAEILGALLS+L IWVVTGVLVYLA +RL+  D
Sbjct:    94 FASMLISLFSLWVSSRPATKTMNFGWQRAEILGALLSVLSIWVVTGVLVYLAVQRLISGD 153

Query:   122 YQIQATVMIIVSSCAVAANIVLTVVLHQRCLGHNH-------KEVQANASVRAAFVHAPG 174
             Y+I+   M+I S CAVA NI++ + LHQ   GH+H         + Q N SVRAAF+H  G
Sbjct:   154 YEIKGDTMLITSGCAVAVNIIMGLALHQSGHGHSHGHSHEDSSQQQQNPSVRAAFIHVVG 213

Query:   175 DLFQSISVLISALIIYFKPEYKIADPICTFIFSILVLASTITILKDFSILLMEGVPKSLN 234
             DL QS+ VL++A IIYFKPEYK  DPICTF+FSILVL +T+TIL+D  ++LMEG PK ++
Sbjct:   214 DLLQSVGVLVAAYIIYFKPEYKYVDPICTFLFSILVLGTTLTILRDVILVLMEGTPKGVD 273

Query:   235 YSGVKELILAVDGVLSVHCLHIWSLTMNQVILSAHVATAASRDSQVVRREIAKALSKSFT 294
             ++ VK L+L+VDGV ++H LHIW+LT+ Q +LS H+A A + D+Q V +     L    F
Sbjct:   274 FTTVKNLLLSVDGVEALHSLHIWALTVAQPVLSVHIAIAQNVDAQAVLKVARDRLQGKFN 333
```

```
Query:   295 MHSLTIQMESPVDQDPDCLFCEDPCD 320
             H++TIQ+ES  +    C  C+ P +
Sbjct:   334 FHTMTIQIESYSEDMKSCQECQGPSE 359
```

Pedant information for DKFZphfbr2_62f10, frame 2

Report for DKFZphfbr2_62f10.2

```
[LENGTH]      320
[MW]          35053.51
[pI]          6.48
[HOMOL]       PIR:S70632 zinc transporter ZnT-2 - rat 3e-84
[FUNCAT]      30.02 organization of plasma membrane      [S. cerevisiae, YMR243c] 2e-16
[FUNCAT]      13.01 homeostasis of metal ions     [S. cerevisiae, YMR243c] 2e-16
[FUNCAT]      08.19 cellular import  [S. cerevisiae, YMR243c] 2e-16 ,
[FUNCAT]      11.07 detoxificaton    [S. cerevisiae, YMR243c] 2e-16
[FUNCAT]      07.04.01 metal ion transporters (cu, fe, etc.)      [S. cerevisiae, YMR243c]
2e-16
[FUNCAT]      08.04 mitochondrial transport        [S. cerevisiae, YOR316c] 3e-13
[FUNCAT]      30.16 mitochondrial organization     [S. cerevisiae, YOR316c] 3e-13
[FUNCAT]      99 unclassified proteins     [S. cerevisiae, YDR205w] 4e-07
[PIRKW]       transmembrane protein 2e-30
[PIRKW]       mitochondrial inner membrane 6e-12
[PIRKW]       mitochondrion 6e-12
[PIRKW]       membrane protein 1e-11
[SUPFAM]      zinc transporter ZnT-2 2e-30
[SUPFAM]      membrane protein czcD 1e-11
[PROSITE]     MYRISTYL       4
[PROSITE]     CAMP_PHOSPHO_SITE      1
[PROSITE]     CK2_PHOSPHO_SITE       1
[PROSITE]     PROKAR_LIPOPROTEIN     1
[PROSITE]     TYR_PHOSPHO_SITE       1
[PROSITE]     PKC_PHOSPHO_SITE       4
[PROSITE]     ASN_GLYCOSYLATION      2
[KW]          TRANSMEMBRANE  5
[KW]          LOW_COMPLEXITY     8.12 %
```

```
SEQ    MYHCHSGSKPTEKGANEYAYAKWKLCSASAICFIFMIAEVVGGHIAGSLAVVTDAAHLLI
SEG    .........................................................xxx
PRD    cccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhh
MEM    .......................MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ    DLTSFLLSLFSLWLSSKPPSKRLTFGWHRAEILGALLSILCIWVVTGVLVYLACERLLYP
SEG    xxxxxxxxxxxxxxxxxxxxxxx.....................................
PRD    hhhhhhhhhhhhhhhcccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhc
MEM    MMMMMMMMMMMM...........MMMMMMMMMMMMMMMMMMMMMMMMMMMMM.......

SEQ    DYQIQATVMIIVSSCAVAANIVLTVVLHQRCLGHNHKEVQANASVRAAFVHAPGDLFQSI
SEG    ............................................................
PRD    cccccccceeeehhhhhhhhhhhhhhhhhcccccccccccccchhhhhhhhhhhhhchhh
MEM    MMMMMMMMMMMMMMMMMMMMMMMMM...........MMMMMMMMMMMMMMMMMMMMM...

SEQ    SVLISALIIYFKPEYKIADPICTFIFSILVLASTITILKDFSILLMEGVPKSLNYSGVKE
SEG    ............................................................
PRD    hhhhhhhhhhccccceeeccchhhhhhhhhhhhhchhhhhhhhheeeeecccccccchhhhhh
MEM    ..MMMMMMMMMMMMMMMMMMM.......................................

SEQ    LILAVDGVLSVHCLHIWSLTMNQVILSAHVATAASRDSQVVRREIAKALSKSFTMHSLTI
SEG    ............................................................
PRD    hhhhhhceeeccccceeeeecccchhhhheeeeecccchhhhhhhhhhhhhhhhhccccee
MEM    ............................................................

SEQ    QMESPVDQDPDCLFCEDPCD
SEG    ....................
PRD    eeeccccccccccccccccc
MEM    ....................
```

Prosite for DKFZphfbr2_62f10.2

PS00001	162->166	ASN_GLYCOSYLATION	PDOC00001
PS00001	234->238	ASN_GLYCOSYLATION	PDOC00001
PS00004	81->85	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	11->14	PKC_PHOSPHO_SITE	PDOC00005
PS00005	75->78	PKC_PHOSPHO_SITE	PDOC00005

PS00005	80->83	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00007	13->21	TYR_PHOSPHO_SITE	PDOC00007
PS00008	7->13	MYRISTYL	PDOC00008
PS00008	42->48	MYRISTYL	PDOC00008
PS00008	94->100	MYRISTYL	PDOC00008
PS00008	228->234	MYRISTYL	PDOC00008
PS00013	125->136	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphfbr2_62f10.2)

DKFZphfbr2_62n10
----

group: brain derived

DKFZphfbr2_62n10 encodes a novel 541 amino acid protein with similarity to Plasmodium vivax reticulocyte-binding protein 1.

The novel protein contains one Leucine Zipper, involved in protein-protein-interaction. No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to reticulocyte-binding protein

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="13"

Insert length: 3522 bp
Poly A stretch at pos. 3503, polyadenylation signal at pos. 3479

```
   1 GGGGCGTGTT GGCGGGATTC TGAACGCTGC CATGGCTCAG ACCGTGTAGA
  51 ATGTTACATT GTCGCTCACT CTGCCCATCA CGTGCCACAT TTGCTTGGGG
 101 AAGGTACGTC AGCCTGTCAT ATGCATCAAC AACCATGTAT TTTGTTCGAT
 151 TTGTATTGAT TTGTGGTTGA AGAATAATAG CCAGTGTCCA GCTTGCAGAG
 201 TCCCCATCAC TCCTGAAAAT CCTTGCAAAG AAATTATAGG AGGAACAAGT
 251 GAAAGTGAAC CTATGCTAAG CCATACGGTC AGGAAGCATC TTCGGAAAAC
 301 TAGACTTGAA TTACTACACA AAGAATATGA GGACGAAATA GATTGTTTAC
 351 AGAAAGAAGT AGAAGAGCTT AAGAGTAAAA ATCTCAGCTT GGAGTCACAG
 401 ATCAAAGCTA TTCTGGATCC TTTAACCTTG GTGCAGGGCA ACCAAAATGA
 451 AGACAAACAT CTAGTCACAG ATAATCCAAG TATAATTAAC CCAGAAACTG
 501 TAGCAGAGTG GAAGAAAAAA CTCAGAACAG CTAATGAAAT CTATGAAAAA
 551 GTGAAAGATG ATGTGGATAA GCTAAAGGAG GCAAATAAAA AATTGAAATT
 601 GGAAAATGGT GGTCTGGTGA GGGAGAATTT ACGACTGAAG GCTGAAGTTG
 651 ATAACAGATC ACCTCAAAAG TTTGGAAGGT TTGCAGTTGC TGCTCTTCAG
 701 TCCAAAGTAG AACAGTATGA GCGTGAAACC AATCGCCTCA AGAAAGCCCT
 751 GGAACGAAGT GATAAGTATA TAGAGGAACT AGAATCTCAA GTTGCACAGC
 801 TAAAAAATTC AAGTGAAGAG AAAGAGGCTA TGAATTCCAT TTGCCAGACA
 851 GCACTTTCTG CAGATGGCAA AGGGAGCAAA GGCAGTGAGG AGGATGTGGT
 901 GTCAAAGAAT CAAGGCGATA GTGCCAGAAA GCAGCCTGGC TCATCCACCT
 951 CCAGTTCTTC TCACCTAGCG AAGCCTTCCA GCAGCAGACT GTGTGACACC
1001 AGTTCTGCAA GGCAGGAAAG TACCAGCAAA GCAGACCTTA ACTGTTCTAA
1051 GAACAAAGAC CTATATCAAG AACAGGTAGA AGTAATGTTA GATGTGACAG
1101 ATACAAGTAT GGATACTTAT TTGGAAAGAG AATGGGGGAA TAAACCAAGT
1151 GACTGTGTAC CCTACAAAGA TGAAGAACTT TATGATTTTC CAGCTCCTTG
1201 TACTCCTTTG TCCCTTAGTT GCCTTCAGCT CAGTACTCCA GAAAATAGAG
1251 AGAGCTCTGT GGTCCAAGCA GGAGGTTCCA AAAAGCACTC AAACCATCTC
1301 AGAAAATTGG TGTTTGATGA TTTTTGTGAT TCTTCAAATG TTTCTAATAA
1351 AGATTCTTCA GAAGATGATA TAAGTAGAAG TGAAAATGAG AAGAAATCAG
1401 AATGTTTTTC TTCCACAAAG ACAGGATTTT GGGACTGTTG TTCCACAAGC
1451 TATGCCCAAA ACTTAGATTT TGAAAGTTCA GAGGGGAACA CGATAGCAAA
1501 TTCTGTTGGA GAAATATCTT CAAAATTGAG TGAGAAATCA GGCTTATGTT
1551 TATCCAAAAG GTTGAATTCT ATTCGCTCTT TTGAAATGAA CCGGACAAGA
1601 ACATCCAGTG AAGCATCGAT GGATGCTGCT TACCTTGACA AAATCTCTGA
1651 GTTGGATTCA ATGATGTCAG AGTCAGACAA CAGCAAGAGC CCTTGTAATA
1701 ACGGTTTTAA GTCACTGGAT TTGGATGGGT TATCAAAGTC ATCTCAAGGC
1751 AGTGAATTTC TTGAGGAACC TGATAAGTTG GAAGAAAAAA CTGAGCTAAA
1801 CCTTTCCAAA GGTTCTCTAA CTAATGATCA GTTAGAAAAT GGAAGTGAAT
1851 GGAAACCCAC TTCTTTTTTT TCTCCTCTCT CCATCTGACC AAGAAATGAA
1901 TGAAGATTTT TCACTCCATT CCAGTTCTTG TCCAGTAACT AATGAAATCA
1951 AACCCCCAAG CTGCTTGTTT CAGACAGAGT TTTCCCAGGG CATTTTGTTA
2001 AGCAGTTCAC ATCGACTATT GGAAGATCAA AGATTTGGGT CATCTTTGTT
2051 TAAGATGTCC TCAGAGATGC ACAGTCTTCA TAACCACCTT CAGTCTCCTT
2101 GGTCTACTTC CTTTGTGCCT GAAAAGAGGA ATAAAAATGT GAATCAATCA
2151 ACAAAAAGAA AAATCCAGAG CAGCCTTTCC AGTGCCAGCC CATCAAAAGC
2201 AACTAAAAGT TGACTCATTA GAAAGGTGTC ATTTGTGGTT TTGTCCTGAG
2251 AGAAATAGAA AAGTTGTTAA AGTTACCTTT TTTCCTCATA AAAGTTCTAT
2301 ACAAATTGGA ATTGATAATC TTTAGTCAAG TATCAAGTCA GGATGGTGGA
2351 TTAACCTGTA CCCAGAATAC TTATTGTTCA TTTTGAAAAG ACTTTGTTCT
2401 TTTCATTTTT ATTTGGGAGT CTTTGTGACC AGAGAAGTTA GGGAGGAGGT
2451 TATTTTTGTG TTTTGGGGTT GGTTGGTTGG TTGGTTTTGT TTTTGGTTTT
2501 GTTTTTTTAC TGAATTTGAT ATGTATCTCG GTTGGATATA CATTGTTTTT
2551 TTAAAAAATG TTATTTAACT GTTAGATACA GTGGCCTGTT GATAAGCCCC
2601 ACTTGTCTTC AGAACTTGGA TTTCTTAAAT AAAACTTTTA GTGTTGTCTA
```

```
2651 TACACTGCTC AATAAGACAC TTGAGTTTAA GCTTTTCCCA GGGTGGAAAT
2701 TATTTTACCT GTCCCTTTTT ATTTATGTTT AGTGATGGCC TAGTTTTTCT
2751 GCAGGGCCAT GATGGAGAAA TAGCACTCTA GCCTTAGTCC AATATTGATT
2801 TACTTTCTTT TTTTAGGTTT TATGTATATG TTTGCATTTT TTAGCATTGT
2851 GTTTTGTCCA GTTTTGTGAA AATGTTCTGC TAGTATGAAA GAAAACATTT
2901 TCTATATGAA GACATTTGTT TTATGTTAGG TAGCTTACAT TTTCTCCTCT
2951 GCGTGTGTGT GTATGTGTGT AAAATCAGAA ATTTAGCATA CTATGGAAAG
3001 AAGGCATGGA GCACTTGGGT TTAGAGGAAC CTAAAACATC ATAGCTTCAT
3051 TGTTCCAGAT GTAACAGGTT TGAAAGAGCT CATCGCCAAG TTCTTGATCC
3101 ACTTGCATTC CAGGGGAGTT CTCTTTTGAG TAGTATGTTT CTTGTTTGCA
3151 TGTTCCTGTT CTTTGTGGAA ACTATGCATG GTAGCATTTT TGCTTGCTGT
3201 GTTTTCCATA CTTAAGAAAA AGAGGTTTCA GTTGGCTGAT AGAATATCTT
3251 TTATGTAGGA CAAAACTTTT CTGTGAAGAG TGTTGAGGGG GTGAAGATAG
3301 GTAAGAGGTA AGCACAATTT TTAATTTAGG CTCTGAAAAA GTGTATTGTT
3351 CTAAACGTAT TTGGTATGCC TATATAGGTC TTTAAAAATG GGTTTGTATG
3401 CTGTTTAATG TGCACTGAAC ATTTTACATT AATATTGTAC TGTTTTACAT
3451 TAATACTGCA TGCTTTTCTA TGTGAATTGA ATAAAGAATG TCATAAGCAC
3501 TGGAAAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry HS658254 from database EMBL:
human STS SHGC-11774.
Score = 1643, P = 8.0e-67, identities = 345/355

Entry HS513217 from database EMBL:
human STS SHGC-14656.
Score = 1193, P = 5.8e-46, identities = 241/244

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 263 bp to 1885 bp; peptide length: 541
Category: similarity to known protein

```
  1 MLSHTVRKHL RKTRLELLHK EYEDEIDCLQ KEVEELKSKN LSLESQIKAI
 51 LDPLTLVQGN QNEDKHLVTD NPSIINPETV AEWKKKLRTA NEIYEKVKDD
101 VDKLKEANKK LKLENGGLVR ENLRLKAEVD NRSPQKFGRF AVAALQSKVE
151 QYERETNRLK KALERSDKYI EELESQVAQL KNSSEEKEAM NSICQTALSA
201 DGKGSKGSEE DVVSKNQGDS ARKQPGSSTS SSSHLAKPSS SRLCDTSSAR
251 QESTSKADLN CSKNKDLYQE QVEVMLDVTD TSMDTYLERE WGNKPSDCVP
301 YKDEELYDFP APCTPLSLSC LQLSTPENRE SSVVQAGGSK KHSNHLRKLV
351 FDDFCDSSNV SNKDSSEDDI SRSENEKKSE CFSSTKTGFW DCCSTSYAQN
401 LDFESSEGNT IANSVGEISS KLSEKSGLCL SKRLNSIRSF EMNRTRTSSE
451 ASMDAAYLDK ISELDSMMSE SDNSKSPCNN GFKSLDLDGL SKSSQGSEFL
501 EEPDKLEEKT ELNLSKGSLT NDQLENGSEW KPTSFFSPLS I
```

BLASTP hits

Entry A42771 from database PIR:
reticulocyte-binding protein 1 - Plasmodium vivax
Score = 127, P = 3.7e-08, identities = 68/300, positives = 145/300

Entry RBP1_PLAVB from database SWISSPROT:
RETICULOCYTE BINDING PROTEIN 1 PRECURSOR.
Score = 127, P = 3.9e-08, identities = 68/300, positives = 145/300

Entry MMDSPPG_1 from database TREMBL:
gene: "DSPP"; product: "dentin sialophosphoprotein"; Mus musculus DSPP gene
Score = 160, P = 5.2e-08, identities = 87/373, positives = 146/373

Alert BLASTP hits for DKFZphfbr2_62n10, frame 2

No Alert BLASTP hits found

```
Pedant information for DKFZphfbr2_62n10, frame 2
------------------------------------------------

            Report for DKFZphfbr2_62n10.2

[LENGTH]       541
[MW]           60533.06
[pI]           5.10
[FUNCAT]       04.99 other transcription activities  [S. cerevisiae, YKR092c] 3e-05
[FUNCAT]       30.10 nuclear organization    [S. cerevisiae, YKR092c] 3e-05
[PROSITE]      LEUCINE_ZIPPER 1
[PROSITE]      MYRISTYL        7
[PROSITE]      CAMP_PHOSPHO_SITE      1
[PROSITE]      CK2_PHOSPHO_SITE       18
[PROSITE]      PROKAR_LIPOPROTEIN     1
[PROSITE]      TYR_PHOSPHO_SITE       1
[PROSITE]      PKC_PHOSPHO_SITE       14
[PROSITE]      ASN_GLYCOSYLATION      7
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY     9.24 %
[KW]           COILED_COIL       22.55 %

SEQ     MLSHTVRKHLRKTRLELLHKEYEDEIDCLQKEVEELKSKNLSLESQIKAILDPLTLVQGN
SEG     ............................................................
PRD     ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcchhhhhhhccccccccc
COILS   ........CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC........

SEQ     QNEDKHLVTDNPSIINPETVAEWKKKLRTANEIYEKVKDDVDKLKEANKKLKLENGGLVR
SEG     ...................................xxxxxxxxxxxxxxxxxxxx.....
PRD     cccceeeeeccccccchhhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhccccceee
COILS   .................CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....

SEQ     ENLRLKAEVDNRSPQKFGRFAVAALQSKVEQYERETNRLKKALERSDKYIEELESQVAQL
SEG     ............................................................
PRD     ehhhhhhhcccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   ..........................CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ     KNSSEEKEAMNSICQTALSADGKGSKGSEEDVVSKNQGDSARKQPGSSTSSSSHLAKPSS
SEG     ..............................................xxxxxxxxxxxxxx
PRD     hcchhhhhhhhhhhhhhhccccccccccceeeeecccccccccccccccccccccccccc
COILS   CCCCCC......................................................

SEQ     SRLCDTSSARQESTSKADLNCSKNKDLYQEQVEVMLDVTDTSMDTYLEREWGNKPSDCVP
SEG     x...........................................................
PRD     ccccccccccccccccccccccccchhhhhhhhhccccccccchhhhhhhhccccccccc
COILS   ............................................................

SEQ     YKDEELYDFPAPCTPLSLSCLQLSTPENRESSVVQAGGSKKHSNHLRKLVFDDFCDSSNV
SEG     ............................................................
PRD     cccccccccccccccccceeeeccccccceeeeecccccccccccccccccccccccccc
COILS   ............................................................

SEQ     SNKDSSEDDISRSENEKKSECFSSTKTGFWDCCSTSYAQNLDFESSEGNTIANSVGEISS
SEG     ............................................................
PRD     cccccccchhhhcccccccccccccccccccccccccccccccccccccccccccccccc
COILS   ............................................................

SEQ     KLSEKSGLCLSKRLNSIRSFEMNRTRTSSEASMDAAYLDKISELDSMMSESDNSKSPCNN
SEG     ............................................................
PRD     ccccccccchhhhccccccccccccchhhhhhhhhhhhhhhhhccccccccccccccccc
COILS   ............................................................

SEQ     GFKSLDLDGLSKSSQGSEFLEEPDKLEEKTELNLSKGSLTNDQLENGSEWKPTSFFSPLS
SEG     ..xxxxxxxxxxxxxxx...........................................
PRD     ccccccccccccccccceeeccchhhhhhhhhhccccccccccccccccccccccccccc
COILS   ............................................................

SEQ     I
SEG     .
PRD     c
COILS   .


            Prosite for DKFZphfbr2_62n10.2

PS00001      40->44    ASN_GLYCOSYLATION      PDOC00001
PS00001     182->186   ASN_GLYCOSYLATION      PDOC00001
PS00001     260->264   ASN_GLYCOSYLATION      PDOC00001
```

PS00001	359->363	ASN_GLYCOSYLATION	PDOC00001
PS00001	443->447	ASN_GLYCOSYLATION	PDOC00001
PS00001	513->517	ASN_GLYCOSYLATION	PDOC00001
PS00001	526->530	ASN_GLYCOSYLATION	PDOC00001
PS00004	340->344	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	5->8	PKC_PHOSPHO_SITE	PDOC00005
PS00005	156->159	PKC_PHOSPHO_SITE	PDOC00005
PS00005	166->169	PKC_PHOSPHO_SITE	PDOC00005
PS00005	220->223	PKC_PHOSPHO_SITE	PDOC00005
PS00005	240->243	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	254->257	PKC_PHOSPHO_SITE	PDOC00005
PS00005	339->342	PKC_PHOSPHO_SITE	PDOC00005
PS00005	361->364	PKC_PHOSPHO_SITE	PDOC00005
PS00005	384->387	PKC_PHOSPHO_SITE	PDOC00005
PS00005	419->422	PKC_PHOSPHO_SITE	PDOC00005
PS00005	423->426	PKC_PHOSPHO_SITE	PDOC00005
PS00005	431->434	PKC_PHOSPHO_SITE	PDOC00005
PS00005	436->439	PKC_PHOSPHO_SITE	PDOC00005
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	89->93	CK2_PHOSPHO_SITE	PDOC00006
PS00006	147->151	CK2_PHOSPHO_SITE	PDOC00006
PS00006	183->187	CK2_PHOSPHO_SITE	PDOC00006
PS00006	208->212	CK2_PHOSPHO_SITE	PDOC00006
PS00006	255->259	CK2_PHOSPHO_SITE	PDOC00006
PS00006	281->285	CK2_PHOSPHO_SITE	PDOC00006
PS00006	285->289	CK2_PHOSPHO_SITE	PDOC00006
PS00006	324->328	CK2_PHOSPHO_SITE	PDOC00006
PS00006	361->365	CK2_PHOSPHO_SITE	PDOC00006
PS00006	365->369	CK2_PHOSPHO_SITE	PDOC00006
PS00006	371->375	CK2_PHOSPHO_SITE	PDOC00006
PS00006	373->377	CK2_PHOSPHO_SITE	PDOC00006
PS00006	414->418	CK2_PHOSPHO_SITE	PDOC00006
PS00006	447->451	CK2_PHOSPHO_SITE	PDOC00006
PS00006	462->466	CK2_PHOSPHO_SITE	PDOC00006
PS00006	469->473	CK2_PHOSPHO_SITE	PDOC00006
PS00007	294->302	TYR_PHOSPHO_SITE	PDOC00007
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	226->232	MYRISTYL	PDOC00008
PS00008	292->298	MYRISTYL	PDOC00008
PS00008	408->414	MYRISTYL	PDOC00008
PS00008	427->433	MYRISTYL	PDOC00008
PS00008	489->495	MYRISTYL	PDOC00008
PS00008	517->523	MYRISTYL	PDOC00008
PS00013	310->321	PROKAR_LIPOPROTEIN	PDOC00013
PS00029	104->126	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2_62n10.2)

DKFZphfbr2_62o17
----

group: metabolism

DKFZphfbr2_62o17.2 encodes a novel 282 amino acid protein with weak similarity to the apolipoprotein E receptor.

The new protein contains a leucine zipper for protein-protein interaction, and three LDL-receptor class A domain (LDLRA_1) patterns. In LDL-receptors the class A domains form the binding site for LDL and calcium. The acidic residues between the fourth and sixth cysteines are important for high-affinity binding of positively charged sequences in LDLR's ligands.

The new protein can find application in modulation of cholesterol binding and transport by LDL-receptors and LDL-binding proteins

similarity to apolipoprotein E receptor

complete cDNA, complete cds, start at Bp 56 matches kozak consensus
ANCatg EST hits

Sequenced by LMU

Locus: unknown

Insert length: 1260 bp
Poly A stretch at pos. 1240, polyadenylation signal at pos. 1218

```
   1 GGGGGATAAG AGAGCGGTCT GGACAGCGCG TGGCCGGCGC CGCTGTGGGG
  51 ACAGCATGAG CGGCGGTTGG ATGGCGCAGG TTGGAGCGTG GCGAACAGGG
 101 GCTCTGGGCC TGGCGCTGCT GCTGCTGCTC GGCCTCGGAC TAGGCCTGGA
 151 GGCCGCCGCG AGCCCGCTTT CCACCCCGAC CTCTGCCCAG GCCGCAGGCC
 201 CCAGCTCAGG CTCGTGCCCA CCCACCAAGT TCCAGTGCCG CACCAGTGGC
 251 TTATGCGTGC CCCTCACCTG GCGCTGCGAC AGGGACTTGG ACTGCAGCGA
 301 TGGCAGCGAT GAGGAGGAGT GCAGGATTGA GCCATGTACC CAGAAAGGGC
 351 AATGCCCACC GCCCCCTGGC CTCCCCTGCC CCTGCACCGG CGTCAGTGAC
 401 TGCTCTGGGG GAACTGACAA GAAACTGCGC AACTGCAGCC GCCTGGCCTG
 451 CCTAGCAGGC GAGCTCCGTT GCACGCTGAG CGATGACTGC ATTCCACTCA
 501 CGTGGCGCTG CGACGGCCAC CCAGACTGTC CCGACTCCAG CGACGAGCTC
 551 GGCTGTGGAA CCAATGAGAT CCTCCCGGAA GGGGATGCCA CAACCATGGG
 601 GCCCCCTGTG ACCCTGGAGA GCGTCACCTC TCTCAGGAAT GCCACAACCA
 651 TGGGGCCCCC TGTGACCCTG GAGAGTGTCC CCTCTGTCGG GAATGCCACA
 701 TCCTCCTCTG CCGGAGACCA GTCTGGAAGC CCAACTGCCT ATGGGGTTAT
 751 TGCAGCTGCT GCGGTGCTCA GTGCAAGCCT GGTCACCGCC ACCCTCCTCC
 801 TTTTGTCCTG GCTCCGAGCC CAGGAGCGCC TCCGCCCACT GGGGTTACTG
 851 GTGGCCATGA AGGAGTCCCT GCTGCTGTCA GAACAGAAGA CCTCGCTGCC
 901 CTGAGGACAA GCACTTGCCA CCACCGTCAC TCAGCCCTGG GCGTAGCCGG
 951 ACAGGAGGAG AGCAGTGATG CGGATGGGTA CCCGGGCACA CCAGCCCTCA
1001 GAGACCTGAG CTCTTCTGGC CACGTGGAAC CTCGAACCCG AGCTCCTGCA
1051 GAAGTGGCCC TGGAGATTGA GGGTCCCTGG ACACTCCCTA TGGAGATCCG
1101 GGGAGCTAGG ATGGGGAACC TGCCACAGCC AGAACCGAGG GGCTGGCCCC
1151 AGGCAGCTCC CAGGGGGTAG GACGGCCCTG TGCTTAAGAC ACTCCTGCTG
1201 CCCCGTCTGA GGGTGGCGAT TAAAGTTGCT TCACATCCTC AAAAAAAAAA
1251 AAAAAAAAAC
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 56 bp to 901 bp; peptide length: 282
Category: similarity to known protein
Classification: unset
Prosite motifs: LDLRA_1 (67-90)
LDLRA_1 (67-90)
LDLRA_1 (145-168)

LEUCINE_ZIPPER (17-39)

```
  1 MSGGWMAQVG AWRTGALGLA LLLLLGLGLG LEAAASPLST PTSAQAAGPS
 51 SGSCPPTKFQ CRTSGLCVPL TWRCDRDLDC SDGSDEEECR IEPCTQKGQC
101 PPPPGLPCPC TGVSDCSGGT DKKLRNCSRL ACLAGELRCT LSDDCIPLTW
151 RCDGHPDCPD SSDELGCGTN EILPEGDATT MGPPVTLESV TSLRNATTMG
201 PPVTLESVPS VGNATSSSAG DQSGSPTAYG VIAAAAVLSA SLVTATLLLL
251 SWLRAQERLR PLGLLVAMKE SLLLSEQKTS LP
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_62o17, frame 2

TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial cds; and unknown gene., N = 1, Score = 733, P = 1.5e-72

PIR:JE0237 apolipoprotein E receptor 2 precursor - mouse, N = 2, Score = 290, P = 1.1e-26

TREMBL:HSZ75190_1 product: "apolipoprotein E receptor 2 906"; H.sapiens mRNA for apolipoprotein E receptor 2, N = 1, Score = 279, P = 1.8e-23

>TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial cds; and unknown gene.
Length = 260

HSPs:

Score = 733 (110.0 bits), Expect = 1.5e-72, P = 1.5e-72
Identities = 157/276 (56%), Positives = 178/276 (64%)

```
Query:    6 MAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSG 65
            MA+ GA R  ALGL L LL GL  GLEAA +P  T    Q +G  + SCP   FQC TSG
Sbjct:    1 MARGGAGRAVALGLVLRLLFGLRTGLEAAPAPAHT--RVQVSGSRADSCPTDTFQCLTSG 58

Query:   66 LCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKLR 125
             CVPL+WRCD D DCSDGSDEE+CRIE C Q GQC P   LPC C  +S CS  +DK L
Sbjct:   59 YCVPLSWRCDGDQDCSDGSDEEDCRIESCAQNGQCQPQSALPCSCDNISGCSDVSDKNL- 117

Query:  126 NCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPV 185
            NCSR  C   EL C L D CIP TWRCDGHPDC DSSDEL C T+
Sbjct:  118 NCSRPPCQESELHCILDDVCIPHTWRCDGHPDCLDSSDELSCDTD--------------T 163

Query:  186 TLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTA 245
             ++ +    NATT     T+E+  S  N T +SAGD S +P+AYGVIAAA VLSA LV+A
Sbjct:  164 EIDKIFQEENATTTRISTTMENETSFRNVTFTSAGDSSRNPSAYGVIAAAGVLSAILVSA 223

Query:  246 TLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSL 281
            TLL+L  LR Q  L P GLLVA+KESLLLSE+KTSL
Sbjct:  224 TLLILLRLRGQGYLPPPGLLVAVKESLLLSERKTSL 259
```

Pedant information for DKFZphfbr2_62o17, frame 2

Report for DKFZphfbr2_62o17.2

[LENGTH] 282
[MW] 28991.19
[pI] 4.61
[HOMOL] TREMBL:AF110520_6 product: "NG29"; Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial cds; and unknown gene. 5e-55
[BLOCKS] BL01209 LDL-receptor class A (LDLRA) domain proteins
[SCOP] d1ajj__ 7.11.1.1.1 Ligand-binding domain of low-density lipoprotei 2e-10

```
[PIRKW]         duplication 1e-19
[PIRKW]         tandem repeat 1e-15
[PIRKW]         heterodimer 6e-18
[PIRKW]         endocytosis 4e-18
[PIRKW]         heparan sulfate 2e-12
[PIRKW]         VLDL 1e-19
[PIRKW]         transmembrane protein 1e-19
[PIRKW]         coated pits 4e-18
[PIRKW]         fatty acid metabolism 1e-19
[PIRKW]         G protein-coupled receptor 1e-10
[PIRKW]         receptor 1e-19
[PIRKW]         glycoprotein 1e-19
[PIRKW]         lipid transport 4e-18
[PIRKW]         LDL 5e-14
[PIRKW]         calcium binding 6e-18
[PIRKW]         extracellular protein 6e-13
[PIRKW]         alternative splicing 1e-19
[PIRKW]         extracellular matrix 3e-10
[PIRKW]         chondroitin sulfate proteoglycan 2e-12
[PIRKW]         cholesterol 4e-18
[SUPFAM]        leucine-rich alpha-2-glycoprotein repeat homology 1e-10
[SUPFAM]        LDL receptor YWTD-containing repeat homology 1e-19
[SUPFAM]        trypsin homology 6e-13
[SUPFAM]        alpha-2-macroglobulin receptor 6e-18
[SUPFAM]        LDL receptor 1e-19
[SUPFAM]        LDL receptor ligand-binding repeat homology 1e-19
[SUPFAM]        EGF homology 1e-19
[PROSITE]       LDLRA_1 3
[PROSITE]       LEUCINE_ZIPPER 1
[PFAM]          Low-density lipoprotein receptor domain class A
[PFAM]          TNFR/NGFR cysteine-rich region
[KW]            SIGNAL_PEPTIDE 31
[KW]            TRANSMEMBRANE  1
[KW]            LOW_COMPLEXITY    22.34 %
```

```
SEQ  MSGGWMAQVGAWRTGALGLALLLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQ
SEG  ..............xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx............
PRD  cccccccccccchhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccceee
MEM  ............................................................

SEQ  CRTSGLCVPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGT
SEG  ......................................xxxxxxxxxxx..........
PRD  ecccccceeeeecccccccccccccccccccccccccccccccccccccccccccccccc
MEM  ............................................................

SEQ  DKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATT
SEG  ............................................................
PRD  cccccccccccccccccceeeccccccccccccccccccccccccccccccccccccccc
MEM  ............................................................

SEQ  MGPPVTLESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSA
SEG  ....................................................xxxxxxxx
PRD  ccccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhh
MEM  ...................................................MMMMMMM

SEQ  SLVTATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
SEG  xxxxxxxxxxx...............................
PRD  hhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhcccccc
MEM  MMMMMMMMMM................................
```

Prosite for DKFZphfbr2_62o17.2

PS01209	67->90	LDLRA_1	PDOC00929
PS01209	67->90	LDLRA_1	PDOC00929
PS01209	145->168	LDLRA_1	PDOC00929
PS00029	17->39	LEUCINE_ZIPPER	PDOC00029

Pfam for DKFZphfbr2_62o17.2

```
HMM_NAME      TNFR/NGFR cysteine-rich region

HMM              *CpeGtYtD.WNHvpqClpC.trCePEMGQYMvqPCTwTQNT.VC*
                  CP+  ++  +    + C+P   RC+    ++      +C + ++  +C
Query          54 CPPTKFQCRTS--GLCVPLTWRCDR--DL----DCSDGSDEEEC      89
```

```
HMM_NAME       Low-density lipoprotein receptor domain class A

HMM                *tTCeGPDEFQCgSGeMRCIPMsWvCDGDpDCeDWSDEWPeNChp*
                    C  P +FQC+++   C+P+ W+CD D DC D+SDE  E+C+
Query          52  GSCP-PTKFQCRTSG-LCVPLTWRCDRDLDCSDGSDE--EECRI    91

54.99 (bits) f: 130 t: 169 Target: dkfzphfbr2_62o17.2 similarity to apolipoprotein E
receptor
  Alignment to HMM consensus:
Query               *tTCeGPDEFQCgSGeMRCIPMsWvCDGDpDCeDWSDEWPeNChp*
                     C  + E +C  +    CIP+ W+CDG PDC D SDE  ++C+
  dkfzphfbr2   130  LACL-AGELRCTLSD-DCIPLTWRCDGHPDCPDSSDE--LGCGT    169
```

DKFZphfbr2_64a15
----

group: nucleic acid management

DKFZphfbr2_64a15 encodes a novel 255 amino acid protein with strong similarity to inorganic pyrophosphatases

Inorganic pyrophosphatase (EC 3.6.1.1) (PPase) is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed as the product of the many biosynthetic reactions that utilize ATP. All known PPases require the presence of divalent metal cations, with magnesium conferring the highest activity.

The new protein can find application as a new enzyme for biotechnologic processes.

strong similarity to inorganic pyrophosphatases

unspliced Intron 212-256 see EST HS1190948

Sequenced by Qiagen

Locus: unknown

Insert length: 1188 bp
Poly A stretch at pos. 1170, polyadenylation signal at pos. 1151

```
   1 GGGGGTTGGG GACCAGTGCA GGGACCGGGT CGCGCCGTGC TATGGCCCTG
  51 TACCACACTG AGGAGCGCGG CCAGCCCTGC TCGCAGAATT ACCGCCTCTT
 101 CTTTAAGAAT GTAACTGGTC ACTACATTTC CCCCTTTCAT GATATTCCTC
 151 TGAAGGTGAA CTCTAAAGAG GACACTGAGG CTCAAGGCAT TTTTATAGAC
 201 TTGTCTAAGA TCTGGAAAAT GGCATTCCTA TGAAGAAAGC ACGAAATGAT
 251 GAATATGAGA ATCTGTTTAA TATGATTGTA GAAATACCTC GGTGGACAAA
 301 GGCTAAAATG GAGATTGCCA CCAAGGAGCC AATGAATCCC ATTAAACAAT
 351 ATGTAAAGGA TGGAAAGCTA CGCTATGTGG CGAATATCTT CCCTTACAAG
 401 GGTTATATAT GGAATTATGG TACCCTCCCT CAGACTTGGG AAGATCCCCA
 451 TGAAAAAGAT AAGAGCACGA ACTGCTTTGG AGATAATGAT CCTATTGATG
 501 TTTGCGAAAT AGGCTCAAAG ATTCTTTCTT GTGGAGAAGT TATTCATGTG
 551 AAGATCCTTG GAATTTTGGC TCTTATTGAT GAAGGTGAAA CAGATTGGAA
 601 ATTAATTGCT ATCAATGCGA ATGATCCTGA AGCCTCAAAG TTTCATGATA
 651 TTGATGATGT TAAGAAGTTC AAACCGGGTT ACCTGGAAGC TACTCTTAAT
 701 TGGTTTAGAT TATGTAAGGT ACCAGATGGA AAACCAGAAA ACCAGTTTGC
 751 TTTTAATGGA GAATTCAAAA ACAAGGCTTT TGCTCTTGAA GTTATTAAAT
 801 CCACTCATCA ATGTTGGAAA GCATTGCTTA TGAAGAACTG TAATGGAGGA
 851 GCTACAAATT GCACAAACGT GCAGATATCT GATAGCCCTT TCCGTTGCAC
 901 TCAAGAGGAA GCAAGATCAT TAGTTGAATC GGTATCATCT TCACCAAATA
 951 AAGAAAGTAA TGAAGAAGAG CAAGTGTGGC ACTTCCTTGG CAAGTGATTG
1001 AAACATCTGA AATTCTGCTG TCAAGATTCC CATCTCTAAG GACTCCAAGA
1051 CTCTTTTTCC CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTTACTGA
1101 CTTCCTGTTA AAACTTCATT TTTTCAAACT TTTTGAGCTA TGCAATATAT
1151 AAATAAACAG TAAGAATTTT AAAAAAAAAA AAAAAAAA
```

BLAST Results

Entry HSPPASEMR from database EMBL:
H.sapiens partial mRNA for pyrophosphatase.
Score = 1706, P = 1.6e-70, identities = 342/343

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 230 bp to 994 bp; peptide length: 255
Category: strong similarity to known protein
Classification: unset
Prosite motifs: PPASE (85-92)

```
  1 MKKARNDEYE NLFNMIVEIP RWTKAKMEIA TKEPMNPIKQ YVKDGKLRYV
 51 ANIFPYKGYI WNYGTLPQTW EDPHEKDKST NCFGDNDPID VCEIGSKILS
101 CGEVIHVKIL GILALIDEGE TDWKLIAINA NDPEASKFHD IDDVKKFKPG
151 YLEATLNWFR LCKVPDGKPE NQFAFNGEFK NKAFALEVIK STHQCWKALL
201 MKNCNGGATN CTNVQISDSP FRCTQEEARS LVESVSSSPN KESNEEEQVW
251 HFLGK
```

BLASTP hits

Entry IPYR_KLULA from database SWISSPROT:
INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE).
Score = 689, P = 6.0e-68, identities = 128/248, positives = 170/248

Entry A45153 from database PIR:
inorganic pyrophosphatase (EC 3.6.1.1) - bovine
Score = 862, P = 2.8e-86, identities = 146/226, positives = 190/226

Entry AF085600_1 from database TREMBLNEW:
gene: "Nurf-38"; product: "inorganic pyrophosphatase NURF-38";
Drosophila melanogaster inorganic pyrophosphatase NURF-38 (Nurf-38) gene, complete cds.
Score = 731, P = 2.1e-72, identities = 134/248, positives = 177/248

Entry PWBY from database PIR:
inorganic pyrophosphatase (EC 3.6.1.1) - yeast (Saccharomyces cerevisiae)
Score = 688, P = 7.7e-68, identities = 133/251, positives = 174/251

Alert BLASTP hits for DKFZphfbr2_64a15, frame 2

SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE)., N = 1, Score = 731, P = 2.4e-72

```
>SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
     PHOSPHO- HYDROLASE) (PPASE).
            Length = 290

  HSPs:

 Score = 731 (109.7 bits), Expect = 2.4e-72, P = 2.4e-72
 Identities = 134/248 (54%), Positives = 177/248 (71%)

Query:     7 DEYENLFNMIVEIPRWTKAKMEIATKEPMNPIKQYVKDGKLRYVANIFPYKGYIWNYGTL 66
               +E + ++NM+VE+PRWT AKMEI+ K PMNPIKQ +K GKLR+VAN FP+KGYIWNYG L
Sbjct:    40 NEEKTIYNMVVEVPRWTNAKMEISLKTPMNPIKQDIKKGKLRFVANCFPHKGYIWNYGAL 99

Query:    67 PQTWEDPHEKDKSTNCFGDNDPIDVCEIGSKILSCGEVIHVKILGILALIDEGETDWKLI 126
             PQTWE+P    + ST C GDNDPIDV EIG ++   G+V+ VK+LG  ALIDEGETDWK+I
Sbjct:   100 PQTWENPDHIEPSTGCKGDNDPIDVIEIGYRVAKRGDVLKVKVLGQFALIDEGETDWKII 159

Query:   127 AINANDPEASKFHDIDDVKKFKPGYLEATLNWFRLCKVPDGKPENQFAFNGEFKNKAFAL 186
             AI+ NDP ASK +DI DV ++ PG L AT+ WF++ K+PDGKPENQFAFNG+ KN  FA
Sbjct:   160 AIDVNDPLASKVNDIADVDQYFPGLLRATVEWFKIYKIPDGKPENQFAFNGDAKNADFAN 219

Query:   187 EVIKSTHQCWKALLMKNCNGGATNCTNVQISDSPFRCTQEEARS-LVESVSSSPNKESNE 245
              +I  TH+ W+ L+ ++   G+ + TN+   +S    +EEA   L E+      +E ++
Sbjct:   220 TIIAETHKFWQNLVHQSPASGSISTTNITNRNSEHVIPKEEAEKILAEAPDGGQVEEVSD 279

Query:   246 EEQVWHFL 253
                 WHF+
Sbjct:   280 TVDTWHFI 287
```

Peptide information for frame 3

ORF from 42 bp to 230 bp; peptide length: 63
Category: strong similarity to known protein
Classification: unset

```
  1 MALYHTEERG QPCSQNYRLF FKNVTGHYIS PFHDIPLKVN SKEDTEAQGI
 51 FIDLSKIWKM AFL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64a15, frame 3

SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE)., N = 1, Score = 118, P = 8.8e-07

PIR:A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine, N = 1, Score = 113, P = 3.1e-06

TREMBLNEW:AF108211_1 product: "cytosolic inorganic pyrophosphatase"; Homo sapiens cytosolic inorganic pyrophosphatase mRNA, partial cds., N = 1, Score = 106, P = 1.8e-05

```
>SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
     PHOSPHO- HYDROLASE) (PPASE).
            Length = 290

  HSPs:

 Score = 118 (17.7 bits), Expect = 8.8e-07, P = 8.8e-07
 Identities = 23/43 (53%), Positives = 29/43 (67%)

Query:     1 MALYHTEERGQPCSQNYRLFFKNVTGHYISPFHDIPLKVNSKE 43
             MALY T E+G   S +Y L+FKN  G+ ISP HDIPL  N ++
Sbjct:     1 MALYETVEKGAKNSPSYSLYFKNKCGNVISPMHDIPLYANEEK 43
```

Pedant information for DKFZphfbr2_64a15, frame 2

Report for DKFZphfbr2_64a15.2

```
[LENGTH]       255
[MW]           29177.34
[pI]           5.67
[HOMOL]        TREMBLNEW:AF108211_1 product: "cytosolic inorganic pyrophosphatase"; Homo
sapiens cytosolic inorganic pyrophosphatase mRNA, partial cds. 2e-93
[FUNCAT]       01.04.01 phosphate utilization        [S. cerevisiae, YBR011c] 9e-73
[FUNCAT]       30.03 organization of cytoplasm       [S. cerevisiae, YBR011c] 9e-73
[FUNCAT]       02.99 other energy generation activities     [S. cerevisiae, YMR267w] 1e-58
[FUNCAT]       30.16 mitochondrial organization      [S. cerevisiae, YMR267w] 1e-58
[FUNCAT]       1 genome replication, transcription, recombination and repair      [M.
genitalium, MG351] 1e-06
[FUNCAT]       g carbohydrate metabolism and transport      [H. influenzae, HI0124] 2e-06
[BLOCKS]       BL00387D
[BLOCKS]       BL00387C
[BLOCKS]       BL00387B
[BLOCKS]       BL00387A
[SCOP]         d1wgja_ 2.29.5.1.1 Inorganic pyrophosphatase  [baker's yeas 1e-113
[EC]           3.6.1.1 Inorganic pyrophosphatase 7e-92
[PIRKW]        mitochondrion 3e-57
[PIRKW]        hydrolase 7e-92
[PIRKW]        homodimer 2e-71
[SUPFAM]       inorganic pyrophosphatase 7e-92
[PROSITE]      PPASE   1
[KW]           Alpha_Beta
[KW]           3D
[KW]           LOW_COMPLEXITY     6.27 %

SEQ    MKKARNDEYENLFNMIVEIPRWTKAKMEIATKEPMNPIKQYVKDGKLRYVANIFPYKGYI
SEG    ............................................................
1hukB  ......EGGGCEEEEEEEETTTbCBCEEETTTTTTTCEEECEETTEECBCCBBTTBTTbT

SEQ    WNYGTLPQTWEDPHEKDKSTNCFGDNDPIDVCEIGSKILSCGEVIHVKILGILALIDEGE
SEG    ............................................................
1hukB  CEEEETTTTCBTTTTEETTTTEECCCBCCEEEECCCCCCTTTEEEEEEEEEEEEETTTTB

SEQ    TDWKLIAINANDPEASKFHDIDDVKKFKPGYLEATLNWFRLCKVPDGKPENQFAFNGEFK
SEG    ............................................................
1hukB  CEEEEEEEETTTTTGGGCCCHHHHHHHTTTHHHHHHHHHHHCGGGCCCCCCBCGGGCCB

SEQ    NKAFALEVIKSTHQCWKALLMKNCNGGATNCTNVQISDSPFRCTQEEARSLVESVSSSPN
SEG    ...................................................xxxxxxxxx
1hukB  CHHHHHHHHHHHHHHHHHHHHCTTTTTTTCCCBTTTTTTT....................
```

```
SEQ     KESNEEEQVWHFLGK
SEG     xxxxxxx........
1hukB   ...............
```

Prosite for DKFZphfbr2_64a15.2

```
PS00387       85->92    PPASE                 PDOC00325
```

(No Pfam data available for DKFZphfbr2_64a15.2)

Pedant information for DKFZphfbr2_64a15, frame 3

Report for DKFZphfbr2_64a15.3

```
[LENGTH]        63
[MW]            7405.54
[pI]            6.81
[HOMOL]         SWISSPROT:IPYR_DROME INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE
PHOSPHO- HYDROLASE) (PPASE). 1e-06
[EC]            3.6.1.1 Inorganic pyrophosphatase 5e-06
[PIRKW]         hydrolase 5e-06
[SUPFAM]        inorganic pyrophosphatase 5e-06
[KW]            All_Beta
```

```
SEQ     MALYHTEERGQPCSQNYRLFFKNVTGHYISPFHDIPLKVNSKEDTEAQGIFIDLSKIWKM
PRD     cccccccccccccccceeeeeecccccccccccccccccccccccccccceeeechhhhhhh

SEQ     AFL
PRD     ccc
```

(No Prosite data available for DKFZphfbr2_64a15.3)

(No Pfam data available for DKFZphfbr2_64a15.3)

DKFZphfbr2_64c16
----

group: brain derived

DKFZphfbr2_64a16.2 encodes a novel 101 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: /map="745_A_2; 756_F_2; 842_C_2"

Insert length: 1866 bp
Poly A stretch at pos. 1848, polyadenylation signal at pos. 1829

```
   1 GGGCGCGGCG CCGGAGGAGG AAGTGGTGAG GTTGTTGCTC CTTCAGCGCC
  51 TATCGCTGGC TCTTGGGGCG CAGAGAGGGG CCGCAGTCTC CGCGGCTGCG
 101 TCGAGCTCCC TTGCAGTCCC CTCCATGTTC CCCGGCGCCA CTACTCCCCT
 151 TCCTAAGGCC GCCGCTTACC CCGGGGTCTA TGGAAGTAAT GGAAGGACCC
 201 CTCAACCTGG CTCATCAACA GAGCAGACGA GCAGACCGTT TATTAGCTGC
 251 AGGCAAATAC GAAGAGGCTA TTTCTTGTCA CAAAAAGGCT GCAGCATATC
 301 TTTCTGAAGC CATGAAGCTG ACACAGTCAG AGCAGGCTCA TCTTTCACTG
 351 GAATTGCAAA GGGATAGCCA TATGAAACAG CTCCTCCTCA TCCAAGAGAG
 401 ATGGAAAAGG GCCCAGCGTG AAGAAAGATT GAAAGCCCAG CAGAACACAG
 451 ACAAGGATGC AGCTGCCCAT CTTCAGACAT CTCACAAACC CTCTGCAGAG
 501 GATGCAGAGG GCCAGAGTCC CCTTTCTCAG AAGTACAGCC CTTCCACAGA
 551 GAAATGCCTG CCTGAGATTC AGGGGATCTT TGACAGGGAT CCAGACACAC
 601 TACTTTATTT ACTTCAGCAA AAGAGTGAGC CAGCAGAGCC ATGTATTGGA
 651 AGCAAAGCCC CAAAAGATGA TAAAACAATT ATAGAGGAGC AGGCAACCAA
 701 AATTGCAGAT TTGAAGAGGC ATGTGGAATT CCTTGTGGCT GAGAATGAAA
 751 GATTAAGGAA AGAAAATAAA CAACTAAAGG CTGAAAAGGC CAGACTTCTA
 801 AAAGGTCCAA TAGAAAAGGA GCTGGATGTA GATGCTGATT TTGTAGAAAC
 851 GTCAGAGTTA TGGAGCTTGC CACCACATGC AGAAACTGCT ACAGCCTCCT
 901 CAACCTGGCA GAAGTTCGCA GCAAATACTG GGAAAGCCAA GGACATTCCA
 951 ATCCCCAATC TTCCTCCCTT GGATTTTCCA TCTCCAGAAC TTCCTCTTAT
1001 GGAGCTCTCT GAGGATATTC TGAAAGGACT TATGAATAAT TAAAATGGAA
1051 GGCCACAGAA AAGGGGAAAA GAGGAAATAA TACAGTAATC GTTAATCCAG
1101 CAAAAAGAAA TGAAAAGGGA AAACCACATA GAAGGGTAAT CCCGGAAATG
1151 CTTCATCTGG TGGACTGTGG GAGCAGAGGC ATTGCCAGGA CTTGGGAAAC
1201 AGTCACTGTG AAATGCGCTG CGTATCTCAT TCACTCACTT CAGCTAATGA
1251 CTCCGACTTG GCAGACGCTA AACTCATGGA GGTTCGGTTT CTCCTGATAC
1301 AAACCAAATG GCTACCTGGA AGAATTTCTT TCAAGCAACA GTTATTTTTC
1351 TTATCTTCAG GGTTAAAATG TATAAAAGTT ATGTGTAATT AATCTATAAT
1401 GCCATAAATG ATAATGCAAA ACCTAAATAA TATGGTGGCC GGAGGGGCTG
1451 CCTTATATTT GAAACATGCT TTCTATCATG CATTGACTGT ATGCATTTTG
1501 TTAATGCACA TTCTGTTTGT TTAAGGTGTG TGAGATACAC ACCTTTCTAG
1551 ATGAAACTAT ATGTGCCACA CTTTGCACTA CTCATAATGA TAACCTCAAG
1601 ACTATCAGAA GAAATATTTA AATTTCCATT TTATGAAGAA AGGAACCAAA
1651 TTATTATGCT TTTTAAAACA AATTACCAGT TTACATAATT AATCAGGGTG
1701 CATTTTAAGT TCTAACTTCG TTTATTGTAT AATGCATCAT TTGAAAATAC
1751 CAAGGAGGAA ATACCCTTTG TTTTTAATGA TGCAAGAGTG GACGTAATGC
1801 TAGTTGGCAG TATTTTATTG TAAGAAATCA ATAAAGTAAT TGTGTTTTAA
1851 AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HS286143 from database EMBL:
human STS WI-6844.
Score = 1460, P = 3.4e-61, identities = 292/292

Medline entries

No Medline entry

Peptide information for frame 2

ORF from the beginning to 304 bp; peptide length: 102
Category: questionable ORF
Classification: unset

```
  1 GAAPEEEVVR LLLLQRLSLA LGAQRGAAVS AAASSSLAVP SMFPGATTPL
 51 PKAAAYPGVY GSNGRTPQPG SSTEQTSRPF ISCRQIRRGY FLSQKGCSIS
101 F
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64c16, frame 2

No Alert BLASTP hits found

Peptide information for frame 3

ORF from 180 bp to 1040 bp; peptide length: 287
Category: putative protein
Classification: unset
Prosite motifs: LEUCINE_ZIPPER (178-200)
LEUCINE_ZIPPER (185-207)

```
  1 MEVMEGPLNL AHQQSRRADR LLAAGKYEEA ISCHKKAAAY LSEAMKLTQS
 51 EQAHLSLELQ RDSHMKQLLL IQERWKRAQR EERLKAQQNT DKDAAAHLQT
101 SHKPSAEDAE GQSPLSQKYS PSTEKCLPEI QGIFDRDPDT LLYLLQQKSE
151 PAEPCIGSKA PKDDKTIIEE QATKIADLKR HVEFLVAENE RLRKENKQLK
201 AEKARLLKGP IEKELDVDAD FVETSELWSL PPHAETATAS STWQKFAANT
251 GKAKDIPIPN LPPLDFPSPE LPLMELSEDI LKGLMNN
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64c16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_64c16, frame 2

Report for DKFZphfbr2_64c16.2

```
[LENGTH]    101
[MW]        10469.94
[pI]        10.18
[KW]        All_Alpha
[KW]        LOW_COMPLEXITY    29.70 %

SEQ    GAAPEEEVVRLLLLQRLSLALGAQRGAAVSAAASSSLAVPSMFPGATTPLPKAAAYPGVY
SEG    .........xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.....................
PRD    ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccc

SEQ    GSNGRTPQPGSSTEQTSRPFISCRQIRRGYFLSQKGCSISF
SEG    .........................................
PRD    ccccccccccccccccccccchhhhhcccccccccccccccc
```

(No Prosite data available for DKFZphfbr2_64c16.2)

(No Pfam data available for DKFZphfbr2_64c16.2)

Pedant information for DKFZphfbr2_64c16, frame 3

Report for DKFZphfbr2_64c16.3

```
[LENGTH]        287
[MW]            32343.79
[pI]            5.61
[PROSITE]       LEUCINE_ZIPPER 2
[KW]            All_Alpha
[KW]            COILED_COIL       14.98 %

SEQ     MEVMEGPLNLAHQQSRRADRLLAAGKYEEAISCHKKAAAYLSEAMKLTQSEQAHLSLELQ
PRD     cccccchhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   ............................................................

SEQ     RDSHMKQLLLIQERWKRAQREERLKAQQNTDKDAAAHLQTSHKPSAEDAEGQSPLSQKYS
PRD     hhcchhhhhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhccccccccccccccccccc
COILS   ............................................................

SEQ     PSTEKCLPEIQGIFDRDPDTLLYLLQQKSEPAEPCIGSKAPKDDKTIIEEQATKIADLKR
PRD     cccccccchhhhhcccccchhhhhhhhhcccccccccccccccchhhhhhhhhhhhhhhh
COILS   ..............................................CCCCCCCCCCCCCC

SEQ     HVEFLVAENERLRKENKQLKAEKARLLKGPIEKELDVDADFVETSELWSLPPHAETATAS
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccccccccccccccc
COILS   CCCCCCCCCCCCCCCCCCCCCCCCCCCCC...............................

SEQ     STWQKFAANTGKAKDIPIPNLPPLDFPSPELPLMELSEDILKGLMNN
PRD     hhhhhhhhhcccccccccccccccccccccccchhhhhhhhhhhhhhccc
COILS   ...............................................
```

Prosite for DKFZphfbr2_64c16.3

```
PS00029     178->200    LEUCINE_ZIPPER          PDOC00029
PS00029     185->207    LEUCINE_ZIPPER          PDOC00029
```

(No Pfam data available for DKFZphfbr2_64c16.3)

DKFZphfbr2_64c4
----

group: brain derived

DKFZphfbr2_64c4 encodes a novel 467 amino acid protein with similarity to A. thaliana T08I13.5

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A. thaliana T08I13.5

complete cDNA, complete cds, EST hits
on genomic level encoded by AC005043 11 exons

Sequenced by Qiagen

Locus: unknown

Insert length: 1559 bp
Poly A stretch at pos. 1540, no polyadenylation signal found

```
   1 TGGGACCGCC GGAAGTTTCT GCCGCGGCTT TGCGGGGACG GGGGAGTGGT
  51 AGTGGGGGCT GCAGCTGCCG GACCCAGGCG CGATGGCTAC GGGCGCGGAT
 101 GTACGGGACA TTCTAGAACT CGGGGGTCCA GAAGGGGATG CAGCCTCTGG
 151 GACCATCAGC AAGAAGGACA TTATCAACCC GGACAAGAAA AAATCCAAGA
 201 AGTCCTCTGA GACACTGACT TTCAAGAGGC CCGAGGGCAT GCACCGGGAA
 251 GTCTATGCCT TGCTCTACTC TGACAAGAAG GATGCACCCC CACTGCTACC
 301 CAGTGACACT GGCCAGGGAT ACCGTACAGT GAAGGCCAAG TTGGGCTCCA
 351 AGAAGGTGCG GCCTTGGAAG TGGATGCCAT TCACCAACCC GGCCCGCAAG
 401 GACGGAGCAA TGTTCTTCCA CTGGCGACGT GCAGCGGAGG AGGGCAAGGA
 451 CTACCCCTTT GCCAGGTTCA ATAAGACTGT GCAGGAGCCT GTGTACTCGG
 501 AGCAGGAGTA CCAGCTTTAT CTCCACGATA ATGCTTGGAC TAAGGCAGAA
 551 ACTGACCACC TCTTTGACCT CAGCCGCCGC TTTGACCTGC GTTTTGTTGT
 601 TATCCATGAC CGGTATGACC ACCAGCAGTT CAAGAAGCGT TCTGTGGAAG
 651 ACCTGAAGGA GCGGTACTAC CACATCTGTG CTAAGCTTGC CAACGTGCGG
 701 GCTGTGCCAG GCACAGACCT TAAGATACCA GTATTTGATG CTGGGCACGA
 751 ACGACGGCGG AAGGAACAGC TTGAGCGTCT CTACAACCGG ACCCCAGAGC
 801 AGGTGGCAGA GGAGGAGTAC CTGCTACAGG AGCTGCGCAA GATTGAGGCC
 851 CGGAAGAAGG AGCGGGAGAA ACGCAGCCAG GACCTGCAGA AGCTGATCAC
 901 AGCGGCAGAC ACCACTGCAG AGCAGCGGCG CACGGAACGC AAGGCCCCCA
 951 AAAAGAAGCT ACCCCAGAAA AAGGAGGCTG AGAAGCCGGC TGTTCCTGAG
1001 ACTGCAGGCA TCAAGTTTCC AGACTTCAAG TCTGCAGGTG TCACGCTGCG
1051 GAGCCAACGG ATGAAGCTGC CAAGCTCTGT GGGACAGAAG AAGATCAAGG
1101 CCCTGGAACA GATGCTGCTG GAGCTTGGTG TGGAGCTGAG CCCGACACCT
1151 ACGGAGGAGC TGGTGCACAT GTTCAATGAG CTGCGAAGCG ACCTGGTGCT
1201 GCTCTACGAG CTCAAGCAGG CCTGTGCCAA CTGCGAGTAT GAGCTGCAGA
1251 TGCTGCGGCA CCGTCATGAG GCACTGGCCC GGGCTGGTGT GCTAGGGGGC
1301 CCTGCCACAC CAGCATCAGG CCCAGGCCCG GCCTCTGCTG AGCCGGCAGT
1351 GTCTGAACCC GGACTTGGTC CTGACCCCAA GGACACCATC ATTGATGTGG
1401 TGGGCGCACC CCTCACGCCC AATTCGAGAA AGCGACGGGA GTCGGCCTCC
1451 AGCTCATCTT CCGTGAAGAA AGCCAAGAAG CCGTGAGAGG CCCCACGGGG
1501 TGTGGGCGAC GCTGTTATGT AAATAGAGCT GCTGAGTTGG AAAAAAAAAA
1551 AAAAAAAAA
```

BLAST Results

Entry AC005043 from database EMBL:
Homo sapiens clone NH0576N21; HTGS phase 1, 5 unordered pieces.
Score = 1506, P = 4.6e-244, identities = 316/330

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 83 bp to 1483 bp; peptide length: 467

Category: similarity to unknown protein

```
  1 MATGADVRDI LELGGPEGDA ASGTISKKDI INPDKKKSKK SSETLTFKRP
 51 EGMHREVYAL LYSDKKDAPP LLPSDTGQGY RTVKAKLGSK KVRPWKWMPF
101 TNPARKDGAM FFHWRRAAEE GKDYPFARFN KTVQEPVYSE QEYQLYLHDN
151 AWTKAETDHL FDLSRRFDLR FVVIHDRYDH QQFKKRSVED LKERYYHICA
201 KLANVRAVPG TDLKIPVFDA GHERRRKEQL ERLYNRTPEQ VAEEEYLLQE
251 LRKIEARKKE REKRSQDLQK LITAADTTAE QRRTERKAPK KKLPQKKEAE
301 KPAVPETAGI KFPDFKSAGV TLRSQRMKLP SSVGQKKIKA LEQMLLELGV
351 ELSPTPTEEL VHMFNELRSD LVLLYELKQA CANCEYELQM LRHRHEALAR
401 AGVLGGPATP ASGPGPASAE PAVSEPGLGP DPKDTIIDVV GAPLTPNSRK
451 RRESASSSSS VKKAKKP
```

BLASTP hits

Entry ATAC2337_5 from database TREMBLNEW:
gene: "T08I13.5"; Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence.
Score = 340, P = 2.6e-30, identities = 115/374, positives = 176/374

Entry YE8D_SCHPO from database SWISSPROT:
HYPOTHETICAL 47.1 KD PROTEIN C9G1.13C IN CHROMOSOME I.
Score = 221, P = 1.9e-20, identities = 67/192, positives = 97/192

Entry S64291 from database PIR:
hypothetical protein YGR002c - yeast (Saccharomyces cerevisiae)
Score = 202, P = 2.8e-13, identities = 71/260, positives = 124/260

Alert BLASTP hits for DKFZphfbr2_64c4, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_64c4, frame 2

Report for DKFZphfbr2_64c4.2

```
[LENGTH]        467
[MW]            53007.60
[pI]            9.51
[HOMOL]         TREMBL:ATAC2337_5 gene: "T08I13.5"; Arabidopsis thaliana chromosome II BAC
T08I13 genomic sequence, complete sequence. 4e-29
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YGR002c] 1e-19
[PROSITE]       MYRISTYL          1
[PROSITE]       CAMP_PHOSPHO_SITE      4
[PROSITE]       CK2_PHOSPHO_SITE       10
[PROSITE]       TYR_PHOSPHO_SITE       3
[PROSITE]       GLYCOSAMINOGLYCAN      1
[PROSITE]       PKC_PHOSPHO_SITE       12
[PROSITE]       ASN_GLYCOSYLATION      1
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY    20.13 %

SEQ     MATGADVRDILELGGPEGDAASGTISKKDIINPDKKKSKKSSETLTFKRPEGMHREVYAL
SEG     ......................xxxxxxxxxxxxxxxxxx..................
PRD     ccceeeeeeeeeeccccccccccccccccccccccccccccccccccccccchhhhhhhh

SEQ     LYSDKKDAPPLLPSDTGQGYRTVKAKLGSKKVRPWKWMPFTNPARKDGAMFFHWRRAAEE
SEG     ............................................................
PRD     hhhhccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhc

SEQ     GKDYPFARFNKTVQEPVYSEQEYQLYLHDNAWTKAETDHLFDLSRRFDLRFVVIHDRYDH
SEG     ............................................................
PRD     cccccccccccccccchhhhhhhhhhhcchhhhhhhhhhhhhhhhccceeeeeeecccc

SEQ     QQFKKRSVEDLKERYYHICAKLANVRAVPGTDLKIPVFDAGHERRRKEQLERLYNRTPEQ
SEG     ............................................................
PRD     chhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccchhhhhhhhhhhhhhhhcchhh

SEQ     VAEEEYLLQELRKIEARKKEREKRSQDLQKLITAADTTAEQRRTERKAPKKKLPQKKEAE
SEG     .........xxxxxxxxxxxxxxx...................xxxxxxxxxxxxxxxx
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhh

SEQ     KPAVPETAGIKFPDFKSAGVTLRSQRMKLPSSVGQKKIKALEQMLLELGVELSPTPTEEL
SEG     xxx.........................................................
```

```
PRD     hcccccccccccccccccceeehhhhhhhccccccchhhhhhhhhhhhhhhhcccccchhh

SEQ     VHMFNELRSDLVLLYELKQACANCEYELQMLRHRHEALARAGVLGGPATPASGPGPASAE
SEG     ............................................xxxxxxxxxxxxxxxx
PRD     hhhhhhcccchhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhcccccccccccccccccc

SEQ     PAVSEPGLGPDPKDTIIDVVGAPLTPNSRKRRESASSSSSVKKAKKP
SEG     xxxxxxx...................xxxxxxxxxxxxxxxxxxx.
PRD     ccccccccccccceeeeecccccccccccccccccccccceeecccc
```

Prosite for DKFZphfbr2_64c4.2

PS00001	130->134	ASN_GLYCOSYLATION	PDOC00001
PS00002	412->416	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	35->39	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	39->43	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	184->188	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	451->455	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	46->49	PKC_PHOSPHO_SITE	PDOC00005
PS00005	63->66	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00005	284->287	PKC_PHOSPHO_SITE	PDOC00005
PS00005	321->324	PKC_PHOSPHO_SITE	PDOC00005
PS00005	324->327	PKC_PHOSPHO_SITE	PDOC00005
PS00005	448->451	PKC_PHOSPHO_SITE	PDOC00005
PS00005	460->463	PKC_PHOSPHO_SITE	PDOC00005
PS00006	3->7	CK2_PHOSPHO_SITE	PDOC00006
PS00006	26->30	CK2_PHOSPHO_SITE	PDOC00006
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	139->143	CK2_PHOSPHO_SITE	PDOC00006
PS00006	153->157	CK2_PHOSPHO_SITE	PDOC00006
PS00006	187->191	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	355->359	CK2_PHOSPHO_SITE	PDOC00006
PS00006	435->439	CK2_PHOSPHO_SITE	PDOC00006
PS00007	131->139	TYR_PHOSPHO_SITE	PDOC00007
PS00007	227->235	TYR_PHOSPHO_SITE	PDOC00007
PS00007	116->125	TYR_PHOSPHO_SITE	PDOC00007
PS00008	14->20	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_64c4.2)

DKFZphfbr2_64h6
----

group: brain derived

DKFZphfbr2_64h6 encodes a novel 176 amino acid protein with similarity to predicted yeast proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to S.pombe SPBC337.09 and S.cerevisiae YER044c

complete cDNA, complete cds accoring to YER044c/SPBC337.09, start at Bp 111, EST hits

Sequenced by Qiagen

Locus: /map="14"

Insert length: 1212 bp
Poly A stretch at pos. 1192, polyadenylation signal at pos. 1168

```
   1 GGGCTGGAGC TGTCCTGGGG GAGCTTGTTT GCGGCAGCGG CTGCTGCTGC
  51 CACTGCTGTG CTGGGGGCCC GGTCGCCAGG CAAAAAGCCC TCCCACGTTT
 101 GAGGGGAGTC ATGAGCCGTT TCCTGAATGT GTTAAGAAGT TGGCTGGTTA
 151 TGGTGTCCAT CATAGCCATG GGGAACACGC TGCAGAGCTT CCGAGACCAC
 201 ACTTTTCTCT ATGAAAAGCT CTACACTGGC AAGCCAAACC TTGTGAATGG
 251 CCTCCAAGCT CGGACCTTTG GGATCTGGAC GCTGCTCTCA TCAGTGATCC
 301 GCTGCCTCTG TGCCATTGAC ATTCACAACA AGACGCTCTA TCACATCACA
 351 CTCTGGACCT TCCTCCTTGC CCTGGGGCAT TTCCTCTCTG AGTTGTTTGT
 401 CTATGGAACT GCAGCTCCCA CGATTGGCGT CCTGGCACCC CTGATGGTGG
 451 CAAGTTTCTC CATCCTGGGT ATGCTGGTCG GGCTCCGGTA TCTAGAAGTA
 501 GAACCAGTAT CCAGACAGAA GAAGAGAAAC TGAGGCCAGC ATTATCACCT
 551 CCAGGACTTT CTCGTTTTCC ACCTTGGCCA TCTTCTTCCT TCGTCGTCTC
 601 TCCCCTTTAA TTTCTTTTCT ATTCCATCAT CTGCCCTTTT ACTCACTTTT
 651 AGCCTCTTTT TTTAATTTTT AAAATTTAAA GATATGCATA CTGAAAAGTA
 701 TATAACATGT ACGTACAATT TAAAGAATAA TTTTAAAGTG AATACTACGT
 751 AACTCCATCC AAGTCAAGAA ATTGCCAGCT TCTCGGAAGC CCACTGTGTC
 801 TCCTTCCCCT ACCTGCAACC TCTTCCAGGC TCCCTTTTCC AGCCTTCCCC
 851 TTTTTCCCTT TTATTTTCAT GCCTTGATTT GACTTGTGTG GTGGGAACAT
 901 GTGAACTATG AAACTTAAAC CTGCTGCCCA CCCAGAGCAG CTGTGACCAA
 951 GGGCTGCCTC AAGGGGTTGT CCACGCAGGT TGGGCTCCTC TCTGCTGCTG
1001 GACCCAAGAC TCTGAACCTT CCAAGGGACA GGCAGTTCTT CTGAGAAGGG
1051 CTCCCCTGTG TGTGAGCAAG ACCACAGCTC TCCTTCTATC TACAGATGCA
1101 TGAGGGTTGG AAGAGTCTGG GCTGTTTTTA GACCTTCTGG TCAGCTGTAT
1151 TTGTGTAACA ACTTTTGTAA TAAATAGAAA AACCCTCTGC TCAAAAAAAA
1201 AAAAAAAAAA AA
```

BLAST Results

Entry G38566 from database EMBL:
SHGC-64295 Human Homo sapiens STS genomic, sequence tagged site.
Score = 1398, P = 1.4e-56, identities = 284/288

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 0 bp to 530 bp; peptide length: 177
Category: similarity to unknown protein
Classification: unclassified

```
   1 AGAVLGELVC GSGCCCHCCA GGPVARQKAL PRLRGVMSRF LNVLRSWLVM
  51 VSIIAMGNTL QSFRDHTFLY EKLYTGKPNL VNGLQARTFG IWTLLSSVIR
 101 CLCAIDIHNK TLYHITLWTF LLALGHFLSE LFVYGTAAPT IGVLAPLMVA
```

```
151 SFSILGMLVG LRYLEVEPVS RQKKRN
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64h6, frame 3

TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical protein"; S.pombe chromosome II cosmid c337., N = 1, Score = 224, P = 1.4e-18

PIR:S50547 hypothetical protein YER044c - yeast (Saccharomyces cerevisiae), N = 1, Score = 192, P = 3.4e-15

```
>TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical
     protein"; S.pombe chromosome II cosmid c337.
            Length = 136

  HSPs:

 Score = 224 (33.6 bits), Expect = 1.4e-18, P = 1.4e-18
 Identities = 49/113 (43%), Positives = 74/113 (65%)

Query:    42 NVLRSWLVMVSIIAMGNTLQSFRDHTFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRC 101
             +++  W V+VS+ A+ NT+QSF      L +++Y+    N VNGLQ RTFGIWTLLS+++R
Sbjct:    11 SLVAKWNVVVSVAALFNTVQSFLTPK-LTKRVYSNT-NEVNGLQGRTFGIWTLLSAIVRF 68

Query:   102 LCAIDIHNKTLYHITLWTFLLALGHFLSELFVYGTAAPTIGVLAPLMVASFSI 154
              CA  I N  +Y +   T+ LA  HFLSE  ++ T     G+L+P++V++ SI
Sbjct:    69 YCAYHITNPDVYFLCQCTYYLACFHFLSEWLLFRTTNLGPGLLSPIVVSTVSI 121
```

Pedant information for DKFZphfbr2_64h6, frame 3

Report for DKFZphfbr2_64h6.3

```
[LENGTH]        176
[MW]            19359.31
[pI]            9.53
[HOMOL]         TREMBL:SPBC337_9 gene: "SPBC337.09"; product: "conserved hypothetical protein";
S.pombe chromosome II cosmid c337. 2e-17
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YER044c] 7e-16
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY      7.39 %

SEQ     AGAVLGELVCGSGCCCHCCAGGPVARQKALPRLRGVMSRFLNVLRSWLVMVSIIAMGNTL
SEG     .........xxxxxxxxxxxx.......................................
PRD     ccceeeeeeeeccceeeecccccccccccccccccchhhhhhhhhhhhhheeeeccccccc
MEM     .......................................MMMMMMMMMMMMMMMMM....

SEQ     QSFRDHTFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRCLCAIDIHNKTLYHITLWTF
SEG     ............................................................
PRD     cccccchhhhhhhhhccccccccccccccchhhhhhhhhhhhhhhcccccceeeehhhhh
MEM     ............................................................

SEQ     LLALGHFLSELFVYGTAAPTIGVLAPLMVASFSILGMLVGLRYLEVEPVSRQKKRN
SEG     ........................................................
PRD     hhhhhhhhhhhhhhhhcccccccccccceeehhhhhhhhhhhhheeeeeeccccccccccc
MEM     ......................MMMMMMMMMMMMMMMMMM.................
```

(No Prosite data available for DKFZphfbr2_64h6.3)

(No Pfam data available for DKFZphfbr2_64h6.3)

DKFZphfbr2_64j18
----

group: Intracellular transport and trafficking

DKFZphfbr2_624j18.1 encodes a novel 180 amino acid protein nearly identical to the microsomal signal peptidase 23 kd subunit of canis familiaris, gallus gallus and C. elegans.

The new protein is identical to canine and chicken microsomal signal peptidase 23 kd subunit. The canine microsomal signal peptidase is a protein complex comprised of five subunits (25, 22/23, 21, 18, and 12 kDa). The 23kDa subunit is tightly associated with the 18- and 21-kDa subunits, that are integral membrane proteins.

The new protein can find application in modulation of protein transport into microsomal compartments and as a tool for proteomic analysis.

strong similarity to dog signal peptidase (EC 3.4.99.-)

complete cDNA, complete cds, potential start at Bp 109, EST hits,

Sequenced by Qiagen

Locus: unknown

Insert length: 690 bp
Poly A stretch at pos. 666, polyadenylation signal at pos. 646

```
  1 GCCGGAACGC GCGCACCGCA GACGGCGCGG ATCGCAGGGA GCCGGTCCGC
 51 CGCCGGAACG GGAGCCTGGG TGTGCGTGTG GAGTCCGGAC TCGTGGGAGA
101 CGATCGCGAT GAACACGGTG CTGTCGCGGG CGAACTCACT GTTCGCCTTC
151 TCGCTGAGCG TGATGGCGGC GCTCACCTTC GGCTGCTTCA TCACCACCGC
201 CTTCAAAGAC AGGAGCGTCC CGGTGCGGCT GCACGTCTCG CGGATCATGC
251 TAAAAAATGT AGAAGATTTC ACTGGACCTA GAGAAAGAAG TGATCTGGGA
301 TTTATCACAT CTGATATAAC TGCTGATCTA GAGAATATAT TTGATTGGAA
351 TGTTAAGCAG TTGTTTCTTT ATTTATCAGC AGAATATTCA ACAAAAAATA
401 ATGCTCTGAA CCAAGTTGTC CTATGGGACA AGATTGTTTT GAGAGGTGAT
451 AATCCGAAGC TGCTGCTGAA AGATATGAAA ACAAAATATT TTTTCTTTGA
501 CGATGGAAAT GGTCTCAAGG GAAACAGGAA TGTCACTTTG ACCCTGTCTT
551 GGAACGTCGT ACCAAATGCT GGAATTCTAC CTCTTGTGAC AGGATCAGGA
601 CACGTATCTG TCCCATTTCC AGATACATAT GAAATAACGA AGAGTTATTA
651 AATTATTCTG AATTTGAAAC AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

89034208:
cDNA-derived primary structure of the glycoprotein component of canine microsomal
signal peptidase complex.

Peptide information for frame 1

ORF from 109 bp to 648 bp; peptide length: 180
Category: strong similarity to known protein
Prosite motifs: TONB_DEPENDENT_REC_1 (1-58)
RGD (148-151)

```
  1 MNTVLSRANS LFAFSLSVMA ALTFGCFITT AFKDRSVPVR LHVSRIMLKN
 51 VEDFTGPRER SDLGFITSDI TADLENIFDW NVKQLFLYLS AEYSTKNNAL
101 NQVVLWDKIV LRGDNPKLLL KDMKTKYFFF DDGNGLKGNR NVTLTLSWNV
151 VPNAGILPLV TGSGHVSVPF PDTYEITKSY
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64j18, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_64j18, frame 1

Report for DKFZphfbr2_64j18.1

```
[LENGTH]        180
[MW]            20253.39
[pI]            8.66
[HOMOL]         PIR:A31788 signal peptidase (EC 3.4.99.-) (SPC 22/23) - dog 1e-100
[FUNCAT]        30.07 organization of endoplasmatic reticulum       [S. cerevisiae, YLR066w]
6e-15
[FUNCAT]        06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)        [S. cerevisiae, YLR066w] 6e-15
[PIRKW]         transmembrane protein 2e-92
[PIRKW]         glycoprotein 2e-92
[PIRKW]         hydrolase 2e-92
[PROSITE]       RGD     1
[PROSITE]       MYRISTYL        2
[PROSITE]       PROKAR_LIPOPROTEIN      1
[PROSITE]       TONB_DEPENDENT_REC_1    1
[PROSITE]       PKC_PHOSPHO_SITE        1
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            Alpha_Beta
[KW]            SIGNAL_PEPTIDE 32
```

```
SEQ    MNTVLSRANSLFAFSLSVMAALTFGCFITTAFKDRSVPVRLHVSRIMLKNVEDFTGPRER
PRD    cccccccchhhhhhhhhhhhhhhhhhhhhheeeccccccceeehhhhhhhhhhhhccccccc

SEQ    SDLGFITSDITADLENIFDWNVKQLFLYLSAEYSTKNNALNQVVLWDKIVLRGDNPKLLL
PRD    cccccchhhhhhhhcccccchhhhhhhhhhhhhhhhcccccceeeeeeeceeeccccchhhhh

SEQ    KDMKTKYFFFDDGNGLKGNRNVTLTLSWNVVPNAGILPLVTGSGHVSVPFPDTYEITKSY
PRD    hhccccceeeecccccccccceeeeeeeecccccceeeeeccccceeeecccccccccccc
```

Prosite for DKFZphfbr2_64j18.1

PS00001	141->145	ASN_GLYCOSYLATION	PDOC00001
PS00005	94->97	PKC_PHOSPHO_SITE	PDOC00005
PS00008	25->31	MYRISTYL	PDOC00008
PS00008	135->141	MYRISTYL	PDOC00008
PS00013	16->27	PROKAR_LIPOPROTEIN	PDOC00013
PS00016	112->115	RGD	PDOC00016
PS00430	1->22	TONB_DEPENDENT_REC_1	PDOC00354

(No Pfam data available for DKFZphfbr2_64j18.1)

DKFZphfbr2_64k24
----

group: transmembrane proteins

DKFZphfbr2_64k24 encodes a novel 412 amino acid protein with weak similarity to several known proteins.

The novel protein contains 5 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to AMAC1 "testicular condensing enzyme" ;
membrane regions: 5
Summary DKFZphfbr2_64k24 encodes a novel 412 amino acid protein, with similarity to AMAC1"; product: "testicular condensing enzyme

similarity to AMAC1 "testicular condensing enzyme"

complete cDNA, complete cds, EST hits

Sequenced by Qiagen

Locus: unknown

Insert length: 1958 bp
Poly A stretch at pos. 1939, polyadenylation signal at pos. 1918

```
   1 GGGCCCGCCT CGATTTTCCC AGGCGAGGGC ACGCCCGCGT CAGTCGCCTC
  51 CGGGGCACCT TCCTCGCCAC GACACGCAGG TAACCGGGCC CCGGGAGCCG
 101 GTCGGCGGCG GCGGACTGGG ACCTTGATCC TGCCTGCCCG GCCGCCCGAC
 151 AAGGGAATGA GAGCGGACCC CGAACTCCAC ACACCCGCGT TTAGCCGCCA
 201 CACCTAAGGG GCAGAACAGT CTTTTTGGGT AAGGGCCGGG CTGGGGGCGA
 251 CGCGCCCCGC CCGCTTTGCA GACTTCGGGG TGCTCTGCAC GACGCCTGAA
 301 AGGCCGCGGG GCCCGCATTT CTCTGTGCTG CCCTCCTGGA GAACCGGGAC
 351 ACGGGGACGG GAGGGCCAGC ATCGGCTACG GCCCGGTTTC CCGTTTCTTT
 401 CCTCTGTCGC GTCTGGGCCC TCCTGCAGCG TCCATGATGA AGGCCAGGGG
 451 CTGTTGCTTT CCTCTCGCCC AGTAGCCAAC CCAAGCAAGG GAATTAATTA
 501 TCTGAAGAAA TGGATACTTC TCCCTCCAGA AAATATCCAG TTAAAAAACG
 551 GGTGAAAATA CATCCCAACA CAGTGATGGT GAAATATACT TCTCATTATC
 601 CCCAGCCTGG CGATGATGGA TATGAAGAAA TCAATGAAGG CTATGGGAAT
 651 TTTATGGAGG AAAATCCAAA GAAAGGTCTG CTGAGTGAAA TGAAAAAAAA
 701 AGGGAGAGCT TTCTTTGGAA CCATGGATAC CCTACCTCCA CCAACAGAAG
 751 ACCCAATGAT CAATGAGATT GGACAATTCC AGAGCTTTGC AGAAAAAAAC
 801 ATTTTTCAAT CCCGAAAAAT GTGGATAGTG CTGTTTGGAT CTGCTTTGGC
 851 TCATGGATGT GTAGCTCTTA TCACTAGGCT TGTTTCTGAT CGGTCTAAAG
 901 TTCCATCTCT AGAACTGATT TTTATCCGTT CTGTTTTTCA GGTCTTATCT
 951 GTGTTAGTTG TGTGTTACTA TCAGGAGGCC CCCTTTGGAC CCAGTGGATA
1001 CAGATTACGA CTCTTCTTTT ATGGTGTATG CAATGTCATT TCTATCACTT
1051 GTGCTTATAC ATCATTTTCA ATAGTTCCTC CCAGCAATGG GACCACTATG
1101 TGGAGAGCCA CAACTACAGT CTTCAGTGCC ATTTTGGCTT TTTTACTCGT
1151 AGATGAGAAA ATGGCTTATG TTGACATGGC TACAGTTGTT TGCAGCATCT
1201 TAGGTGTTTG TCTTGTCATG ATCCCAAACA TTGTTGATGA AGACAATTCT
1251 TTGTTAAATG CCTGGAAAGA AGCCTTTGGG TACACCATGA CTGTGATGGC
1301 TGGACTGACC ACTGCTCTCT CAATGATAGT ATACAGATCC ATCAAGGAGA
1351 AGATCAGCAT GTGGACTGCG CTGTTTACTT TTGGTTGGAC TGGGACAATT
1401 TGGGGAATAT CTACTATGTT TATTCTTCAA GAACCCATCA TCCCATTAGA
1451 TGGAGAAACC TGGAGTTATC TCATTGCTAT ATGTGTCTGT TCTACTGCAG
1501 CATTCTTAGG AGTTTATTAT GCCTTGGACA AATTCCATCC AGCTTTGGTT
1551 AGCACAGTAC AACATTTGGA GATTGTGGTA GCTATGGTCT TGCAGCTTCT
1601 CGTGCTGCAC ATATTTCCTA GCATCTATGA TGTTTTTGGA GGGGTAATCA
1651 TTATGATTAG TGTTTTTGTC CTTGCTGGCT ATAAACTTTA CTGGAGGAAT
1701 TTAAGAAGGC AGGACTACCA GGAAATACTA GACTCTCCCA TTAAATGAAT
1751 ACCTGATTAT TATTGTCTCA TTAATGTTCA GTTATTAATA TGTATACTGC
1801 CATTTTAATG TTTACCTATG AATGTCTTTT GTGTTATATA ACTGACAGAG
1851 TGCTATAAAA TATATAATAT ATACAAATGC AGAAAATTTA TTCTAGTCTA
1901 ATATATTCAA ATACAAATAT TAAATATATG AAATACGTTA AAAAAAAAAA
1951 AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 510 bp to 1745 bp; peptide length: 412
Category: similarity to known protein

```
  1 MDTSPSRKYP VKKRVKIHPN TVMVKYTSHY PQPGDDGYEE INEGYGNFME
 51 ENPKKGLLSE MKKKGRAFFG TMDTLPPPTE DPMINEIGQF QSFAEKNIFQ
101 SRKMWIVLFG SALAHGCVAL ITRLVSDRSK VPSLELIFIR SVFQVLSVLV
151 VCYYQEAPFG PSGYRLRLFF YGVCNVISIT CAYTSFSIVP PSNGTTMWRA
201 TTTVFSAILA FLLVDEKMAY VDMATVVCSI LGVCLVMIPN IVDEDNSLLN
251 AWKEAFGYTM TVMAGLTTAL SMIVYRSIKE KISMWTALFT FGWTGTIWGI
301 STMFILQEPI IPLDGETWSY LIAICVCSTA AFLGVYYALD KFHPALVSTV
351 QHLEIVVAMV LQLLVLHIFP SIYDVFGGVI IMISVFVLAG YKLYWRNLRR
401 QDYQEILDSP IK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_64k24, frame 3

TREMBLNEW:AF016712_1 gene: "AMAC1"; product: "testicular condensing enzyme"; Mus musculus testicular condensing enzyme (AMAC1) mRNA, complete cds., N = 1, Score = 191, P = 1.9e-12

TREMBL:BMAJ733_6 product: "hypothetical protein"; Bacillus megaterium bgaM gene, N = 1, Score = 137, P = 1.6e-06

PIR:G71841 hypothetical protein jhp1155 - Helicobacter pylori (strain J99), N = 1, Score = 129, P = 1.3e-05

```
>TREMBLNEW:AF016712_1 gene: "AMAC1"; product: "testicular condensing
     enzyme"; Mus musculus testicular condensing enzyme (AMAC1) mRNA, complete
     cds.
            Length = 362

  HSPs:

 Score = 191 (28.7 bits), Expect = 1.9e-12, P = 1.9e-12
 Identities = 39/105 (37%), Positives = 66/105 (62%)

Query:   289 FTFGWTGTIWGISTMFILQEPIIPLDGETWSYLIAICVCSTAAFLGVYYALDKFHPALVS 348
             F FG  G +  +  +F+LQ P++P D  +WS ++A+ + +  +F+ V YA+ K HPALV
Sbjct:   248 FLFGLVGLMVSVPGLFVLQTPVLPQDTLSWSCVVAVGLLALVSFVCVSYAVTKAHPALVC 307

Query:   349 TVQHLEIVVAMVLQLLVLH--IFPSIYDVFGGVIIMISVFVLAGYKL 393
              V H E+VVA++LQ  VL+  + PS  D+ G  +++ S+ ++    L
Sbjct:   308 AVLHSEVVVALMLQYYVLYETVAPS--DIMGAGVVLGSIAIITAQNL 352
```

Pedant information for DKFZphfbr2_64k24, frame 3

Report for DKFZphfbr2_64k24.3

```
[LENGTH]        412
[MW]            46449.87
[pI]            6.99
[HOMOL]         TREMBL:AF016712_1 gene: "AMAC1"; product: "testicular condensing enzyme"; Mus
musculus testicular condensing enzyme (AMAC1) mRNA, complete cds. 8e-14
[PROSITE]       MYRISTYL        6
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            TRANSMEMBRANE   5

SEQ     MDTSPSRKYPVKKRVKIHPNTVMVKYTSHYPQPGDDGYEEINEGYGNFMEENPKKGLLSE
```

```
PRD     cccccccccccccceeeecccceeeeeeeccccccccccceeeeeccccccccccchhhh
MEM     ............................................................

SEQ     MKKKGRAFFGTMDTLPPPTEDPMINEIGQFQSFAEKNIFQSRKMWIVLFGSALAHGCVAL
PRD     hhhhcceeeccccccccccccccceeeeccccchhhhhhhhccceeeeeeeeecccccchhhhhc
MEM     ............................................................

SEQ     ITRLVSDRSKVPSLELIFIRSVFQVLSVLVVCYYQEAPFGPSGYRLRLFFYGVCNVISIT
PRD     chhhhhcccccccccchhhhhhhhhhhheeeeeeeecccccccccceeeeeeeeecceeeeeee
MEM     ................MMMMMMMMMMMMMMMMM...........................

SEQ     CAYTSFSIVPPSNGTTMWRATTTVFSAILAFLLVDEKMAYVDMATVVCSILGVCLVMIPN
PRD     eccceeeecccccccceeeeeeehhhhhhhhhhhhhhhheeeeeeeeeeeeeeeeeeeeeecc
MEM     ............................................................

SEQ     IVDEDNSLLNAWKEAFGYTMTVMAGLTTALSMIVYRSIKEKISMWTALFTFGWTGTIWGI
PRD     cccccchhhhhhhhhhhheeeeeeeehhhhhhhcchhhhhhhhhhhhcccccccccceeeec
MEM     .........................................MMMMMMMMMMMMMMMMMMM

SEQ     STMFILQEPIIPLDGETWSYLIAICVCSTAAFLGVYYALDKFHPALVSTVQHLEIVVAMV
PRD     ceeeeeecccccccccceeeeeeccchhhhhhhhhcccccccccccchhhhhhhhhhhhhh
MEM     MMMMMMMMMM.......MMMMMMMMMMMMMMMMMMMMMMM......MMMMMMMMMMMMMM

SEQ     LQLLVLHIFPSIYDVFGGVIIMISVFVLAGYKLYWRNLRRQDYQEILDSPIK
PRD     hhhhhhhhccccccceeeeeeeeeeeeccccccchhhhhhhhhhhhhhhhhccccc
MEM     MMMMMMM....MMMMMMMMMMMMMMMMMMMMM....................
```

Prosite for DKFZphfbr2_64k24.3

PS00001	193->197	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	101->104	PKC_PHOSPHO_SITE	PDOC00005
PS00005	126->129	PKC_PHOSPHO_SITE	PDOC00005
PS00005	277->280	PKC_PHOSPHO_SITE	PDOC00005
PS00006	92->96	CK2_PHOSPHO_SITE	PDOC00006
PS00006	277->281	CK2_PHOSPHO_SITE	PDOC00006
PS00006	371->375	CK2_PHOSPHO_SITE	PDOC00006
PS00008	70->76	MYRISTYL	PDOC00008
PS00008	88->94	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	265->271	MYRISTYL	PDOC00008
PS00008	295->301	MYRISTYL	PDOC00008
PS00008	334->340	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_64k24.3)

DKFZphfbr2_6a17

group: brain derived

DKFZphfbr2_6a17 encodes a novel 100 amino acid protein with very weak similarity to human finger protein zfOC1.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 1424 bp
Poly A stretch at pos. 1405, polyadenylation signal at pos. 1389

```
   1 GGGACTGAGG GGGTGGGCTT ACTCCCTGGG CAGTCTTGGG GGCCAGAGCT
  51 GAGGCCAGTC CATATTACAG TGGCTGGGCT GTTTTTTTCA GTAGCCCCTA
 101 GCATTGGCTG GGATTCCTGT TCCTGGGTGC GCCTCCACCT CCCTTCTGAT
 151 GCTTCCTGGC TATGGTGGGG TGGGAACCTC AGTTTCCCCC AAAGTCTTCC
 201 CTGGATGCTG GCTTCAGGTT GAAGACCCTG GTTCTTCCAG TTCCTCACGG
 251 GTTAGGTAGG GGCTCCTGCA TCACCTTCAG AATCAGTTCC AACCCCCACT
 301 CTCCTTAGGC TTTGTGCTCT GCTCTGCCCT GCCAGGCTGC CCTTGTCCAT
 351 GTGAGTAGCA TGGGCGGGTG GTGGGGACGG CAGTGGTGAT GAAGGGGGTG
 401 CACCACAGGC CTCATGAAGC AGTTCCCACA TGGGCGTGTG GCTGGGGCGT
 451 GGCCACCACA GAGCACATGG CTGTGTCTAG GCGCAAGCAC TTTAGCAGTA
 501 TCTGTTTACA TGCGCAAGGA TCAAGCCGAC TACCTGTGCT GTCTACTGGG
 551 ACAGCAGTCT CCGAGCTACT CCGTACCTCC CTCTGCCAGG TCGTGGAGTT
 601 AGGCCCCAGT CCCTACTTGT CACTGGTTCC CACTGTGCTC CTAACTGTGC
 651 AGCACCTGGG AGCTCTGGCC TGGGGCTGGA GGCCCTGGTA GGAGCTGCAG
 701 TTGGAGGCCG TTCTGTGCCC AGCAGCGGTG AGCGGCTCCC ATGGGCCCTG
 751 TGTCTGCAGG GAGCCAGGGC TGCGGCACAT GTGCTGTGAA ACTGGCACCC
 801 ACCTGGCGTG CTGCTGCCGC CACTTGCTTC CTGCAGCACC TCCTACCCTG
 851 CTCCGTGTCC TCCCTCTCCC CGCGCCTGGC TCAGGAGTGC TGGAAAAGCT
 901 CACGCCTCGG CCTGGGAGCC TGGCCTCTTG ATATACCTCG AGCTTCCCCT
 951 GTGCTCCCCA GCCCCAGGAC CACTGGCCCC TTGGCCTGAG GGGCTGGGGG
1001 CCCCACGACC TGCAGCGTCG AGTCCGGGAG AGAGCCCGGA GCGGCGTGCC
1051 ATCTCGGCTC GGCCTTGCTG AGAGCCTCCG CCCTGGCTTT CTCCCTGTCT
1101 GGTTTCAGTG GCTCACGTTG GTGCTACACA GCTAGAATAG ATATATTTAG
1151 AGAGAGAGAT ATTTTTAAGA CAAAGCCCAC AATTAGCTGT CCTTTAACAC
1201 CGCAGAACCC CCTCCCAGAA GAAGAGCGAT CCCTCGGACG GTCCGGGCGG
1251 GCACCCTCAG CCGGGCTCTT TGCAGAAGCA GCACCGCTGA CTGTGGGCCC
1301 GGCCCTCAGA TGTGTACATA TACGGCTATT TCCTATTTTA CTGTTCTTCA
1351 GATTTAGTAC TTGTAAATAA ACACACACAT TAAGGAGAGA TTAAACATTT
1401 TTGCCAAAAA AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 389 bp to 688 bp; peptide length: 100
Category: putative protein

```
   1 MKGVHHRPHE AVPTWACGWG VATTEHMAVS RRKHFSSICL HAQGSSRLPV
  51 LSTGTAVSEL LRTSLCQVVE LGPSPYLSLV PTVLLTVQHL GALAWGWRPW
```

BLASTP hits

```
Entry S70007 from database PIR:
finger protein zfOC1 - human (fragment)
Length = 183
Score = 62 (21.8 bits), Expect = 0.24, Sum P(2) = 0.22
Identities = 18/47 (38%), Positives = 24/47 (51%)


            Alert BLASTP hits for DKFZphfbr2_6a17, frame 2

No Alert BLASTP hits found

            Pedant information for DKFZphfbr2_6a17, frame 2
            -----------------------------------------------

                      Report for DKFZphfbr2_6a17.2


[LENGTH]        100
[MW]            10944.82
[pI]            9.49
[PROSITE]       MYRISTYL        2
[PROSITE]       PKC_PHOSPHO_SITE        2
[KW]            Alpha_Beta


SEQ     MKGVHHRPHEAVPTWACGWGVATTEHMAVSRRKHFSSICLHAQGSSRLPVLSTGTAVSEL
PRD     cccccccccccccccccccccchhhhhhhhhhcccccceeeccccccccceeeccccchhhhh

SEQ     LRTSLCQVVELGPSPYLSLVPTVLLTVQHLGALAWGWRPW
PRD     hhhhheeeeecccccceeecchhhhhhhhhchhhhhcccc


                      Prosite for DKFZphfbr2_6a17.2

PS00005         30->33    PKC_PHOSPHO_SITE        PDOC00005
PS00005         45->48    PKC_PHOSPHO_SITE        PDOC00005
PS00008         20->26    MYRISTYL                PDOC00008
PS00008         54->60    MYRISTYL                PDOC00008

(No Pfam data available for DKFZphfbr2_6a17.2)
```

DKFZphfbr2_6b24
----

group: metabolism

DKFZphfkd2_6b24 encodes a novel 334 amino acid protein with similarity to several bacterial dTDP-4-dehydrorhamnose reductases (EC 1.1.1.133).

The novel protein seems to be a human enzyme similar to dTDP-4-dehydrorhamnose reductases. EC 1.1.1.133 catalises the reaction: dTDP-6-deoxy-L-mannose + NADP(+) <=> dTDP-4-dehydro-6-deoxy-L-mannose + NADPH.

The new protein can find application in modulation of rhamnose metabolism and as a new enzyme for biotechnologic production processes.

similar to dTDP-6-deoxy-L-mannose-dehydrogenases

complete cDNA, EST hits, complete cds
Nucleotide sugars metabolism seems to be a dehydrogenase
localisation: region of primer A missing

Sequenced by AGOWA

Locus: /map="5"

Insert length: 2054 bp
Poly A stretch at pos. 2028, polyadenylation signal at pos. 2015

```
   1 GGGGGAGGCC CGCGTCGATC CTGGGTTGGA GGAGGTGGCG GCCGCTGAGG
  51 CTGCGGCGTG AAGACGGCGG GCATGGTGGG GCGGGAGAAA GAGCTCTCTA
 101 TACACTTTGT TCCCGGGAGC TGTCGGCTGG TGGAGGAGGA AGTTAACATC
 151 CCTAATAGGA GGGTTCTGGT TACTGGTGCC ACTGGGCTTC TTGGCAGAGC
 201 TGTACACAAA GAATTTCAGC AGAATAATTG GCATGCAGTT GGCTGTGGTT
 251 TCAGAAGAGC AAGACCAAAA TTTGAACAGG TTAATCTGTT GGATTCTAAT
 301 GCAGTTCATC ACATCATTCA TGATTTTCAG CCCCATGTTA TAGTACATTG
 351 TGCAGCAGAG AGAAGACCAG ATGTTGTAGA AAATCAGCCA GATGCTGCCT
 401 CTCAACTTAA TGTGGATGCT TCTGGGAATT TAGCAAAGGA AGCAGCTGCT
 451 GTTGGAGCAT TTCTCATCTA CATTAGCTCA GATTATGTAT TTGATGGAAC
 501 AAATCCACCT TACAGAGAGG AAGACATACC AGCTCCCCTA AATTTGTATG
 551 GCAAAACAAA ATTAGATGGA GAAAAGGCTG TCCTGGAGAA CAATCTAGGA
 601 GCTGCTGTTT TGAGGATTCC TATTCTGTAT GGGGAAGTTG AAAAGCTCGA
 651 AGAAAGTGCA GTGACTGTTA TGTTTGATAA AGTGCAGTTC AGCAACAAGT
 701 CAGCAAACAT GGATCACTGG CAGCAGAGGT TCCCCACACA TGTCAAAGAT
 751 GTGGCCACTG TGTGCCGGCA GCTAGCAGAG AAGAGAATGC TGGATCCATC
 801 AATTAAGGGA ACCTTTCACT GGTCTGGCAA TGAACAGATG ACTAAGTATG
 851 AAATGGCATG TGCAATTGCA GATGCCTTCA ACCTCCCCAG CAGTCACTTA
 901 AGACCTATTA CTGACAGCCC TGTCCTAGGA GCACAACGTC CGAGAAATGC
 951 TCAGCTTGAC TGCTCCAAAT TGGAGACCTT GGGCATTGGC CAACGAACAC
1001 CATTTCGAAT TGGAATCAAA GAATCACTTT GGCCTTTCCT CATTGACAAG
1051 AGATGGAGAC AAACGGTCTT TCATTAGTTT ATTTGTGTTG GGTTCTTTTT
1101 TTTTTAAAT GAAAAGTATA GTATGTGGCC CTTTTTAAAG AACAAAGGAA
1151 ATAGTTTTGT ATGAGTACTT TAATTGTGAC TCTTAGGATC TTTCAGGTAA
1201 ATGATGCTCT TGCACTAGTG AAATTGTCTA AAGAAACTAA AGGGCAGTCA
1251 TGCCCTGTTT GCAGTAATTT TTCTTTTTAT CATTATGTTT GTCCTGGCTA
1301 AACTTGGAGT TTGAGTATAG TAAATTATGA TCCTTAAATA TTTGAGGGTC
1351 AGGATGAAGC AGATCTGCTG TAGACTTTTC AGATGAAATT GTTCATTCTC
1401 GTAACCTCCA TATTTTCAGG ATTTTTGAAG CTGTTGACCA TTTCATGTTG
1451 ATTATTTTAA ATTGTGTGGA ATAGTATAAA AATCATTGGT GTTCATTATT
1501 TGCTTTGCCT GAGCTCAGAT CAAAATGTTT GAAGAAAGGA ACTTTATTTT
1551 TGCAAGTTAC GTACAGTTTT TATGCTTGAG ATATTTCAAC ATGTTATGTA
1601 TATTGGAACT TCTACAGCTT GATGCCTCCT GCTTTTATAG CAGTTTATGG
1651 GGAGCACTTG AAAGAGCGTG TGTACATGTA TTTTTTTTCT AGGCAAACAT
1701 TGAATGCAAA CGTGTATTTT TTTAATATAA ATATATAACT GTCCTTTTCA
1751 TCCCATGTTG CCGCTAAGTG ATATTTCATA TGTGTGGTTA TACTCATAAT
1801 AATGGGCCTT GTAAGTCTTT TCACCATTCA TGAATAATAA TAAATATGTA
1851 CTGCTGGCAT GTAATGCTTA GTTTTCTTGT ATTTACTTCT TTTTTTTAAA
1901 TGTAAGGACC AAACTTCTAA ACTAATTGTT CTTTTGTTGC TTTAATTTTT
1951 AAAAATTACA TTCTTCTGAT GTAACATGTG ATACATACAA AAGAATATAG
2001 TTTAATATGT ATTGAAATAA AACACAATAA AATTAAAAAA AAAAAAAAAA
2051 AAAA
```

BLAST Results

Entry G37115 from database EMBL:
SHGC-56899 Human Homo sapiens STS genomic.
Score = 446, P = 4.6e-14, identities = 90/91

Medline entries

99109950:
The metabolism of 6-deoxyhexoses in bacterial and animal cells.

Peptide information for frame 1

ORF from 73 bp to 1074 bp; peptide length: 334
Category: similarity to known protein

```
  1 MVGREKELSI HFVPGSCRLV EEEVNIPNRR VLVTGATGLL GRAVHKEFQQ
 51 NNWHAVGCGF RRARPKFEQV NLLDSNAVHH IIHDFQPHVI VHCAAERRPD
101 VVENQPDAAS QLNVDASGNL AKEAAAVGAF LIYISSDYVF DGTNPPYREE
151 DIPAPLNLYG KTKLDGEKAV LENNLGAAVL RIPILYGEVE KLEESAVTVM
201 FDKVQFSNKS ANMDHWQQRF PTHVKDVATV CRQLAEKRML DPSIKGTFHW
251 SGNEQMTKYE MACAIADAFN LPSSHLRPIT DSPVLGAQRP RNAQLDCSKL
301 ETLGIGQRTP FRIGIKESLW PFLIDKRWRQ TVFH
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_6b24, frame 1

PIR:T00104 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) - Actinobacillus actinomycetemcomitans, N = 1, Score = 293, P = 6.4e-26

TREMBL:SSU51197_21 gene: "rhsD"; product: "dTDP-6-deoxy-L-mannose-dehydrogenase"; Sphingomonas S88 sphingan polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase (spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase (spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26, ATP-binding cassette trans>., N = 1, Score = 291, P = 1e-25

SWISSPROT:RFBD_RHISN PROBABLE DTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.133) (DTDP-4-KETO- L-RHAMNOSE REDUCTASE) (DTDP-6-DEOXY-L-MANNOSE DEHYDROGENASE) (DTDP-L- RHAMNOSE SYNTHETASE)., N = 1, Score = 283, P = 7.4e-25

>PIR:T00104 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) - Actinobacillus actinomycetemcomitans
Length = 294

HSPs:

Score = 293 (44.0 bits), Expect = 6.4e-26, P = 6.4e-26
Identities = 89/276 (32%), Positives = 151/276 (54%)

```
Query:    30 RVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHHIIHDFQPHV 89
             R+L+TGA G LGR++ K    N  + V          F ++++ + + V  II  F+P+V
Sbjct:     3 RLLITGAGGQLGRSLAKLLVDNGRYEV------LALDFSELDITNKDMVFSIIDSFKPNV 56

Query:    90 IVHCAAERRPDVVENQPDAASQLNVDASGNLAKEAAAVGAFLIYISSDYVFDG-TNPPYR 148
             I++ AA    D  E +  +A  +NV     LA+ A    + ++++S+DYVFDG  +  Y+
Sbjct:    57 IINAAAYTSVDQAELEVSSAYSVNVRGVQYLAEAAIRHNSAILHVSTDYVFDGYKSGKYK 116

Query:   149 EEDIPAPLNLYGKTKLDGEKAVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSN 208
             E DI  PL +YGK+K +GE+ +L  +  + +LR    +GE      + V  M  ++  +
Sbjct:   117 ETDIIHPLCVYGKSKAEGERLLLTLSPKSIILRTSWTFGEYGN---NFVKTML-RLAKNR 172

Query:   209 KSANMDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIK-GTFHWSGNEQMTKYEMACAIAD 267
                 +   Q   PT+  D+A+V  Q+AEK ++  ++K G +H++G   ++ Y+ A AI D
Sbjct:   173 DILGVVADQIGGPTYSGDIASVLIQIAEKIIVGETVKYGIYHFTGEPCVSWYDFAIAIFD 232

Query:   268 AF-------NLPSSHLRPITDSPVLGAQRPRNAQLDCSKLE-TLGI 305
                      N+P  +     D P L A+RP N+ LD +K++   GI
Sbjct:   233 EAVAQKVLENVPLVNAITTADYPTL-AKRPANSCLDLTKIQQAFGI 277
```

Pedant information for DKFZphfbr2_6b24, frame 1

Report for DKFZphfbr2_6b24.1

```
[LENGTH]        334
[MW]            37551.98
[pI]            6.90
[HOMOL]         PIR:T00104 probable dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133) -
Actinobacillus actinomycetemcomitans 6e-25
[FUNCAT]        01.06.01 lipid, fatty-acid and sterol biosynthesis   [S. cerevisiae, YGL001c]
6e-04
[EC]            1.1.1.133 dTDP-4-dehydrorhamnose reductase 2e-16
[PIRKW]         lipopolysaccharide biosynthesis 2e-16
[PIRKW]         NADP 2e-16
[PIRKW]         oxidoreductase 2e-16
[PIRKW]         streptomycin biosynthesis 1e-19
[SUPFAM]        dTDP-dihydrostreptose synthase 1e-20
[PROSITE]       MYRISTYL        1
[PROSITE]       CK2_PHOSPHO_SITE        4
[PROSITE]       PKC_PHOSPHO_SITE        3
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            Alpha_Beta

SEQ     MVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGF
PRD     ccccccеeeccccccceeeeeccccccccceeeeeccccchhhhhhhhhhhccceeeeecc

SEQ     RRARPKFEQVNLLDSNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNL
PRD     cccccccccccccchhhhhhhhhhhcccеeeehhhhhhhhhhhhhhhhhhhhhhhcchhh

SEQ     AKEAAAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEKAVLENNLGAAVL
PRD     hhhhhhhhheeeeeeccccccccccccccccccccccccchhhhhhhhhcccccccceeee

SEQ     RIPILYGEVEKLEESAVTVMFDKVQFSNKSANMDHWQQRFPTHVKDVATVCRQLAEKRML
PRD     eeeeeecccccccchhhhhhhhhhhhcccеeeeccccccccccchhhhhhhhhhhhhhhh

SEQ     DPSIKGTFHWSGNEQMTKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
PRD     cccccceeeecccccchhhhhhhhhhhhhcccccccccccccccccccccccchhhhhh

SEQ     ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
PRD     hhhhccccchhhhhhhhhhhhhhhhhhhhhcccc
```

Prosite for DKFZphfbr2_6b24.1

PS00001	208->212	ASN_GLYCOSYLATION	PDOC00001
PS00005	16->19	PKC_PHOSPHO_SITE	PDOC00005
PS00005	207->210	PKC_PHOSPHO_SITE	PDOC00005
PS00005	243->246	PKC_PHOSPHO_SITE	PDOC00005
PS00006	162->166	CK2_PHOSPHO_SITE	PDOC00006
PS00006	251->255	CK2_PHOSPHO_SITE	PDOC00006
PS00006	257->261	CK2_PHOSPHO_SITE	PDOC00006
PS00006	298->302	CK2_PHOSPHO_SITE	PDOC00006
PS00008	314->320	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_6b24.1)

DKFZphfbr2_6i20
----

group: brain derived

DKFZphfbr2_6i20 encodes a novel 296 amino acid protein with similarity to ribosomal protein L15 precursor of S. cerevisiae mitochondria.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to ribosomal protein L15 precursor, mitochondrial

complete cDNA, complete cds, EST hits
potential miochondrial L15 ribosomal protein

Sequenced by AGOWA

Locus: /map="377.5 cR from top of Chr8 linkage group"

Insert length: 1122 bp
Poly A stretch at pos. 1099, polyadenylation signal at pos. 1071

```
   1 GGGGGCCCTT GAAAGTTCTT GGATCTGCGG GTTATGGCCG GTCCCTTGCA
  51 GGGCGGTGGG GCCCGGGCCC TGGACCTACT CCGGGGCCTG CCGCGTGTGA
 101 GCCTGGCCAA CTTAAAGCCG AATCCCGGCT CCAAGAAACC GGAGAGAAGA
 151 CCAAGAGGTC GGAGAAGAGG TAGAAAATGT GGCAGAGGCC ATAAAGGAGA
 201 AAGGCAAAGA GGAACCCGGC CCCGCTTGGG CTTTGAGGGA GGCCAGACTC
 251 CATTTTACAT CCGAATCCCA AAATACGGGT TTAACGAAGG ACATAGTTTC
 301 AGACGCCAGT ATAAGCCTAT GAGTCTCAAT AGACTGCAGT ATCTTATTGA
 351 TTTGGGTCGT GTTGATCCTA GTCAACCTAT TGACTTAACC CAGCTTGTCA
 401 ATGGGAGAGG TGTGACCATC CAGCCACTTA AAAGGGATTA TGATGTCCAG
 451 CTGGTTGAGG AGGGTGCTGA CACCTTTACG GCAAAAGTTA ATATTGAAGT
 501 ACAGTTGGCT TCAGAACTAG CTATTGCTGC CATTGAAAAA AATGGTGGTG
 551 TTGTTACTAC AGCCTTCTAT GATCCAAGAA GTCTGGACAT TGTATGCAAA
 601 CCTGTTCCAT TCTTTCTTCG TGGACAACCC ATTCCAAAAA GAATGCTTCC
 651 ACCAGAAGAA CTGGTACCAT ATTACACTGA TGCAAAGAAC CGTGGGTACC
 701 TGGCGGATCC TGCCAAATTT CCTGAAGCAC GACTTGAACT CGCCAGGAAG
 751 TATGGTTATA TCTTACCTGA TATCACTAAA GATGAACTCT TCAAAATGCT
 801 CTGTACTAGG AAGGATCCAA GGCAGATTTT CTTTGGTCTT GCTCCAGGAT
 851 GGGTGGTGAA TATGGCCGAT AAGAAAATCC TAAAACCTAC AGATGAAAAT
 901 CTCCTTAAGT ATTATACCTC ATGAATTCCC GTCCAAGGAA GCAGAGTTGT
 951 TAAAGAGTAC TGGAATAGGG GCTGAAGGAT CTATATTCCC TTATTGCATT
1001 TTCCTTATGT ATAATTTTCC AGATGGTGAT GTTACTTTTC AGTGTACTCA
1051 TATGTCTCAT TTTCATCTAA AATTAAATGG CAGGAAACAA GGACTGCATA
1101 GAGAAAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry HS500354 from database EMBL:
human STS WI-12392.
Length = 426
Minus Strand HSPs:
Score = 1791 (268.7 bits), Expect = 1.1e-74, P = 1.1e-74
Identities = 375/384 (97%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 34 bp to 921 bp; peptide length: 296
Category: strong similarity to known protein

```
   1 MAGPLQGGGA RALDLLRGLP RVSLANLKPN PGSKKPERRP RGRRRGRKCG
```

```
 51 RGHKGERQRG TRPRLGFEGG QTPFYIRIPK YGFNEGHSFR RQYKPMSLNR
101 LQYLIDLGRV DPSQPIDLTQ LVNGRGVTIQ PLKRDYDVQL VEEGADTFTA
151 KVNIEVQLAS ELAIAAIEKN GGVVTTAFYD PRSLDIVCKP VPFFLRGQPI
201 PKRMLPPEEL VPYYTDAKNR GYLADPAKFP EARLELARKY GYILPDITKD
251 ELFKMLCTRK DPRQIFFGLA PGWVVNMADK KILKPTDENL LKYYTS
```

BLASTP hits

Entry S63258 from database PIR:
ribosomal protein L15 precursor, mitochondrial - yeast (Saccharomyces cerevisiae)
Length = 322
Score = 259 (91.2 bits), Expect = 2.0e-22, P = 2.0e-22
Identities = 71/200 (35%), Positives = 106/200 (53%)

Entry H70161 from database PIR:
ribosomal protein L15 (rplO) - Lyme disease spirochete
Length = 145
Score = 173 (60.9 bits), Expect = 4.8e-13, P = 4.8e-13
Identities = 45/140 (32%), Positives = 73/140 (52%)

Alert BLASTP hits for DKFZphfbr2_6i20, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_6i20, frame 1

Report for DKFZphfbr2_6i20.1

```
[LENGTH]     296
[MW]         33495.98
[pI]         9.98
[HOMOL]      TREMBL:AF067212_1 gene: "F37F2.1"; Caenorhabditis elegans cosmid F37F2. 1e-38

[FUNCAT]     05.01 ribosomal proteins     [S. cerevisiae, YNL284c] 7e-15
[FUNCAT]     30.16 mitochondrial organization      [S. cerevisiae, YNL284c] 7e-15
[FUNCAT]     j mrna translation and ribosome biogenesis   [M. genitalium, MG169] 1e-06
[BLOCKS]     BL00475D
[BLOCKS]     BL00475B Ribosomal protein L15 proteins
[PIRKW]      ribosome 2e-13
[PIRKW]      mitochondrion 2e-13
[PIRKW]      protein biosynthesis 2e-13
[SUPFAM]     Escherichia coli ribosomal protein L15 4e-06
[PROSITE]    MYRISTYL       3
[PROSITE]    AMIDATION      2
[PROSITE]    CK2_PHOSPHO_SITE      2
[PROSITE]    PKC_PHOSPHO_SITE      4
[KW]         Alpha_Beta
[KW]         LOW_COMPLEXITY    12.50 %

SEQ    MAGPLQGGGARALDLLRGLPRVSLANLKPNPGSKKPERRPRGRRRGRKCGRGHKGERQRG
SEG    ......xxxxxxxxxxxxx..............xxxxxxxxxxxxxxxxxxxxxxxxx...
PRD    cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ    TRPRLGFEGGQTPFYIRIPKYGFNEGHSFRRQYKPMSLNRLQYLIDLGRVDPSQPIDLTQ
SEG    ............................................................
PRD    cccccccccccceeeeeccccccccccccccccccccchhhhhhhhcccccccccccccee

SEQ    LVNGRGVTIQPLKRDYDVQLVEEGADTFTAKVNIEVQLASELAIAAIEKNGGVVTTAFYD
SEG    ............................................................
PRD    eccccceeeeccccccceeeeeecccccchhhhhhhhhhhhhhhhhhccceeeeeecc

SEQ    PRSLDIVCKPVPFFLRGQPIPKRMLPPEELVPYYTDAKNRGYLADPAKFPEARLELARKY
SEG    ............................................................
PRD    cccccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhh

SEQ    GYILPDITKDELFKMLCTRKDPRQIFFGLAPGWVVNMADKKILKPTDENLLKYYTS
SEG    ........................................................
PRD    cccccccchhhhhhhhhcccccceeeeeccccceeeecccceeeccccchhhhhcccc
```

Prosite for DKFZphfbr2_6i20.1

```
PS00005     33->36    PKC_PHOSPHO_SITE      PDOC00005
PS00005     88->91    PKC_PHOSPHO_SITE      PDOC00005
```

PS00005	149->152	PKC_PHOSPHO_SITE	PDOC00005
PS00005	258->261	PKC_PHOSPHO_SITE	PDOC00005
PS00006	248->252	CK2_PHOSPHO_SITE	PDOC00006
PS00006	258->262	CK2_PHOSPHO_SITE	PDOC00006
PS00008	8->14	MYRISTYL	PDOC00008
PS00008	171->177	MYRISTYL	PDOC00008
PS00008	268->274	MYRISTYL	PDOC00008
PS00009	41->45	AMIDATION	PDOC00009
PS00009	45->49	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_6i20.1)

DKFZphfbr2_6o17
----

group: nucleic acid management

DKFZphfbr2_6o17 encodes a novel 455 amino acid protein with strong similarity to DEAD-box ATP-dependent RNA helicases YHR065c and T26G10.1.

The S. cerevisiae protein YHR065c is required for maturation of the 35S RNA primary transcript.

The new protein can find application in modulating rRNA maturation.

strong similar to RNA helicases

complete cDNA, complete cds, EST hits
probable start at Bp 27 matchs kozak consensus ANNatgG
involved in maturation of r-RNA ??
YHR065c/Rrp3p is involved in maturation of the 35S primary transcript
Drs1p cold-sensitive mutation has slow 27S to 25S pre-rRNA
conversion and is deficient in 60S ribosomal subunits

Sequenced by AGOWA

Locus: unknown

Insert length: 1840 bp
Poly A stretch at pos. 1815, polyadenylation signal at pos. 1793

```
   1 GGGGACTTCC GGAGACCTCA CACAAGATGG CGGCACCCGA GGAACACGAT
  51 TCTCCGACCG AAGCGTCCCA GCCGATTGTG GAAGAGGAGG AAACTAAAAC
 101 ATTTAAAGAC CTGGGTGTGA CAGATGTGTT GTGTGAAGCT TGTGACCAGT
 151 TGGGATGGAC AAAACCCACC AAGATTCAGA TTGAAGCTAT TCCTTTGGCC
 201 TTACAAGGTC GTGATATCAT TGGGCTTGCA GAAACTGGCT CTGGAAAGAC
 251 AGGCGCCTTT GCTTTGCCCA TTCTAAACGC ACTGCTGGAG ACCCCGCAGC
 301 GTTTGTTTGC CCTAGTTCTT ACCCCGACTC GGGAGCTGGC CTTTCAGATC
 351 TCAGAGCAGT TTGAAGCCCT GGGGTCCTCT ATTGGAGTGC AGAGTGCTGT
 401 GATTGTAGGT GGAATTGATT CAATGTCTCA ATCTTTGGCC CTTGCAAAAA
 451 AACCACATAT AATAATAGCA ACTCCTGGTC GACTGATTGA CCACTTGGAA
 501 AATACGAAAG GTTTCAACTT GAGAGCTCTC AAATACTTGG TCATGGATGA
 551 AGCCGACCGA ATACTGAATA TGGATTTTGA GACAGAGGTT GACAAGATCC
 601 TCAAAGTGAT TCCTCGAGAT CGGAAAACAT TCCTCTTCTC TGCCACCATG
 651 ACCAAGAAGG TTCAAAAACT TCAGCGAGCA GCTCTGAAGA ATCCTGTGAA
 701 ATGTGCCGTT TCCTCTAAAT ACCAGACAGT TGAAAAATTA CAGCAATATT
 751 ATATTTTTAT TCCCTCTAAA TTCAAGGATA CCTACCTGGT TTATATTCTA
 801 AATGAATTGG CTGGAAACTC CTTTATGATA TTCTGCAGCA CCTGTAATAA
 851 TACCCAGAGA ACAGCTTTGC TACTGCGAAA TCTTGGCTTC ACTGCCATCC
 901 CCCTCCATGG ACAAATGAGT CAGAGTAAGC GCCTAGGATC CCTTAATAAG
 951 TTTAAGGCCA AGGCCCGTTC CATTCTTCTA GCAACTGACG TTGCCAGCCG
1001 AGGTTTGGAC ATACCTCATG TAGATGTGGT TGTCAACTTT GACATTCCTA
1051 CCCATTCCAA GGATTACATC CATCGAGTAG GTCGAACAGC TAGAGCTGGG
1101 CGCTCCGGAA AGGCTATTAC TTTTGTCACA CAGTATGATG TGGAACTCTT
1151 CCAGCGCATA GAACACTTAA TTGGGAAGAA ACTACCAGGT TTTCCAACAC
1201 AGGATGATGA GGTTATGATG CTGACAGAAC GCGTCGCTGA AGCCCAAAGG
1251 TTTGCCCGAA TGGAGTTAAG GGAGCATGGA GAAAAGAAGA AACGCTCGCG
1301 AGAGGATGCT GGAGATAATG ATGACACAGA GGGTGCTATT GGTGTCAGGA
1351 ACAAGGTGGC TGGAGGAAAA ATGAAGAAGC GGAAAGGCCG TTAATCACTT
1401 TTATGAAGGC TCGAGTTCTG CTGTTCTGTA AAAGAAAATT GGAGAATGAA
1451 ACCTGCTCCA ACAGAGATCA TGAGACTGAA ATTGGTCAGA ATTGTGTCCA
1501 GAATGTGCTC AGCTAATTCA GTATTCTTCC CCATTCTGGG TTGGAGTTTA
1551 CTGCAGAGTA ATTCTTACAG TGCTGATGTC AAGACTGTTA CTGTTCTTCG
1601 ACTTTGATTC CTTGCTCATG ACATGAGTAG GGTGTGCTCT TCTGTCACTT
1651 CACACAGACC TTTTGCCTTT TTTAGCTGCA AGTCAAGGAC TAGGTTGATG
1701 ATGCCCATGA CCTGTAATTG TAAAGAAGCT TGGACATCTG CAAATGATAT
1751 TTAAACCATC TTGGCTTGTG CTTTATTCAA ACTAATGTGA AACAATAAAT
1801 TTAAATATTA TTTTTAAAAG AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 27 bp to 1391 bp; peptide length: 455
Category: strong similarity to known protein

```
  1 MAAPEEHDSP TEASQPIVEE EETKTFKDLG VTDVLCEACD QLGWTKPTKI
 51 QIEAIPLALQ GRDIIGLAET GSGKTGAFAL PILNALLETP QRLFALVLTP
101 TRELAFQISE QFEALGSSIG VQSAVIVGGI DSMSQSLALA KKPHIIIATP
151 GRLIDHLENT KGFNLRALKY LVMDEADRIL NMDFETEVDK ILKVIPRDRK
201 TFLFSATMTK KVQKLQRAAL KNPVKCAVSS KYQTVEKLQQ YYIFIPSKFK
251 DTYLVYILNE LAGNSFMIFC STCNNTQRTA LLLRNLGFTA IPLHGQMSQS
301 KRLGSLNKFK AKARSILLAT DVASRGLDIP HVDVVVNFDI PTHSKDYIHR
351 VGRTARAGRS GKAITFVTQY DVELFQRIEH LIGKKLPGFP TQDDEVMMLT
401 ERVAEAQRFA RMELREHGEK KKRSREDAGD NDDTEGAIGV RNKVAGGKMK
451 KRKGR
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_6o17, frame 3

PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans, N = 1, Score = 1497, P = 1.6e-153

PIR:S46713 hypothetical protein YHR065c - yeast (Saccharomyces cerevisiae), N = 1, Score = 1154, P = 3.6e-117

TREMBL:ATH010462_1 gene: "RH10"; product: "RNA helicase"; Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH10, N = 1, Score = 1122, P = 8.9e-114

TREMBL:AC002985_2 product: "R27090_2"; Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence., N = 1, Score = 950, P = 1.5e-95

>PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans
Length = 489

HSPs:

Score = 1497 (224.6 bits), Expect = 1.6e-153, P = 1.6e-153
Identities = 283/442 (64%), Positives = 364/442 (82%)

```
Query:    19 EEEETKTFKDLGVTDVLCEACDQLGWTKPTKIQIEAIPLALQGRDIIGLAETGSGKTGAF 78
             E+ + K+F +LGV+  LC+AC +LGW KP+KIQ  A+P ALQG+D+IGLAETGSGKTGAF
Sbjct:    39 EDVKEKSFAELGVSQPLCDACQRLGWMKPSKIQQAALPHALQGKDVIGLAETGSGKTGAF 98

Query:    79 ALPILNALLETPQRLFALVLTPTRELAFQISEQFEALGSSIGVQSAVIVGGIDSMSQSLA 138
             A+P+L +LL+ PQ  F LVLTPTRELAFQI +QFEALGS IG+ +AVIVGG+D  +Q++A
Sbjct:    99 AIPVLQSLLDHPQAFFCLVLTPTRELAFQIGQQFEALGSGIGLIAAVIVGGVDMAAQAMA 158

Query:   139 LAKKPHIIIATPGRLIDHLENTKGFNLRALKYLVMDEADRILNMDFETEVDKILKVIPRD 198
             LA++PHII+ATPGRL+DHLENTKGFNL+ALK+L+MDEADRILNMDFE E+DKILKVIPR+
Sbjct:   159 LARRPHIIVATPGRLVDHLENTKGFNLKALKFLIMDEADRILNMDFEVELDKILKVIPRE 218

Query:   199 RKTFLFSATMTKKVQKLQRAALKNPVKCAVSSKYQTVEKLQQYYIFIPSKFKDTYLVYIL 258
             R+T+LFSATMTKKV KL+RA+L++P + +VSS+Y+TV+ L+Q+YIF+P+K+K+TYLVY+L
Sbjct:   219 RRTYLFSATMTKKVSKLERASLRDPARVSVSSRYKTVDNLKQHYIFVPNKYKETYLVYLL 278

Query:   259 NELAGNSFMIFCSTCNNTQRTALLLRNLGFTAIPLHGQMSQSKRLGSLNKFKAKARSILL 318
             NE AGNS ++FC+TC  T + A++LR LG  A+PLHGQMSQ KRLGSLNKFK+KAR IL+
Sbjct:   279 NEHAGNSAIVFCATCATTMQIAVMLRQLGMQAVPLHGQMSQEKRLGSLNKFKSKAREILV 338

Query:   319 ATDVASRGLDIPHVDVVVNFDIPTHSKDYIHRVGRTARAGRSGKAITFVTQYDVELFQRI 378
              TDVA+RGLDIPHVD+V+N+D+P+ SKDY+HRVGRTARAGRSG AIT VTQYDVE +Q+I
Sbjct:   339 CTDVAARGLDIPHVDMVINYDMPSQSKDYVHRVGRTARAGRSGIAITVVTQYDVEAYQKI 398

Query:   379 EHLIGKKLPGFPTQDDEVMMLTERVAEAQRFARMELREHGEKKK-----RSREDAGDNDD 433
             E  +GKKL  +    ++EVM+L ER  EA   AR+E++E  EKKK     R  +D GD ++
Sbjct:   399 EANLGKKLDEYKCVENEVMVLVERTQEATENARIEMKEMDEKKKSGKKRRQNDDFGDTEE 458

Query:   434 TEGAIGVRNKVAGGKMKKRKGR 455
```

```
              + G   + K  GG+     GR
Sbjct:    459 SGGRFKMGIKSMGGRGGSGGGR 480
```

Pedant information for DKFZphfbr2_6o17, frame 3

Report for DKFZphfbr2_6o17.3

```
[LENGTH]        455
[MW]            50646.80
[pI]            9.18
[HOMOL]         PIR:S40731 ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans
1e-167
[FUNCAT]        04.01.04 rrna processing      [S. cerevisiae, YHR065c] 1e-127
[FUNCAT]        30.10 nuclear organization    [S. cerevisiae, YHR065c] 1e-127
[FUNCAT]        04.99 other transcription activities [S. cerevisiae, YHR169w] 2e-79
[FUNCAT]        06.10 assembly of protein complexes  [S. cerevisiae, YLL008w] 1e-71
[FUNCAT]        04.05.01.07 chromatin modification   [S. cerevisiae, YMR290c] 4e-66
[FUNCAT]        j mrna translation and ribosome biogenesis   [H. influenzae, HI0231 RNA] 1e-63
[FUNCAT]        09.01 biogenesis of cell wall       [S. cerevisiae, YJL033w] 1e-58
[FUNCAT]        04.05.03 mrna processing (splicing)  [S. cerevisiae, YDL084w] 1e-55
[FUNCAT]        05.04 translation (initiation, elongation and termination)  [S. cerevisiae,
YOR204w] 5e-55
[FUNCAT]        30.03 organization of cytoplasm      [S. cerevisiae, YOR204w] 5e-55
[FUNCAT]        1 genome replication, transcription, recombination and repair      [H.
influenzae, HI0892] 9e-48
[FUNCAT]        98 classification not yet clear-cut  [S. cerevisiae, YLR276c] 2e-45
[FUNCAT]        30.16 mitochondrial organization     [S. cerevisiae, YDR194c] 4e-42
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YGL064c] 7e-16
[FUNCAT]        03.19 recombination and dna repair   [S. cerevisiae, YMR190c] 7e-12
[FUNCAT]        11.10 cell death       [S. cerevisiae, YMR190c] 7e-12
[FUNCAT]        r general function prediction        [M. jannaschii, MJ1401] 5e-06
[BLOCKS]        BL00175B Phosphoglycerate mutase family phosphohistidine proteins
[BLOCKS]        BL00039D DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039C DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039B DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS]        BL00039A DEAD-box subfamily ATP-dependent helicases proteins
[PIRKW]         nucleus 4e-60
[PIRKW]         RNA binding 7e-69
[PIRKW]         DEAD box 7e-69
[PIRKW]         transmembrane protein 9e-41
[PIRKW]         DNA binding 3e-55
[PIRKW]         recF recombination pathway 3e-11
[PIRKW]         ATP 1e-126
[PIRKW]         purine nucleotide binding 7e-69
[PIRKW]         P-loop 1e-126
[PIRKW]         hydrolase 1e-55
[PIRKW]         protein biosynthesis 7e-69
[PIRKW]         ATP binding 3e-61
[SUPFAM]        ATP-dependent RNA helicase eIF-4A 8e-06
[SUPFAM]        WW repeat homology 4e-58
[SUPFAM]        translation initiation factor eIF-4A 7e-69
[SUPFAM]        DEAD/H box helicase homology 1e-126
[SUPFAM]        recQ helicase homology 5e-12
[SUPFAM]        ATP-dependent RNA helicase homology 8e-06
[SUPFAM]        unassigned DEAD/H box helicases 1e-126
[SUPFAM]        ATP-dependent RNA helicase DBP1 4e-60
[SUPFAM]        ATP-dependent RNA helicase DHH1 1e-58
[SUPFAM]        recQ protein 3e-11
[SUPFAM]        tobacco ATP-dependent RNA helicase DB10 4e-58
[SUPFAM]        Bloom's syndrome helicase 5e-12
[PROSITE]       DEAD_ATP_HELICASE      1
[PROSITE]       ATP_GTP_A       1
[PROSITE]       MYRISTYL        5
[PROSITE]       AMIDATION       1
[PROSITE]       CAMP_PHOSPHO_SITE      1
[PROSITE]       CK2_PHOSPHO_SITE       6
[PROSITE]       PKC_PHOSPHO_SITE       9
[PROSITE]       ASN_GLYCOSYLATION      1
[PFAM]          Helicases conserved C-terminal domain
[PFAM]          DEAD and DEAH box helicases
[KW]            Alpha_Beta
```

```
SEQ    MAAPEEHDSPTEASQPIVEEEETKTFKDLGVTDVLCEACDQLGWTKPTKIQIEAIPLALQ
PRD    cccccccccccccccchhhhhhhhhhhccccchhhhhhhhhhcccccccccccccccccc

SEQ    GRDIIGLAETGSGKTGAFALPILNALLETPQRLFALVLTPTRELAFQISEQFEALGSSIG
PRD    ccceeeeeccccccceeehhhhhhhhcccccceeeeeecchhhhhhhhhhhhhhhhhcc
```

```
SEQ      VQSAVIVGGIDSMSQSLALAKKPHIIIATPGRLIDHLENTKGFNLRALKYLVMDEADRIL
PRD      eeeeeeecchhhhhhhhhccceeeeeccccccccccccccccccceeehhhhhhhh

SEQ      NMDFETEVDKILKVIPRDRKTFLFSATMTKKVQKLQRAALKNPVKCAVSSKYQTVEKLQQ
PRD      hhcchhhhhhhhhhcccchhhhhhhhcchhhhhhhhhhhccceeeeeeecccccchhhhh

SEQ      YYIFIPSKFKDTYLVYILNELAGNSFMIFCSTCNNTQRTALLLRNLGFTAIPLHGQMSQS
PRD      hhhhhhhhhhhhhhhhhhhhhcccceeeeeeecchhhhhhhhhhhhcccceeeccccchhh

SEQ      KRLGSLNKFKAKARSILLATDVASRGLDIPHVDVVVNFDIPTHSKDYIHRVGRTARAGRS
PRD      hhhhhhhhhhhhhhhcchhhhhhhhcccccceeeeeecccccccceeeeecccccccccc

SEQ      GKAITFVTQYDVELFQRIEHLIGKKLPGFPTQDDEVMMLTERVAEAQRFARMELREHGEK
PRD      cceeeeeecchhhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ      KKRSREDAGDNDDTEGAIGVRNKVAGGKMKKRKGR
PRD      hhhhccccccccccccccccccccccccccccccc
```

Prosite for DKFZphfbr2_6o17.3

PS00001	274->278	ASN_GLYCOSYLATION	PDOC00001
PS00004	421->425	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	25->28	PKC_PHOSPHO_SITE	PDOC00005
PS00005	72->75	PKC_PHOSPHO_SITE	PDOC00005
PS00005	209->212	PKC_PHOSPHO_SITE	PDOC00005
PS00005	229->232	PKC_PHOSPHO_SITE	PDOC00005
PS00005	276->279	PKC_PHOSPHO_SITE	PDOC00005
PS00005	300->303	PKC_PHOSPHO_SITE	PDOC00005
PS00005	354->357	PKC_PHOSPHO_SITE	PDOC00005
PS00005	360->363	PKC_PHOSPHO_SITE	PDOC00005
PS00005	400->403	PKC_PHOSPHO_SITE	PDOC00005
PS00006	9->13	CK2_PHOSPHO_SITE	PDOC00006
PS00006	25->29	CK2_PHOSPHO_SITE	PDOC00006
PS00006	186->190	CK2_PHOSPHO_SITE	PDOC00006
PS00006	368->372	CK2_PHOSPHO_SITE	PDOC00006
PS00006	391->395	CK2_PHOSPHO_SITE	PDOC00006
PS00006	424->428	CK2_PHOSPHO_SITE	PDOC00006
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	116->122	MYRISTYL	PDOC00008
PS00008	120->126	MYRISTYL	PDOC00008
PS00008	128->134	MYRISTYL	PDOC00008
PS00009	382->386	AMIDATION	PDOC00009
PS00017	68->76	ATP_GTP_A	PDOC00017
PS00039	172->181	DEAD_ATP_HELICASE	PDOC00039

Pfam for DKFZphfbr2_6o17.3

```
HMM_NAME    DEAD and DEAH box helicases

HMM             *gLpPWILRnIyeMGFEkPTPIQQqAIPiILeGRDVMACAQTGSGKTAAF
                 G ++ ++++++++G++KPT+IQ +AIP++L+GRD+++ A TGSGKT+AF
Query        30  GVTDVLCEACDQLGWTKPTKIQIEAIPLALQGRDIIGLAETGSGKTGAF    78

HMM             lIPMLQHIDwdPWpqpPQdPrALILAPTRELAMQIQEEcRkFgkHMngIR
                ++P+L  ++++P       + ++AL+L+PTRELA QI+E+++++G++++ ++
Query        79 ALPILNALLETP----QR-LFALVLTPTRELAFQISEQFEALGSSIG-VQ   122

HMM             ImcIYGGtnMRdQMRmLeRGpPHIVIATPGRLIDHIER.gtldLDrIeML
                +++I+GG + + Q   L+++P HI+IATPGRLIDH+E+   ++L+++++L
Query       123 SAVIVGGIDSMSQSLALAKKP-HIIIATPGRLIDHLENTKGFNLRALKYL   171

HMM             VMDEADRMLDMGFIDQIRrIMrqIPMpwNRQTMMFSATMPdeIqELARrF
                VMDEADR+L+M+F+ ++++I++ IP  ++R T +FSATM++++Q+L+R+
Query       172 VMDEADRILNMDFETEVDKILKVIP--RDRKTFLFSATMTKKVQKLQRAA   219

HMM             MRNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdcLcrLIe*
                ++NP+  ++ ++++T++  ++Q+YI+++  + K  +L+++++
Query       220 LKNPVKCAVSSKYQTVE-KLQQYYIFIP-SKFKDTYLVYILN    259


HMM_NAME    Helicases conserved C-terminal domain

HMM             *EileeWLknlGIrvmYIHGdMpQeERdeIMddFNnGEynVLIcTDVggR
```

```
                 ++ +  L+NLG++++ +HG+M+Q +R+  +++F++     +L++TDV++R
Query      277  QRTALLLRNLGFTAIPLHGQMSQSKRLGSLNKFKAKARSILLATDVASR   325

HMM             GIDIPdVNHVINYDMPWNPEqYIQRIGRTgRIG*
                G+DIP V++V+N+D+P ++ +YI+R+GRT+R+G
Query      326  GLDIPHVDVVVNFDIPTHSKDYIHRVGRTARAG    358
```

DKFZphfbr2_71o20
----

group: brain derived

DKFZphfbr2_71o20 encodes a novel 232 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits
on genomic level encoded by AC006186 (3 exons)

Sequenced by GBF

Locus: /map="10q22.1"

Insert length: 1768 bp
Poly A stretch at pos. 1742, polyadenylation signal at pos. 1726

```
   1 GGGGGCAGCA GGCCAAGGGG GAGGTGCGAG CGTGGACCTG GGACGGGTCT
  51 GGGCGGCTCT CGGTGGTTGG CACGGGTTCG CACACCCATT CAAGCGGCAG
 101 GACGCACTTG TCTTAGCAGT TCTCGCTGAC CGCGCTAGCT GCGGCTTCTA
 151 CGCTCCGGCA CTCTGAGTTC ATCAGCAAAC GCCCTGGCGT CTGTCCTCAC
 201 CATGCCTAGC CTTTGGGACC GCTTCTCGTC GTCGTCCACC TCCTCTTCGC
 251 CCTCGTCCTT GCCCCGAACT CCCACCCCAG ATCGGCCGCC GCGCTCAGCC
 301 TGGGGGTCGG CGACCCGGGA GGAGGGGTTT GACCGCTCCA CGAGCCTGGA
 351 GAGCTCGGAC TGCGAGTCCC TGGACAGCAG CAACAGTGGC TTCGGGCCGG
 401 AGGAAGACAC GGCTTACCTG GATGGGGTGT CGTTGCCCGA CTTCGAGCTG
 451 CTCAGTGACC CTGAGGATGA ACACTTGTGT GCCAACCTGA TGCAGCTGCT
 501 GCAGGAGAGC CTGGCCCAGG CGCGGCTGGG CTCTCGACGC CCTGCGCGCC
 551 TGCTGATGCC TAGCCAGTTG GTAAGCCAGG TGGGCAAAGA ACTACTGCGC
 601 CTGGCCTACA GCGAGCCGTG CGGCCTGCGG GGGGCGCTGC TGGACGTCTG
 651 CGTGGAGCAG GGCAAGAGCT GCCACAGCGT GGGCCAGCTG GCACTCGACC
 701 CCAGCCTGGT GCCCACCTTC CAGCTGACCC TCGTGCTGCG CCTGGACTCA
 751 CGACTCTGGC CCAAGATCCA GGGGCTGTTT AGCTCCGCCA ACTCTCCCTT
 801 CCTCCCTGGC TTCAGCCAGT CCCTGACGCT GAGCACTGGC TTCCGAGTCA
 851 TCAAGAAGAA GCTGTACAGC TCGGAACAGC TGCCCATTGA GGAGTGTTGA
 901 ACTTCAACCT GAGGGGGCCG ACAGTGCCCT CCAAGACAGA GACGACTGAA
 951 CTTTTGGGGT GGAGACTAGA GGCAGGAGCT GAGGGACTGA TTCCAGTGGT
1001 TGGAAAACTG AGGCAGCCAC CTAAAGTGGA GGTGGGGGAA TAGTGTTTCC
1051 CAGGAAGCTC ATTGAGTTGT GTGCGGGTGG CTGTGCATTG GGGACACATA
1101 CCCCTCAGTA CTGTAGCATG AAACAAAGGC TTAGGGGCCA ACAAGGCTTC
1151 CAGCTGGATG TGTGTGTAGC ATGTACCTTA TTATTTTTGT TACTGACAGT
1201 TAACAGTGGT GTGACATCCA GAGAGCAGCT GGGCTGCTCC CGCCCCAGCC
1251 TGGCCCAGGG TGAAGGAAGA GGCACGTGCT CCTCAGAGCA GCCGGAGGGA
1301 AGGGGGAGGT CGGAGGTCGT GGAGGTGGTT TGTGTATCTT ACTGGTCTGA
1351 AGGGACCAAG TGTGTTTGTT GTTTGTTTTG TATCTTGTTT TTCTGATCGG
1401 AGCATCACTA CTGACCTGTT GTAGGCAGCT ATCTTACAGA CGCATGAATG
1451 TAAGAGTAGG AAGGGGTGGG TGTCAGGGAT CACTTGGGAT CTTTGACACT
1501 TGAAAAATTA CACCTGGCAG CTGCGTTTAA GCCTTCCCCC ATCGTGTACT
1551 GCAGAGTTGA GCTGGCAGGG GAGGGGCTGA GAGGGTGGGG GCTGGAACCC
1601 CTTCCCGGGA GGAGTGCCAT CTGGGTCTTC CATCTAGAAC TGTTTACATG
1651 AAGATAAGAT ACTCACTGTT CATGAATACA CTTGATGTTC AAGTATTAAG
1701 ACCTATGCAA TATTTTTTAC TTTTCTAATA AACATGTTTG TTAAAACAAA
1751 AAAAAAAAAA AAAAAAAA
```

BLAST Results

Entry AC006186 from database EMBLNEW:
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1; HTGS phase 1, 4 unordered pieces.
Score = 6512, P = 0.0e+00, identities = 1326/1345
3 exons

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 202 bp to 897 bp; peptide length: 232
Category: putative protein

```
  1 MPSLWDRFSS SSTSSSPSSL PRTPTPDRPP RSAWGSATRE EGFDRSTSLE
 51 SSDCESLDSS NSGFGPEEDT AYLDGVSLPD FELLSDPEDE HLCANLMQLL
101 QESLAQARLG SRRPARLLMP SQLVSQVGKE LLRLAYSEPC GLRGALLDVC
151 VEQGKSCHSV GQLALDPSLV PTFQLTLVLR LDSRLWPKIQ GLFSSANSPF
201 LPGFSQSLTL STGFRVIKKK LYSSEQLPIE EC
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_71o20, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_71o20, frame 1

Report for DKFZphfbr2_71o20.1

```
[LENGTH]     232
[MW]         25354.60
[pI]         4.87
[PROSITE]    MYRISTYL      2
[PROSITE]    CK2_PHOSPHO_SITE     6
[PROSITE]    GLYCOSAMINOGLYCAN    1
[PROSITE]    PKC_PHOSPHO_SITE     1
[KW]         All_Alpha
[KW]         LOW_COMPLEXITY    17.67 %
```

```
SEQ  MPSLWDRFSSSSTSSSPSSLPRTPTPDRPPRSAWGSATREEGFDRSTSLESSDCESLDSS
SEG  .......xxxxxxxxxxxxxxxxxxxxxxx............xxxxxxxxxxxxxx
PRD  cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ  NSGFGPEEDTAYLDGVSLPDFELLSDPEDEHLCANLMQLLQESLAQARLGSRRPARLLMP
SEG  xx..........................................................
PRD  cccccccccccccccccccceeecccccchhhhhhhhhhhhhhhhhcccccccceeecc

SEQ  SQLVSQVGKELLRLAYSEPCGLRGALLDVCVEQGKSCHSVGQLALDPSLVPTFQLTLVLR
SEG  ............................................................
PRD  cccchhhhhhhhhhhcccccchhhhhhhhcccccccccccccccccccccchhhhhhccc

SEQ  LDSRLWPKIQGLFSSANSPFLPGFSQSLTLSTGFRVIKKKLYSSEQLPIEEC
SEG  ....................................................
PRD  cccccccccccccccccccccccccccceeeecccccccccccccccccccc
```

Prosite for DKFZphfbr2_71o20.1

PS00002	62->66	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	111->114	PKC_PHOSPHO_SITE	PDOC00005
PS00006	3->7	CK2_PHOSPHO_SITE	PDOC00006
PS00006	38->42	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	52->56	CK2_PHOSPHO_SITE	PDOC00006
PS00006	77->81	CK2_PHOSPHO_SITE	PDOC00006
PS00006	85->89	CK2_PHOSPHO_SITE	PDOC00006
PS00008	141->147	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_71o20.1)

DKFZphfbr2_72b18
----

group: nucleic acid management

DKFZphfbr2_72b18 encodes a novel 715 amino acid protein with similarity to E. coli DNA-damage-inducibile protein dinP and other proteins induced by DNA-damage.

The novel protein is similar to dinP of E. coli, yqjH of B. subtilis, dinP of M. tuberculosis and T19K24.15 of A. thaliana. The dinB/P pathway is a second SOS-pathway in E. coli. Therefore the new gene seems to be involved in DNA repair.

The new protein can find application in modulating DNA repair and mutagenesis.

similarity to DNA damage induced genes

complete cDNA, complete cds, potential start at Bp 49, EST hits
localisation primer site B is missing!

Sequenced by LMU

Locus: /map="416.0 cR from top of Chr18 linkage group"??

Insert length: 2475 bp
Poly A stretch at pos. 2452, polyadenylation signal at pos. 2431

```
   1 GGGGGAGGAA GGCGGCGGCG ACGACGAGGA AGACGCCGAG GCCTGGGCCA
  51 TGGAACTGGC GGACGTGGGG GCGGCAGCCA GCTCGCAGGG AGTTCATGAT
 101 CAAGTGTTGC CCACACCAAA TGCTTCATCC AGAGTCATAG TACATGTGGA
 151 TCTGGATTGC TTTTATGCAC AAGTAGAAAT GATCTCAAAT CCAGAGCTAA
 201 AAGACAAACC TTTAGGGGTT CAACAGAAAT ATTTGGTGGT TACCTGCAAC
 251 TATGAAGCTA GGAAACTTGG AGTTAAGAAA CTTATGAATG TCAGAGATGC
 301 AAAAGAAAAG TGTCCACAGT TGGTATTAGT TAATGGAGAA GACCTGACCC
 351 GCTACAGAGA AATGTCTTAT AAGGTTACAG AATTACTGGA AGAATTTAGT
 401 CCAGTTGTTG AGAGACTTGG ATTTGATGAA AATTTTGTGG ATCTAACAGA
 451 AATGGTTGAG AAGAGACTAC AGCAGCTGCA AAGTGATGAA CTTTCTGCGG
 501 TGACTGTGTC GGGTCATGTA TACAATAATC AGTCTATAAA CCTGCTTGAC
 551 GTCTTGCACA TCAGACTACT TGTTGGATCT CAGATTGCAG CAGAGATGCG
 601 GGAAGCCATG TATAATCAGT TGGGGCTCAC TGGCTGTGCT GGAGTGGCTT
 651 CTAATAAACT GTTGGCAAAA TTAGTTTCTG GTGTCTTTAA ACCAAATCAA
 701 CAAACAGTCT TATTACCTGA AAGTTGTCAA CATCTTATTC ATAGTTTGAA
 751 TCACATAAAG GAAATACCTG GTATTGGCTA TAAAACTGCC AAATGTCTTG
 801 AAGCACTGGG TATCAATAGT GTGCGTGATC TCCAAACCTT TTCACCCAAA
 851 ATTTTAGAAA AAGAATTAGG AATTTCAGTT GCTCAGCGTA TCCAAAAGCT
 901 CAGTTTTGGA GAGGATAACT CCCCTGTGAT ACTCTCAGGA CCACCTCAGT
 951 CCTTTAGTGA AGAAGATTCA TTTAAAAAAT GTACATCTGA AGTTGAAGCT
1001 AAAAATAAGA TTGAAGAACT ACTTGCTAGT CTTTTAAACA GAGTATGCCA
1051 AGATGGAAGG AAGCCTCATA CAGTGAGATT AATAATCCGT CGGTATTCCT
1101 CTGAGAAGCA CTATGGTCGT GAGAGTCGTC AGTGCCCTAT TCCTTCACAT
1151 GTAATTCAGA AATTAGGGAC AGGAAATTAT GATGTGATGA CCCCAATGGT
1201 TGATATACTT ATGAAACTTT TTCGAAATAT GGTGAATGTG AAGATGCCAT
1251 TTCACCTTAC CCTTCTAAGT GTGTGCTTCT GCAACCTTAA AGCACTAAAT
1301 ACTGCTAAGA AAGGGCTTAT TGATTATTAT TTAATGCCAT CATTATCAAC
1351 TACTTCACGC TCTGGCAAGC ACAGTTTTAA AATGAAAGAC ACTCATATGG
1401 AAGATTTTCC CAAAGACAAA GAAACAAACC GGGATTTCCT ACCAAGTGGA
1451 AGAATTGAAA GTACAAGAAC TAGGGAGTCT CCACTAGATA CCACAAATTT
1501 TTCTAAAGAA AAAGACATTA ATGAATTCCC ACTCTGTTCA CTTCCTGAAG
1551 GTGTTGACCA AGAAGTCTCC AAGCAGCTTC CAGTAGATAT TCAAGAAGAA
1601 ATCCTTTCTG GAAAATCTAG GGAAAAATTT CAAGGGAAAG GAAGTGTGAG
1651 TTGTCCATTA CATGCCTCTA GAGGAGTATT ATCTTTCTTT TCTAAAAAAC
1701 AAATGCAAGA TATTCCCATA AATCCTAGAG ATCATTTATC CAGTAGCAAA
1751 CAGGTATCCT CTGTATCTCC TTGTGAACCG GGAACATCAG GCTTTAATAG
1801 CAGTAGTTCT TCTTACATGT CTAGCCAAAA GGATTATTCA TATTATTTAG
1851 ATAATAGATT AAAAGATGAA CGAATAAGTC AAGGACCTAA AGAACCTCAA
1901 GGATTCCACT TTACAAATTC AAACCCTGCT GTGTCTGCTT TTCATTCATT
1951 TCCAAACTTG CAGAGTGAGC AACTTTTCTC CAGAAACCAC ACTACAGATA
2001 GCCATAAGCA AACAGTAGCA ACAGACTCTC ATGAAGGACT TACAGAAAAT
2051 AGAGAGCCAG ATTCTGTTGA TGAGAAAATT ACTTTCCCTT CTGACATTGA
2101 TCCTCAAGTT TTCTATGAAC TACCAGAAGC AGTACAAAAG GAACTGCTGG
2151 CAGAGTGGAA GAGAACAGGA TCAGATTTCC ACATTGGACA TAAATAAGCA
2201 TATTCAGCAA AAAGGTCTGA AAAGCAAGGG AATACCATTA TTTTCGGATT
2251 AGCGGTTTAT TAAGCTCTTC TATATTAAAC ACTAATAGAT ATTCAATAAC
2301 GGAGTAAACT GTTCCAGATA AAGCAAGAAT AGTTGCAAGA AGTAAATTCT
2351 GGCACAAAGC GTAAAAATAT AACAGAAGAA ATAATGTAAA ATACTATCTT
2401 TTATGTCTAA AGCCATTTTA TATTACTTTT CAATAAAAAG AATATCATGG
2451 TCAAAAAAAA AAAAAAAAAA AAAAC
```

BLAST Results

Entry HS086339 from database EMBL:
human STS WI-11064.
Score = 1523, P = 3.0e-64, identities = 327/343

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 50 bp to 2194 bp; peptide length: 715
Category: similarity to known protein

```
  1 MELADVGAAA SSQGVHDQVL PTPNASSRVI VHVDLDCFYA QVEMISNPEL
 51 KDKPLGVQQK YLVVTCNYEA RKLGVKKLMN VRDAKEKCPQ LVLVNGEDLT
101 RYREMSYKVT ELLEEFSPVV ERLGFDENFV DLTEMVEKRL QQLQSDELSA
151 VTVSGHVYNN QSINLLDVLH IRLLVGSQIA AEMREAMYNQ LGLTGCAGVA
201 SNKLLAKLVS GVFKPNQQTV LLPESCQHLI HSLNHIKEIP GIGYKTAKCL
251 EALGINSVRD LQTFSPKILE KELGISVAQR IQKLSFGEDN SPVILSGPPQ
301 SFSEEDSFKK CTSEVEAKNK IEELLASLLN RVCQDGRKPH TVRLIIRRYS
351 SEKHYGRESR QCPIPSHVIQ KLGTGNYDVM TPMVDILMKL FRNMVNVKMP
401 FHLTLLSVCF CNLKALNTAK KGLIDYYLMP SLSTTSRSGK HSFKMKDTHM
451 EDFPKDKETN RDFLPSGRIE STRTRESPLD TTNFSKEKDI NEFPLCSLPE
501 GVDQEVSKQL PVDIQEEILS GKSREKFQGK GSVSCPLHAS RGVLSFFSKK
551 QMQDIPINPR DHLSSSKQVS SVSPCEPGTS GFNSSSSSYM SSQKDYSYYL
601 DNRLKDERIS QGPKEPQGFH FTNSNPAVSA FHSFPNLQSE QLFSRNHTTD
651 SHKQTVATDS HEGLTENREP DSVDEKITFP SDIDPQVFYE LPEAVQKELL
701 AEWKRTGSDF HIGHK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72b18, frame 2

PIR:H64747 DNA-damage-inducibile protein dinP - Escherichia coli, N = 2, Score = 212, P = 4.2e-27

PIR:H69963 DNA-damage repair protein homolog yqjH - Bacillus subtilis, N = 2, Score = 230, P = 5.2e-26

>PIR:H69963 DNA-damage repair protein homolog yqjH - Bacillus subtilis
Length = 414

HSPs:

Score = 230 (34.5 bits), Expect = 5.2e-26, Sum P(2) = 5.2e-26
Identities = 47/112 (41%), Positives = 73/112 (65%)

```
Query:    27 SRVIVHVDLDCFYAQVEMISNPELKDKPLGV-----QQKYLVVTCNYEARKLGVKKLMNV 81
             SR+I H+D++ FYA VEM  +P L+ KP+ V     ++K +VVTC+YEAR  GVK  M V
Sbjct:     5 SRIIFHIDMNSFYASVEMAYDPALRGKPVAVAGNVKERKGIVVTCSYEARARGVKTTMPV 64

Query:    82 RDAKEKCPQLVLVNGEDLTRYREMSYKVTELLEEFSPVVERLGFDENFVDLTE 134
               AK  CP+L+++    +  RYR  S  +  +L E++ +VE +  DE ++D+T+
Sbjct:    65 WQAKRHCPELIVLP-PNFDRYRNSSRAMFTILREYTDLVEPVSIDEGYMDMTD 116
```

Score = 137 (20.6 bits), Expect = 5.2e-26, Sum P(2) = 5.2e-26
Identities = 43/148 (29%), Positives = 75/148 (50%)

```
Query:   178 QIAAEMREAMYNQLGLTGCAGVASNKLLAKLVSGVFKPNQQTVLLPESCQHLIHSLNHIK 237
             + A E++  +  +L L    G+A NK LAK+ S + KP    T+L        ++  L  +
Sbjct:   125 ETAKEIQSRLQKELLLPSSIGIAPNKFLAKMASDMKKPLGITILRKRQVPDILWPLP-VG 183

Query:   238 EIPGIGYKTAKCLEALGINSVRDLQTFSPKILEKELGISVAQRIQKLSFGEDNSPVILSG 297
             E+ G+G KTA+ L+ LGI+++ +L         L++ LGI+   R++  + G  ++PV
Sbjct:   184 EMHGVGKKTAEKLKGLGIHTIGELAAADEHSLKRLLGIN-GPRLKNKANGIHHAPV---- 238

Query:   298 PPQSFSEEDSFKKCTSEVEAKNKIEELL 325
               P+   E  S    ++      +  EELL
```

```
Sbjct:   239 DPERIYEFKSVGNSSTLSHDSSDEEELL 266
```

Pedant information for DKFZphfbr2_72b18, frame 2

Report for DKFZphfbr2_72b18.2

```
[LENGTH]        715
[MW]            80300.63
[pI]            6.37
[HOMOL]         TREMBL:SPBC16A3_11 gene: "SPBC16A3.11"; product: "hypothetical protein";
S.pombe chromosome II cosmid c16A3. 5e-30
[FUNCAT]        11.04 dna repair (direct repair, base excision repair and nucleotide excision
repair)         [S. cerevisiae, YDR419w] 2e-15
[FUNCAT]        1 genome replication, transcription, recombination and repair      [M.
genitalium, MG360] 3e-13
[PIRKW]         SOS mutagenesis 2e-11
[PIRKW]         DNA repair 2e-11
[PIRKW]         induced mutagenesis 2e-11
[SUPFAM]        umuC protein 3e-29
[PROSITE]       MYRISTYL        6
[PROSITE]       AMIDATION       1
[PROSITE]       CAMP_PHOSPHO_SITE       2
[PROSITE]       CK2_PHOSPHO_SITE        15
[PROSITE]       PROKAR_LIPOPROTEIN      1
[PROSITE]       TYR_PHOSPHO_SITE        2
[PROSITE]       PKC_PHOSPHO_SITE        21
[PROSITE]       ASN_GLYCOSYLATION       5
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY     4.20 %

SEQ     MELADVGAAASSQGVHDQVLPTPNASSRVIVHVDLDCFYAQVEMISNPELKDKPLGVQQK
SEG     ............................................................
PRD     ccceeeeeeecccccceeecccccccceeeeeeecccchhhhhhhhccccccccceeeecc

SEQ     YLVVTCNYEARKLGVKKLMNVRDAKEKCPQLVLVNGEDLTRYREMSYKVTELLEEFSPVV
SEG     ............................................................
PRD     ceeeehhhhhhhhhhhccccchhhhhhhhcccceeeecccccchhhhhhhhhhhhhhhccce

SEQ     ERLGFDENFVDLTEMVEKRLQQLQSDELSAVTVSGHVYNNQSINLLDVLHIRLLVGSQIA
SEG     ............................................................
PRD     eeecccchhhhhhhhhhhhhhhhhhhcccccceeeeeccccccchhhhhhhhhhhhhhhhh

SEQ     AEMREAMYNQLGLTGCAGVASNKLLAKLVSGVFKPNQQTVLLPESCQHLIHSLNHIKEIP
SEG     ............................................................
PRD     hhhhhhhhhhhcceeeeecccchhhhhhhhhhhhhccccceeeeeecchhhhhhhhhcccccc

SEQ     GIGYKTAKCLEALGINSVRDLQTFSPKILEKELGISVAQRIQKLSFGEDNSPVILSGPPQ
SEG     ............................................................
PRD     ccchhhhhhhhhhccccchhhhhhhhhhhhhhhcchhhhhhhhhhcccccceeeecccccc

SEQ     SFSEEDSFKKCTSEVEAKNKIEELLASLLNRVCQDGRKPHTVRLIIRRYSSEKHYGRESR
SEG     ............................................................
PRD     ccccccccccchhhhhhhhhhhhhhhhhhhhhhhhcccccccceeeehhhhhhhhhhhcccc

SEQ     QCPIPSHVIQKLGTGNYDVMTPMVDILMKLFRNMVNVKMPFHLTLLSVCFCNLKALNTAK
SEG     ............................................................
PRD     ccccccceeeeccccccccchhhhhhhhhhhhhhhhcccceeeeeeeeeechhhhhhhhh

SEQ     KGLIDYYLMPSLSTTSRSGKHSFKMKDTHMEDFPKDKETNRDFLPSGRIESTRTRESPLD
SEG     ............................................................
PRD     hhhheeeccccccccccccccceeecccccccccccccccccccccccccccccccccccc

SEQ     TTNFSKEKDINEFPLCSLPEGVDQEVSKQLPVDIQEEILSGKSREKFQGKGSVSCPLHAS
SEG     ............................................................
PRD     ccccccccccccccccccchhhhhhhhhhhhhhhhhhhccccceeeeeccccccccchhhh

SEQ     RGVLSFFSKKQMQDIPINPRDHLSSSKQVSSVSPCEPGTSGFNSSSSSYMSSQKDYSYYL
SEG     ......................xxxxxxxxxx......xxxxxxxxxxxxxxxxxxx.
PRD     hccccccccccccccccccccccccccccccccccccccccccccccccccccchhhhh

SEQ     DNRLKDERISQGPKEPQGFHFTNSNPAVSAFHSFPNLQSEQLFSRNHTTDSHKQTVATDS
SEG     ............................................................
PRD     hhhhhhhhhhcccccccceeeeccccceeeccccccccchhhhhhhcccccceeeeeecc

SEQ     HEGLTENREPDSVDEKITFPSDIDPQVFYELPEAVQKELLAEWKRTGSDFHIGHK
SEG     .......................................................
PRD     cccccccccccccccccccccccceeehhhhhhhhhhhhhhhhhcccccccccc
```

Prosite for DKFZphfbr2_72b18.2

PS00001	24->28	ASN_GLYCOSYLATION	PDOC00001
PS00001	160->164	ASN_GLYCOSYLATION	PDOC00001
PS00001	483->487	ASN_GLYCOSYLATION	PDOC00001
PS00001	583->587	ASN_GLYCOSYLATION	PDOC00001
PS00001	646->650	ASN_GLYCOSYLATION	PDOC00001
PS00004	309->313	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	347->351	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	106->109	PKC_PHOSPHO_SITE	PDOC00005
PS00005	201->204	PKC_PHOSPHO_SITE	PDOC00005
PS00005	246->249	PKC_PHOSPHO_SITE	PDOC00005
PS00005	257->260	PKC_PHOSPHO_SITE	PDOC00005
PS00005	265->268	PKC_PHOSPHO_SITE	PDOC00005
PS00005	307->310	PKC_PHOSPHO_SITE	PDOC00005
PS00005	341->344	PKC_PHOSPHO_SITE	PDOC00005
PS00005	351->354	PKC_PHOSPHO_SITE	PDOC00005
PS00005	418->421	PKC_PHOSPHO_SITE	PDOC00005
PS00005	435->438	PKC_PHOSPHO_SITE	PDOC00005
PS00005	438->441	PKC_PHOSPHO_SITE	PDOC00005
PS00005	442->445	PKC_PHOSPHO_SITE	PDOC00005
PS00005	459->462	PKC_PHOSPHO_SITE	PDOC00005
PS00005	466->469	PKC_PHOSPHO_SITE	PDOC00005
PS00005	471->474	PKC_PHOSPHO_SITE	PDOC00005
PS00005	520->523	PKC_PHOSPHO_SITE	PDOC00005
PS00005	548->551	PKC_PHOSPHO_SITE	PDOC00005
PS00005	565->568	PKC_PHOSPHO_SITE	PDOC00005
PS00005	592->595	PKC_PHOSPHO_SITE	PDOC00005
PS00005	651->654	PKC_PHOSPHO_SITE	PDOC00005
PS00006	46->50	CK2_PHOSPHO_SITE	PDOC00006
PS00006	257->261	CK2_PHOSPHO_SITE	PDOC00006
PS00006	285->289	CK2_PHOSPHO_SITE	PDOC00006
PS00006	301->305	CK2_PHOSPHO_SITE	PDOC00006
PS00006	303->307	CK2_PHOSPHO_SITE	PDOC00006
PS00006	313->317	CK2_PHOSPHO_SITE	PDOC00006
PS00006	448->452	CK2_PHOSPHO_SITE	PDOC00006
PS00006	459->463	CK2_PHOSPHO_SITE	PDOC00006
PS00006	477->481	CK2_PHOSPHO_SITE	PDOC00006
PS00006	497->501	CK2_PHOSPHO_SITE	PDOC00006
PS00006	573->577	CK2_PHOSPHO_SITE	PDOC00006
PS00006	592->596	CK2_PHOSPHO_SITE	PDOC00006
PS00006	672->676	CK2_PHOSPHO_SITE	PDOC00006
PS00006	681->685	CK2_PHOSPHO_SITE	PDOC00006
PS00006	706->710	CK2_PHOSPHO_SITE	PDOC00006
PS00007	101->108	TYR_PHOSPHO_SITE	PDOC00007
PS00007	348->356	TYR_PHOSPHO_SITE	PDOC00007
PS00008	7->13	MYRISTYL	PDOC00008
PS00008	176->182	MYRISTYL	PDOC00008
PS00008	192->198	MYRISTYL	PDOC00008
PS00008	198->204	MYRISTYL	PDOC00008
PS00008	274->280	MYRISTYL	PDOC00008
PS00008	663->669	MYRISTYL	PDOC00008
PS00009	335->339	AMIDATION	PDOC00009
PS00013	186->197	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphfbr2_72b18.2)

DKFZphfbr2_72d13
----

group: brain derived

DKFZphfbr2_72d13 encodes a novel 165 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

seems to be testis specific 9 of 10 EST hits are from testis librarys

Sequenced by LMU

Locus: unknown

Insert length: 723 bp
Poly A stretch at pos. 704, no polyadenylation signal found

```
  1 AGGGGGGGTA TGGGGGAGGG GGAGACTCTG CAGGAGCCTA ATTCCCCACT
 51 CTGAGCTCAC CCTTCTGTCT GCCCGGGCCC TACCCCTTCC CCTACTCTCA
101 CCCTTATAAT CCTTTTCAGC ACTAGGTCTT CCCGTCACCT CCACCTCTCT
151 CCATGACCCG GCTCTGCTTA CCCAGACCCG AAGCACGTGA GGATCCGATC
201 CCAGTTCCTC CAAGGGGCCT GGGTGCTGGG GAGGGGTCAG GTAGTCCAGT
251 GCGTCCACCT GTATCCACCT GGGGCCCTAG CTGGGCCCAG CTCCTGGACA
301 GTGTCCTATG GCTGGGGGCA CTAGGACTGA CAATCCAGGC AGTCTTTTCC
351 ACCACTGGCC CAGCCCTGCT GCTGCTTCTG GTCAGCTTCC TCACCTTTGA
401 CCTGCTCCAT AGGCCCGCAG GTCACACTCT GCCACAGCGC AAACTTCTCA
451 CCAGGGGCCA GAGTCAGGGG GCCGGTGAAG GTCCTGGACA GCAGGAGGCT
501 CTACTCCTGC AAATGGGTAC AGTCTCAGGA CAACTTAGCC TCCAGGACGC
551 ACTGCTGCTG CTGCTCATGG GGCTGGGCCC GCTCCTGAGA GCCTGTGGCA
601 TGCCCTTGAC CCTGCTTGGC CTGGCTTTCT GCCTCCATCC TTGGGCCTGA
651 GAGCCCCTCC CCACAACTCA GTGTCCTTCA AATATACAAT GACCACCCTT
701 CTTCAAAAAA AAAAAAAAAA AAC
```

BLAST Results

Entry HS860F19 from database EMBLNEW:
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 860F19
Score = 2059, P = 1.1e-85, identities = 423/434
2 exons

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 153 bp to 647 bp; peptide length: 165
Category: putative protein
Classification: no clue

```
  1 MTRLCLPRPE AREDPIPVPP RGLGAGEGSG SPVRPPVSTW GPSWAQLLDS
 51 VLWLGALGLT IQAVFSTTGP ALLLLLVSFL TFDLLHRPAG HTLPQRKLLT
101 RGQSQGAGEG PGQQEALLLQ MGTVSGQLSL QDALLLLLMG LGPLLRACGM
151 PLTLLGLAFC LHPWA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72d13, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_72d13, frame 3

Report for DKFZphfbr2_72d13.3

```
[LENGTH]        165
[MW]            17393.73
[pI]            7.80
[BLOCKS]        BL00068A Malate dehydrogenase proteins
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY     29.70 %

SEQ      MTRLCLPRPEAREDPIPVPPRGLGAGEGSGSPVRPPVSTWGPSWAQLLDSVLWLGALGLT
SEG      ............................................................
PRD      cccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhcccccc
MEM      ............................................................

SEQ      IQAVFSTTGPALLLLLVSFLTFDLLHRPAGHTLPQRKLLTRGQSQGAGEGPGQQEALLLQ
SEG      ...........xxxxxxxxxxxxxx................xxxxxxxxxxxxxxx....
PRD      eeeecccccchhhhhhhhhhhhhcccccccccccccccccccccccccccccchhhhhhhh
MEM      ........MMMMMMMMMMMMMMMMM...................................

SEQ      MGTVSGQLSLQDALLLLLMGLGPLLRACGMPLTLLGLAFCLHPWA
SEG      .....xxxxxxxxxxxxxxxxxxxx....................
PRD      hccccccchhhhhhhhhhhhhhhcchhhhcccccchhhhhccccc
MEM      .............MMMMMMMMMMMMMMMMM...............
```

(No Prosite data available for DKFZphfbr2_72d13.3)

(No Pfam data available for DKFZphfbr2_72d13.3)

DKFZphfbr2_72112

group: nucleic acid management

Summary DKFZphfbr2_72112 encodes a novel 344 amino acid protein with similarity to YDR126w and other S. cerevisiae proteins.

The novel protein contains a myc-type, helix-loop-helix dimerization domain signature. This helix-loop-helix domain mediates protein dimerization and has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers. Therefore, the protein could be a novel DNA-binding protein.

The new protein can application in modulating gene expression.

similarity to YDR126w ;
membrane regions: 2

similarity to YDR126w

complete cDNA complete cds, EST hits

Sequenced by LMU

Locus: unknown

Insert length: 1270 bp
Poly A stretch at pos. 1251, no polyadenylation signal found

```
   1 GGGGGCGCCC GGGAGGCGCC GGAGCCCAGC GGCTGGCGCC AGATCCAGGC
  51 TCCTGGAAGA ACCATGTCCG GCAGCTACTG GTCATGCCAG GCACACACTG
 101 CTGCCCAAGA GGAGCTGCTG TTTGAATTAT CTGTGAATGT TGGGAAGAGG
 151 AATGCCAGAG CTGCCGGCTG AAAATTACCC AACCAAGAGA AATCTGCAGG
 201 ATGGACTTTC TGGTCCTCTT CTTGTTCTAC CTGGCTTCGG TGCTGATGGG
 251 TCTTGTTCTT ATCTGCGTCT GCTCGAAAAC CCATAGCTTG AAAGGCCTGG
 301 CCAGGGGAGG AGCACAGATA TTTTCCTGTA TAATTCCAGA ATGTCTTCAG
 351 AGAGCCGTGC ATGGATTGCT TCATTACCTT TTCCATACGA GAAACCACAC
 401 CTTCATTGTC CTGCACCTGG TCTTGCAAGG GATGGTTTAT ACTGAGTACA
 451 CCTGGGAAGT ATTTGGCTAC TGTCAGGAGC TGGAGTTGTC CTTGCATTAC
 501 CTTCTTCTGC CCTATCTGCT GCTAGGTGTA AACCTGTTTT TTTTCACCCT
 551 GACTTGTGGA ACCAATCCTG GCATTATAAC AAAAGCAAAT GAATTATTAT
 601 TTCTTCATGT TTATGAATTT GATGAAGTGA TGTTTCCAAA GAACGTGAGG
 651 TGCTCTACTT GTGATTTAAG GAAACCAGCT CGATCCAAGC ACTGCAGTGT
 701 GTGTAACTGG TGTGTGCACC GTTTCGACCA TCACTGTGTT TGGGTGAACA
 751 ACTGCATCGG GGCCTGGAAC ATCAGGTACT TCCTCATCTA CGTCTTGACC
 801 TTGACGGCCT CGGCTGCCAC CGTCGCCATT GTGAGCACCA CTTTTCTGGT
 851 CCACTTGGTG GTGATGTCAG ATTTATACCA GGAGACTTAC ATCGATGACC
 901 TTGGACACCT CCATGTTATG GACACGGTCA TTCTTATTCA GTACCTGTTC
 951 CTGACTTTTC CACGGATTGT CTTCATGCTG GGCTTTGTCG TGGTCCTGAG
1001 CTTCCTCCTG GGTGGCTACC TGTTGTCTGT CCTGTATCTG GCGGCCACCA
1051 ACCAGACTAC TAACGAGTGG TACAGAGGTG TCTGGGCCTG GTGCCAGCGT
1101 TGTCCCCTTG TGGCCTGGCC TCCGTCAGCA GAGCCCCAAG TCCACCGGAA
1151 CATTCACTCC CATGGGCTTC GGAGCAACCT TCAAGAGATC TTTCTACCTG
1201 CCTTTCCATG TCATGAGAGG AAGAAACAAG AATGACAAGT GTATGACTGC
1251 CAAAAAAAAA AAAAAAAAAC
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 201 bp to 1232 bp; peptide length: 344
Category: similarity to unknown protein

```
  1 MDFLVLFLFY LASVLMGLVL ICVCSKTHSL KGLARGGAQI FSCIIPECLQ
 51 RAVHGLLHYL FHTRNHTFIV LHLVLQGMVY TEYTWEVFGY CQELELSLHY
101 LLLPYLLLGV NLFFFTLTCG TNPGIITKAN ELLFLHVYEF DEVMFPKNVR
151 CSTCDLRKPA RSKHCSVCNW CVHRFDHHCV WVNNCIGAWN IRYFLIYVLT
201 LTASAATVAI VSTTFLVHLV VMSDLYQETY IDDLGHLHVM DTVILIQYLF
251 LTFPRIVFML GFVVVLSFLL GGYLLSVLYL AATNQTTNEW YRGVWAWCQR
301 CPLVAWPPSA EPQVHRNIHS HGLRSNLQEI FLPAFPCHER KKQE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72112, frame 3

TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein"; S.pombe chromosome II cosmid c13G1., N = 2, Score = 247, P = 1.4e-22

TREMBL:CED2021_3 gene: "D2021.2"; Caenorhabditis elegans cosmid D2021., N = 1, Score = 209, P = 9e-17

TREMBL:CEC43H6_2 gene: "C43H6.7"; Caenorhabditis elegans cosmid C43H6., N = 1, Score = 206, P = 5.2e-15

PIR:S52691 probable membrane protein YDR126w - yeast (Saccharomyces cerevisiae), N = 1, Score = 207, P = 8.4e-15

PIR:E71607 metal binding protein (DHHC domain) PFB0725c - malaria parasite (Plasmodium falciparum), N = 1, Score = 182, P = 1.1e-13

```
>TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein";
     S.pombe chromosome II cosmid c13G1.
            Length = 356

  HSPs:

 Score = 247 (37.1 bits), Expect = 1.4e-22, Sum P(2) = 1.4e-22
 Identities = 55/148 (37%), Positives = 85/148 (57%)

Query:    52 AVHGLLHYLFHTRNH--TFIVLHLVLQGM----VYTEYTWEVFGYCQELELSLHYLLLPY 105
             A+  L +Y+ +  N     F+ L L+ G+      +Y      + F      + + L  +LLPY
Sbjct:    64 AMRSLSNYVLYKNNPLVVFLYLALITIGIASFFIYGSSLTQKFSIIDWISV-LTSVLLPY 122

Query:   106 LLLGVNLFFFTLTCGTNPGIITKANELLFLHVYEFD-EVMFPKNVRCSTCDLRKPARSKH 164
                  ++L+    +   +NPG I   N          + +D ++ FP    +CSTC    KPARSKH
Sbjct:   123 ----ISLY---IAAKSNPGKIDLKNWNEASRRFPYDYKIFFPN--KCSTCKFEKPARSKH 173

Query:   165 CSVCNWCVHRFDHHCVWVNNCIGAWNIRYFLIYVL 199
             C +CN CV +FDHHC+W+NNC+G  N RYF +++L
Sbjct:   174 CRLCNICVEKFDHHCIWINNCVGLNNARYFFLFLL 208

 Score = 43 (6.5 bits), Expect = 1.4e-22, Sum P(2) = 1.4e-22
 Identities = 10/35 (28%), Positives = 17/35 (48%)

Query:   257 VFMLGFVV-VLSFLLGGYLLSVLYLAATNQTTNEW 290
             VF++  +  VL   L GY   ++Y   T   + +W
Sbjct:   254 VFLISLICSVLVLCLLGYEFFLVYAGYTTNESEKW 288
```

Pedant information for DKFZphfbr2_72112, frame 3

Report for DKFZphfbr2_72112.3

[LENGTH] 344
[MW] 39677.23
[pI] 7.26
[HOMOL] TREMBL:SPBC13G1_7 gene: "SPBC13G1.07"; product: "hypothetical protein"; S.pombe chromosome II cosmid c13G1. 3e-17
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YDR126w] 1e-16
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YDR264c] 8e-05
[FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YDR264c] 8e-05
[PIRKW] transmembrane protein 4e-15
[SUPFAM] ankyrin repeat homology 1e-10
[SUPFAM] unassigned ankyrin repeat proteins 1e-10
[PROSITE] MYRISTYL 4
[PROSITE] CK2_PHOSPHO_SITE 3

```
[PROSITE]       PKC_PHOSPHO_SITE       1
[PROSITE]       ASN_GLYCOSYLATION      2
[KW]            SIGNAL_PEPTIDE 30
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY    16.57 %

SEQ    MDFLVLFLFYLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIIPECLQRAVHGLLHYL
SEG    ............................................................
PRD    cchhhhhhhhhhhhhhhheeeeeccccceeeeeecccceeeeeeeehhhhhhhhhhhheee
MEM    ............................................................

SEQ    FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCG
SEG    .................................xxxxxxxxxxxxxxxxxxx........
PRD    eccccchhhhhhhhhhhhccchhhhhhheeeeccceeehhhhhhhhhhhhhhcccceeeecc
MEM    ...................................MMMMMMMMMMMMMMMMMMMMMMMMM

SEQ    TNPGIITKANELLFLHVYEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
SEG    ............................................................
PRD    ccccccccccchhhhhhhhhhcccccceeeeccccccccccccccccccceeeeccccccc
MEM    M..............MMMMMMMMMMMMMMMMMMMMMMMMMMMM.................

SEQ    WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
SEG    .................xxxxxxxxxxxxxxxxx..........................
PRD    cccccccccccchhhhhhhhhccchhhhhhhhhhhhhhhhhccccccccccccccccchh
MEM    ............................................................

SEQ    DTVILIQYLFLTFPRIVFMLGFVVVLSFLLGGYLLSVLYLAATNQTTNEWYRGVWAWCQR
SEG    ...................xxxxxxxxxxxxxxxxxxxxx....................
PRD    hhhhhhhhhhhhhhhhccccccccceeecccchhhhhhhhcccchhhhhhhhhhhhcccc
MEM    ............................................................

SEQ    CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
SEG    ............................................
PRD    ccccccccccccccceeeccccccccccceeeeeccccccccccc
MEM    ............................................
```

Prosite for DKFZphfbr2_72112.3

PS00001	65->69	ASN_GLYCOSYLATION	PDOC00001
PS00001	284->288	ASN_GLYCOSYLATION	PDOC00001
PS00005	29->32	PKC_PHOSPHO_SITE	PDOC00005
PS00006	152->156	CK2_PHOSPHO_SITE	PDOC00006
PS00006	229->233	CK2_PHOSPHO_SITE	PDOC00006
PS00006	286->290	CK2_PHOSPHO_SITE	PDOC00006
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	77->83	MYRISTYL	PDOC00008
PS00008	120->126	MYRISTYL	PDOC00008
PS00008	322->328	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_72112.3)

DKFZphfbr2_72m16

group: unknown

DKFZphfbr2_72m16 encodes a novel 287 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="26.2 cR from top of Chr16 linkage group"

Insert length: 1462 bp
Poly A stretch at pos. 1441, polyadenylation signal at pos. 1421

```
   1 GGGGAGGACC GGAGGACCGA GGACAGAAAG ATTGGTGGAC AGGAGCAGCG
  51 GCCGGTGGGG AGGGCGCTCG GCGGCGGCCT GCGGCCATGG CCACCGTGAT
 101 GGCAGCGACG GCGGCGGAGC GGGCGGTGCT GGAGGAGGAG TTCCGCTGGC
 151 TGCTGCACGA CGAGGTGCAC GCTGTGTTGA AGCAGCTGCA GGACATCCTC
 201 AAGGAGGCCT CTCTGCGCTT CACTCTGCCG GGCTCCGGCA CTGAGGGGCC
 251 CGCCAAGCAA GAGAACTTCA TCCTAGGCAG CTGTGGCACA GACCAGGTGA
 301 AGGGTGTGCT GACTCTGCAG GGGGATGCCC TCAGCCAGGC GGATGTGAAC
 351 CTGAAGATGC CCCGGAACAA CCAGCTGCTG CACTTCGCCT TCCGGGAGGA
 401 CAAGCAGTGG AAGCTGCAGC AGATCCAGGA TGCCAGAAAC CATGTGAGCC
 451 AAGCCATTTA CCTGCTTACC AGCCGGGACC AGAGCTACCA GTTCAAGACG
 501 GGCGCTGAGG TCCTCAAGCT GATGGACGCA GTGATGCTGC AGCTGACCAG
 551 AGCCCGAAAC CGGCTCACCA CCCCCGCCAC CCTCACCCTC CCCGAGATCG
 601 CCGCCAGCGG CCTCACGCGG ATGTTCGCCC CTGCCCTGCC GTCCGACCTG
 651 CTGGTCAACG TCTACATCAA CCTCAACAAG CTCTGCCTCA CGGTGTACCA
 701 GCTGCATGCC CTGCAGCCCA ACTCCACCAA GAACTTCCGC CCAGCTGGGG
 751 GCGCGGTGCT GCATAGCCCT GGGGCCATGT TCGAGTGGGG CTCTCAGCGC
 801 CTGGAGGTGA GCCACGTGCA CAAAGTGGAG TGCGTGATCC CCTGGCTCAA
 851 CGACGCCCTG GTCTACTTCA CCGTCTCCCT GCAGCTCTGC CAGCAGCTTA
 901 AGGACAAGAT CTCCGTGTTC TCCAGCTACT GGAGCTACAG ACCCTTCTGA
 951 TCACAGCACC CAGGAGCTTG TCTCCAGGAA GGCGGCCCCG TCCCCTACTC
1001 ATACCCACCA CAGAGCACCA GCCAGTGCCA ACGCCAGGCT GCTATTTATC
1051 TCCCTATCCC ACCCCCTACC CCACCTAACA CATTTGCACT GCCGGGAATG
1101 GACACTGGAA GTGCCAGGAG GAAGGAAGGC TGGTTTGGTG GGGTAGTGGG
1151 GAGGTCAGGG AGGCGGGGCC AAGGGTGTCC CACATTCCCA ACACCGCCCT
1201 CTGATCACCA TGGGAATCTT TGGACTCAGG ACAGGGCCAG GCGCAGGGCT
1251 CTCCCTCCTC TCCCCTTCGC TGTCCCCTCC CCCTGGAGGG CATGGTGTCG
1301 GGGGGTGGCA CTGAGCTATG AGTCCCGGGG ATGGTGAGGA ACGCCACAGA
1351 CAGAGCCACC CTAGGAGTGA GTATAGTGCT GGTGACTGTG TTTCATAGCC
1401 CCAGTCCAGG GCTGTCTAAG AAATAAAGAT CATCAGACTC CAAAAAAAAA
1451 AAAAAAAAAA AC
```

BLAST Results

Entry HS604351 from database EMBL:
human STS WI-18474.
Score = 1178, P = 1.5e-48, identities = 250/268

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 87 bp to 947 bp; peptide length: 287
Category: similarity to unknown protein

```
  1 MATVMAATAA ERAVLEEEFR WLLHDEVHAV LKQLQDILKE ASLRFTLPGS
 51 GTEGPAKQEN FILGSCGTDQ VKGVLTLQGD ALSQADVNLK MPRNNQLLHF
101 AFREDKQWKL QQIQDARNHV SQAIYLLTSR DQSYQFKTGA EVLKLMDAVM
151 LQLTRARNRL TTPATLTLPE IAASGLTRMF APALPSDLLV NVYINLNKLC
201 LTVYQLHALQ PNSTKNFRPA GGAVLHSPGA MFEWGSQRLE VSHVHKVECV
251 IPWLNDALVY FTVSLQLCQQ LKDKISVFSS YWSYRPF
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_72m16, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfbr2_72m16, frame 3

Report for DKFZphfbr2_72m16.3

```
[LENGTH]        287
[MW]            32254.40
[pI]            8.30
[HOMOL]         TREMBL:AF025459_2 gene: "H14A12.3"; Caenorhabditis elegans cosmid H14A12. 3e-14

[PROSITE]       MYRISTYL        1
[PROSITE]       CK2_PHOSPHO_SITE        6
[PROSITE]       PKC_PHOSPHO_SITE        5
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY      6.27 %
```

```
SEQ    MATVMAATAAERAVLEEEFRWLLHDEVHAVLKQLQDILKEASLRFTLPGSGTEGPAKQEN
SEG    xxxxxxxxxxxxxxxxxx..........................................
PRD    cchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccchhhh

SEQ    FILGSCGTDQVKGVLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDARNHV
SEG    ............................................................
PRD    hhcccccceeeeeeeecccchhhhhhhcccccchhhhhhhhchhhhhhhhhhhhchh

SEQ    SQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLTTPATLTLPEIAASGLTRMF
SEG    ............................................................
PRD    hhhhhhhhcccccceeecchhhhhhhhhhhhhhhhhhhhhcccccccccccccccccccc

SEQ    APALPSDLLVNVYINLNKLCLTVYQLHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLE
SEG    ............................................................
PRD    cccccccceeeeehhhhhhhhhheeeecccccccccccccceeecccccccccccccee

SEQ    VSHVHKVECVIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
SEG    ...............................................
PRD    eeeeeeeeeeeccccceeeeeeehhhhhhhhhhhheeeeeeeeccc
```

Prosite for DKFZphfbr2_72m16.3

```
PS00001    212->216   ASN_GLYCOSYLATION    PDOC00001
PS00005     42->45    PKC_PHOSPHO_SITE     PDOC00005
PS00005    128->131   PKC_PHOSPHO_SITE     PDOC00005
PS00005    213->216   PKC_PHOSPHO_SITE     PDOC00005
PS00005    236->239   PKC_PHOSPHO_SITE     PDOC00005
PS00005    283->286   PKC_PHOSPHO_SITE     PDOC00005
PS00006      8->12    CK2_PHOSPHO_SITE     PDOC00006
PS00006     50->54    CK2_PHOSPHO_SITE     PDOC00006
PS00006     83->87    CK2_PHOSPHO_SITE     PDOC00006
PS00006    128->132   CK2_PHOSPHO_SITE     PDOC00006
PS00006    138->142   CK2_PHOSPHO_SITE     PDOC00006
PS00006    167->171   CK2_PHOSPHO_SITE     PDOC00006
PS00008     64->70    MYRISTYL             PDOC00008
```

(No Pfam data available for DKFZphfbr2_72m16.3)

DKFZphfbr2_72n12
----

group: brain derived

DKFZphfbr2_72n12 encodes a novel 117 amino acid protein with similarity to a protein with conserved sequence in bacteria and eukariota.

The novel protein is very similar to human MM46, human and rat gangliosiode expression factor-2 (GEF2), C. elegans 14.8 kD protein C32D5.9 and Laccaria bicolor symbiosis-related protein LBU93506_1. The function of this highly conserved proteins is not known.

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to rat GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2)

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: /map="12"

Insert length: 1880 bp
Poly A stretch at pos. 1859, polyadenylation signal at pos. 1830

```
   1 GGGGGCCGGT ATTTCTCCAT CTGGCTCTCC TCTACCTCCA GGCAGGCTCA
  51 CCCGAGATCC CCGCCCCGAA CCCCCCCTGC ACACTCGGCC CAGCGCTGTT
 101 GCCCCCGGAG CGGACGTTTC TGCAGCTATT CTGAGCACAC CTTGACGTCG
 151 GCTGAGGGAG CGGGACAGGG TCAGCGGCGA AGGAGGCAGG CCCCGCGCGG
 201 GGATCTCGGA AGCCCTGCGG TGCATCATGA AGTTCCAGTA CAAGGAGGAC
 251 CATCCCTTTG AGTATCGGAA AAAGGAAGGA GAAAAGATCC GGAAGAAATA
 301 TCCGGACAGG GTCCCCGTGA TTGTAGAGAA GGCTCCAAAA GCCAGGGTGC
 351 CTGATCTGGA CAAGAGGAAG TACCTAGTGC CCTCTGACCT TACTGTTGGC
 401 CAGTTCTACT TCTTAATCCG GAAGAGAATC CACCTGAGAC CTGAGGACGC
 451 CTTATTCTTC TTTGTCAACA ACACCATCCC TCCCACCAGT GCTACCATGG
 501 GCCAACTGTA TGAGGACAAT CATGAGGAAG ACTATTTTCT GTATGTGGCC
 551 TACAGTGATG AGAGTGTCTA TGGGAAATGA GTGGTTGGAA GCCCAGCAGA
 601 TGGGAGCACC TGGACTTGGG GGTAGGGGAG GGGTGTGTGT GCGCGACATG
 651 GGGAAAGAGG GTGGCTCCCA CCGCAAGGAG ACAGAAGGTG AAGACATCTA
 701 GAAACATTAC ACCACACACA CCGTCATCAC ATTTTCACAT GCTCAATTGA
 751 TATTTTTTGC TGCTTCCTCG GCCCAGGGAG AAAGCATGTC AGGACAGAGC
 801 TGTTGGATTG GCTTTGATAG AGGAATGGGG ATGATGTAAG TTTACAGTAT
 851 TCCTGGGGTT TAATTGTTGT GCAGTTTCAT AGATGGGTCA GGAGGTGGAC
 901 AAGTTGGGGC CAGAGATGAT GGCAGTCCAG CAGCAACTCC CTGTGCTCCC
 951 TTCTCTTTGG GCAGAGATTC TATTTTTGAC ATTTGCACAA GACAGGTAGG
1001 GAAAGGGGAC TTGTGGTAGT GGACCATACC TGGGGACCAA AAGAGACCCA
1051 CTGTAATTGA TGCATTGTGG CCCCTGATCT TCCCTGTCTC ACACTTCTTT
1101 TCTCCCATCC CGGTTGCAAT CTCACTCAGA CATCACAGTA CCACCCCAGG
1151 GGTGGCAGTA GACAACAACC CAGAAATTTA GACAGGGATC TCTTACCTTT
1201 GGAAAATAGG GGTTAGGCAT GAAGGTGGTT GTGATTAAGA AGATGGTTTT
1251 GTTATTAAAT AGCATTAAAC TGGAATTGAC AAGAGTGTTG AGCATCCCTG
1301 TCTAACCTGC TCTTTCTCTT TGGTGCCCCT TATCTCACCC CTTCCTTGGA
1351 ATTTAATAAG TCTCAGGCAT TTCCAATTGT AGACTAAAAC CACTCTTAGC
1401 ATCTCCTCTA GTATTTTCCA TGTATCAGGA AAGAGGTGTC TTATGTAGGG
1451 AGGGGGCAAG TATGAAGTAA GGTAATTATA TACTACTCTC ATTCAGGATT
1501 CTTGCTCCCA TGCTGCTGTC CCTTCAGGCT CACATGCACA GGAATGCTAC
1551 ATGATGGCCA GCTGCTTCCC TCCTTGGTTA TCATCCACTG CAGCTGCTAG
1601 TTAGAAAGGT TTGGAGGGAT GACTTTTAGT AAATCATGGG GATTTTATTG
1651 ATTTATTTTC ACTTTTGGGA TTTTGTGGGG TGGGAGTGGG GAGCAGGAAT
1701 TGCACTCAGA CATGACATTT CAATTCATCT CTGCTAATGA AAAGGGTTCT
1751 TTCTCTTGGG GGAAATGTGT GTGTCAGTTC TGTCAGCTGC AAGTTCTTGT
1801 ATAATGAAGT CAATGCCATC AGGCCAAGGA AATAAAATAA TTGCTTACCT
1851 TAAAAATCGA AAAAAAAAAA AAAAAAAAAC
```

BLAST Results

Entry HS418210 from database EMBL:
human STS SHGC-10496.
Score = 1916, P = 4.0e-80, identities = 394/400

Entry AC006514 from database EMBLNEW:
*** SEQUENCING IN PROGRESS *** Homo sapiens; HTGS phase 1, 68 unordered pieces.
Score = 610, P = 2.7e-16, identities = 128/134
4 exons

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 227 bp to 577 bp; peptide length: 117
Category: strong similarity to known protein

```
  1 MKFQYKEDHP FEYRKKEGEK IRKKYPDRVP VIVEKAPKAR VPDLDKRKYL
 51 VPSDLTVGQF YFLIRKRIHL RPEDALFFFV NNTIPPTSAT MGQLYEDNHE
101 EDYFLYVAYS DESVYGK
```

BLASTP hits

Entry YQD9_CAEEL from database SWISSPROT:
HYPOTHETICAL 14.8 KD PROTEIN C32D5.9 IN CHROMOSOME II.
Score = 496, P = 1.8e-47, identities = 91/116, positives = 105/116

Entry SYRP_LACBI from database SWISSPROT:
SYMBIOSIS-RELATED PROTEIN.
Score = 390, P = 3.1e-36, identities = 68/117, positives = 94/117

Entry LBU93506_1 from database TREMBL:
product: "symbiosis-related protein"; Laccaria bicolor
symbiosis-related protein mRNA, partial cds.
Score = 390, P = 3.1e-36, identities = 68/117, positives = 94/117

Entry GEF2_RAT from database SWISSPROT:
GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2).
Score = 373, P = 2.0e-34, identities = 71/116, positives = 88/116

Alert BLASTP hits for DKFZphfbr2_72n12, frame 2

TREMBLNEW:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete
cds., N = 1, Score = 549, P = 4.7e-53

SWISSPROT:GEF2_HUMAN GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2)., N = 1,
Score = 373, P = 2.1e-34

```
>TREMBLNEW:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete
     cds.
            Length = 117

  HSPs:

 Score = 549 (82.4 bits), Expect = 4.7e-53, P = 4.7e-53
 Identities = 101/116 (87%), Positives = 110/116 (94%)

Query:     1 MKFQYKEDHPFEYRKKEGEKIRKKYPDRVPVIVEKAPKARVPDLDKRKYLVPSDLTVGQF 60
             MKF YKE+HPFE R+ EGEKIRKKYPDRVPVIVEKAPKAR+ DLDK+KYLVPSDLTVGQF
Sbjct:     1 MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKKKYLVPSDLTVGQF 60

Query:    61 YFLIRKRIHLRPEDALFFFVNNTIPPTSATMGQLYEDNHEEDYFLYVAYSDESVYG 116
             YFLIRKRIHLR EDALFFFVNN IPPTSATMGQLY+++HEED+FLY+AYSDESVYG
Sbjct:    61 YFLIRKRIHLRAEDALFFFVNNVIPPTSATMGQLYQEHHEEDFFLYIAYSDESVYG 116
```

Pedant information for DKFZphfbr2_72n12, frame 2

Report for DKFZphfbr2_72n12.2

[LENGTH]	117
[MW]	14044.07
[pI]	8.67
[HOMOL]	TREMBL:AF044671_1 product: "MM46"; Homo sapiens MM46 mRNA, complete cds. 1e-56

[FUNCAT]	30.03 organization of cytoplasm	[S. cerevisiae, YBL078c] 4e-36
[FUNCAT]	08.22 cytoskeleton-dependent transport	[S. cerevisiae, YBL078c] 4e-36
[FUNCAT]	06.13.04 lysosomal and vacuolar degradation	[S. cerevisiae, YBL078c] 4e-36
[SUPFAM]	hypothetical protein YBL078c 8e-35	
[PROSITE]	ASN_GLYCOSYLATION 1	
[KW]	Alpha_Beta	

```
SEQ     MKFQYKEDHPFEYRKKEGEKIRKKYPDRVPVIVEKAPKARVPDLDKRKYLVPSDLTVGQF
PRD     cccccccccchhhhhhhhhhhhhhcccccceeeeeccccccccccccceeecccccchhhh

SEQ     YFLIRKRIHLRPEDALFFFVNNTIPPTSATMGQLYEDNHEEDYFLYVAYSDESVYGK
PRD     hhhhhhhhhhcccccceeeeeccccccccchhhhhhhhhcccccceeeeeeeccccccccc
```

Prosite for DKFZphfbr2_72n12.2

PS00001	81->85	ASN_GLYCOSYLATION	PDOC00001

(No Pfam data available for DKFZphfbr2_72n12.2)

DKFZphfbr2_78c24
----

group: signal transduction

DKFZphfbr2_78c24 encodes a novel 563 amino acid protein with strong similarity to guanylate-binding proteins (GBPs).

GBPs were originally described as proteins that are strongly induced by interferons and are capable of binding to agarose-immobilized guanine nucleotides. hGBP1, the first of two members of this protein family in humans, represents a novel type of GTPase. The novel protein contains an ATP/GTP-binding site motif A (P-loop) and a RGD cell attachment site. It seems to be a new member of the GBP-family and shows a splicing pattern not described previously.

The new protein can find application in modulating/blocking the response of cells to interferons.

strong similarity to guanine nucleotide-binding protein 1/2
but different "splice variant" aa 211-245 of GBP1/2 missing

Sequenced by MediGenomix

Locus: unknown

Insert length: 2952 bp
Poly A stretch at pos. 2927, polyadenylation signal at pos. 2914

```
   1 CAGTTTCATT AGGCTCTGAA GCCATTACAA AGGTTGCTTA ACTTCTAATT
  51 ATTTGATCAC TGAGGAAAAT CCAGAAAGCT ACACAACACT GAAGGGGTGA
 101 AATAAAAGTC CAGCGATCCA GCGAAAGAAA AGAGAAGTGA CAGAAACAAC
 151 TTTACCTGGA CTGAAGATAA AAGCACAGAC AAGAGAACAA TGCCCTGGAC
 201 ATGGCTCCAG AGATCCACAT GACAGGCCCA ATGTGCCTCA TTGAGAACAC
 251 TAATGGGGAA CTGGTGGCGA ATCCAGAAGC TCTGAAAATC CTGTCTGCCA
 301 TTACACAGCC TGTGGTGGTG GTGGCAATTG TGGGCCTCTA CCGCACAGGA
 351 AAATCCTACC TGATGAACAA GCTAGCTGGG AAGAATAAGG GCTTCTCTCT
 401 GGGCTCCACA GTGAAATCTC ACACCAAAGG AATCTGGATG TGGTGTGTGC
 451 CTCACCCCAA AAAGCCAGAA CACACCTTAG TCCTGCTTGA CACTGAGGGC
 501 CTGGGAGATG TAAAGAAGGG TGACAACCAG AATGACTCCT GGATCTTCAC
 551 CCTGGCCGTC CTCCTGAGCA GCACTCTCGT GTACAATAGC ATGGGAACCA
 601 TCAACCAGCA GGCTATGGAC CAACTGTACT ATGTGACAGA GCTGACACAT
 651 CGAATCCGAT CAAAATCCTC ACCTGATGAG AATGAGAATG AGGATTCAGC
 701 TGACTTTGTG AGCTTCTTCC CAGATTTTGT GTGGACACTG AGAGATTTCT
 751 CCCTGGACTT GGAAGCAGAT GGACAACCCC TCACACCAGA TGAGTACCTG
 801 GAGTATTCCC TGAAGCTAAC GCAAGGTAAC AGGAAGCTTG CCCAGCTTGA
 851 GAAACTACAA GATGAAGAGC TGGACCCTGA ATTTGTGCAA CAAGTAGCAG
 901 ACTTCTGTTC CTACATCTTT AGCAATTCCA AAACTAAAAC TCTTTCAGGA
 951 GGCATCAAGG TCAATGGGCC TTGTCTAGAG AGCCTAGTGC TGACCTATAT
1001 CAATGCTATC AGCAGAGGGG ATCTGCCCTG CATGGAGAAC GCAGTCCTGG
1051 CCTTGGCCCA GATAGAGAAC TCAGCCGCAG TGCAAAAGGC TATTGCCCAC
1101 TATGACCAGC AGATGGGCCA GAAGGTGCAG CTGCCCGCAG AAACCCTCCA
1151 GGAGCTGCTG GACCTGCACA GGGTTAGTGA GAGGGAGGCC ACTGAAGTCT
1201 ATATGAAGAA CTCTTTCAAG GATGTGGACC ATCTGTTTCA AAAGAAATTA
1251 GCGGCCCAGC TAGACAAAAA GCGGGATGAC TTTTGTAAAC AGAATCAAGA
1301 AGCATCATCA GATCGTTGCT CAGCTTTACT TCAGGTCATT TTCAGTCCTC
1351 TAGAAGAAGA AGTGAAGGCG GGAATTTATT CGAAACCAGG GGGCTATTGT
1401 CTCTTTATTC AGAAGCTACA AGACCTGGAG AAAAAGTACT ATGAGGAACC
1451 AAGGAAGGGG ATACAGGCTG AAGAGATTCT GCAGACATAC TTGAAATCCA
1501 AGGAGTCTGT GACCGATGCA ATTCTACAGA CAGACCAGAT TCTCACAGAA
1551 AAGGAAAAGG AGATTGAAGT GGAATGTGTA AAAGCTGAAT CTGCACAGGC
1601 TTCAGCAAAA ATGGTGGAGG AAATGCAAAT AAAGTATCAG CAGATGATGG
1651 AAGAGAAAGA GAAGAGTTAT CAAGAACATG TGAAACAATT GACTGAGAAG
1701 ATGGAGAGGG AGAGGGCCCA GTTGCTGGAA GAGCAAGAGA AGACCCTCAC
1751 TAGTAAACTT CAGGAACAGG CCCGAGTACT AAAGGAGAGA TGCCAAGGTG
1801 AAAGTACCCA ACTTCAAAAT GAGATACAAA AGCTACAGAA GACCCTGAAA
1851 AAAAAAACCA AGAGATATAT GTCGCATAAG CTAAAGATCT AAACAACAGA
1901 GCTTTTCTGT CATCCTAACC CAAGGCATAA CTGAAACAAT TTTAGAATTT
1951 GGAACAAGTG TCACTATATT TGATAATAAT TAGATCTTGC ATCATAACAC
2001 TAAAAGTTTA CAAGAACATG CAGTTCAATG ATCAAAATCA TGTTTTTTCC
2051 TTAAAAAGAT TGTAAATTGT GCAACAAAGA TGCATTTACC TCTGTACCAA
2101 CAGAGGAGGG ATCATGAGTT GCCACCACTC AGAAGTTTAT TCTTCCAGAC
2151 GACCAGTGGA TACTGAGGAA AGTCTTAGGT AAAAATCTTG GGACATATTT
2201 GGGCACTGGT TTGGCCAAGT GTACAATAGG TCCCAATATC AGAAACAACC
2251 ATCCTAGCTT CCTAGGGAAG ACAGTGTACA GTTCTCCATT ATATCAAGGC
2301 TACAAGGTCT ATGAGCAATA ATGTGATTTC TGGACATTGC CCATGGATAA
2351 TTCTCACTGA TGGATCTCAA GCTAAAGCAA ACCATCTTAT ACAGAGATCT
2401 AGAATCTTAT ATTTTCCATA GGAAGGTAAA GAAATCATTA GCAAGAGTAG
2451 GAATTGAATC ATAAACAAAT TGGCTAATGA AGAAATCTTT TCTTTCTTGT
2501 TCAATTCATC TAGATTATAA CCTTAATGTG ACACCTGAGA CCTTTAGACA
```

```
2551 GTTGACCCTG AATTAAATAG TCACATGGTA ACAATTATGC ACTGTGTAAT
2601 TTTAGTAATG TATAACATGC AATGATGCAC TTTAACTGAA GATAGAGACT
2651 ATGTTAGAAA ATTGAACTAA TTTAATTATT TGATTGTTTT AATCCTAAAG
2701 CATAAGTTAG TCTTTTCCTG ATTCTTAAAG GTCATACTTG AAATCCTGCC
2751 AATTTTCCCC AAAGGGAATA TGGAATTTTT TTTGACTTTC TTTTGAGCAA
2801 TAAAATAATT GTCTTGCCAT TACTTAGTAT ATGTAGACTT CATCCCAATT
2851 GTCAAACATC CTAGGTAAGT GGTTGACATT TCTTACAGCA ATTACAGATT
2901 ATTTTTGAAC TAGAAATAAA CTAAACTAGA AACAAAAAAA AAAAAAAAAA
2951 AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 201 bp to 1889 bp; peptide length: 563
Category: strong similarity to known protein
Classification: Cell signaling/communication
Prosite motifs: RGD (272-275)
ATP_GTP_A (45-53)

```
  1 MAPEIHMTGP MCLIENTNGE LVANPEALKI LSAITQPVVV VAIVGLYRTG
 51 KSYLMNKLAG KNKGFSLGST VKSHTKGIWM WCVPHPKKPE HTLVLLDTEG
101 LGDVKKGDNQ NDSWIFTLAV LLSSTLVYNS MGTINQQAMD QLYYVTELTH
151 RIRSKSSPDE NENEDSADFV SFFPDFVWTL RDFSLDLEAD GQPLTPDEYL
201 EYSLKLTQGN RKLAQLEKLQ DEELDPEFVQ QVADFCSYIF SNSKTKTLSG
251 GIKVNGPCLE SLVLTYINAI SRGDLPCMEN AVLALAQIEN SAAVQKAIAH
301 YDQQMGQKVQ LPAETLQELL DLHRVSEREA TEVYMKNSFK DVDHLFQKKL
351 AAQLDKKRDD FCKQNQEASS DRCSALLQVI FSPLEEEVKA GIYSKPGGYC
401 LFIQKLQDLE KKYYEEPRKG IQAEEILQTY LKSKESVTDA ILQTDQILTE
451 KEKEIEVECV KAESAQASAK MVEEMQIKYQ QMMEEKEKSY QEHVKQLTEK
501 MERERAQLLE EQEKTLTSKL QEQARVLKER CQGESTQLQN EIQKLQKTLK
551 KKTKRYMSHK LKI
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78c24, frame 3

PIR:A41268 guanine nucleotide-binding protein 1 - human, N = 2, Score = 1306, P = 4.9e-238

PIR:A46459 macrophage-activation gene-1 protein mag-1 - mouse, N = 2, Score = 942, P = 8.9e-184

PIR:S70524 guanine nucleotide-binding protein 2 - human, N = 2, Score = 1131, P = 4.1e-210

TREMBL:AF077007_1 gene: "Gbp2"; product: "interferon-induced guanylate binding protein GBP-2"; Mus musculus interferon-induced guanylate binding protein GBP-2 (Gbp2) mRNA, complete cds., N = 2, Score = 904, P = 1.2e-179

>PIR:A41268 guanine nucleotide-binding protein 1 - human
Length = 592

HSPs:

Score = 1306 (195.9 bits), Expect = 4.9e-238, Sum P(2) = 4.9e-238
Identities = 264/332 (79%), Positives = 288/332 (86%)

```
Query:   211 RKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPCLESLVLTYINAI 270
             RKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGI+VNGP LESLVLTY+NAI
Sbjct:   245 RKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLSGGIQVNGPRLESLVLTYVNAI 304
```

```
Query:   271 SRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQLPAETLQELLDLHRVSEREA 330
             S GDLPCMENAVLALAQIENSAAVQKAIAHY+QQMGQKVQLP E+LQELLDLHR SEREA
Sbjct:   305 SSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTESLQELLDLHRDSEREA 364

Query:   331 TEVYMKNSFKDVDHLFQKKLAAQLDKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKA 390
              EV++++SFKDVDHLFQK+LAAQL+KKRDDFCKQNQEASSDRCS LLQVIFSPLEEEVKA
Sbjct:   365 IEVFIRSSFKDVDHLFQKELAAQLEKKRDDFCKQNQEASSDRCSGLLQVIFSPLEEEVKA 424

Query:   391 GIYSKPGGYCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAILQTDQILTX 450
             GIYSKPGGY LF+QKLQDL+KKYYEEPRKGIQAEEILQTYLKSKES+TDAILQTDQ LT
Sbjct:   425 GIYSKPGGYRLFVQKLQDLKKKYYEEPRKGIQAEEILQTYLKSKESMTDAILQTDQTLTE 484

Query:   451 XXXXXXXXXXXXXSAQASAKMVEEMQIKYQQMMEEKEKSYQEHVKQLTEKMXXXXXXXXX 510
                          SAQASAKM++EMQ K +QMME+KE+SYQEH+KQLTEKM
Sbjct:   485 KEKEIEVERVKAESAQASAKMLQEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRVQLLK 544

Query:   511 XXXKTLTSKLQEQARVLKERCQGESTQLQNEI 542
                +TL  KLQEQ ++LKE  Q ES  ++NEI
Sbjct:   545 EQERTLALKLQEQEQLLKEGFQKESRIMKNEI 576

 Score = 1012 (151.8 bits), Expect = 4.9e-238, Sum P(2) = 4.9e-238
 Identities = 194/211 (91%), Positives = 200/211 (94%)

Query:     1 MAPEIHMTGPMCLIENTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG 60
             MA EIHMTGPMCLIENTNG L+ANPEALKILSAITQP+VVVAIVGLYRTGKSYLMNKLAG
Sbjct:     1 MASEIHMTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAG 60

Query:    61 KNKGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAV 120
             K KGFSLGSTV+SHTKGIWMWCVPHPKKP H LVLLDTEGLGDV+KGDNQNDSWIF LAV
Sbjct:    61 KKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAV 120

Query:   121 LLSSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENE--DSADFVSFFPDFVW 178
             LLSST VYNS+GTINQQAMDQLYYVTELTHRIRSKSSPDENENE  DSADFVSFFPDFVW
Sbjct:   121 LLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVW 180

Query:   179 TLRDFSLDLEADGQPLTPDEYLEYSLKLTQG 209
             TLRDFSLDLEADGQPLTPDEYL YSLKL +G
Sbjct:   181 TLRDFSLDLEADGQPLTPDEYLTYSLKLKKG 211
```

Pedant information for DKFZphfbr2_78c24, frame 3

Report for DKFZphfbr2_78c24.3

```
[LENGTH]      563
[MW]          64127.72
[pI]          5.45
[HOMOL]       PIR:A41268 guanine nucleotide-binding protein 1 - human 0.0
[SUPFAM]      guanine nucleotide-binding protein 1 0.0
[PROSITE]     ATP_GTP_A      1
[PROSITE]     RGD    1
[KW]          TRANSMEMBRANE  1
[KW]          LOW_COMPLEXITY      6.75 %
[KW]          COILED_COIL        10.48 %

SEQ    MAPEIHMTGPMCLIENTNGELVANPEALKILSAITQPVVVVAIVGLYRTGKSYLMNKLAG
SEG    ............................................................
PRD    cccccccccceeeeeccccchhhhhhhhhhhhhhcceeeeeeeeecccccchhhhhhhhh
COILS  ............................................................
MEM    ...........................MMMMMMMMMMMMMMMMM..............

SEQ    KNKGFSLGSTVKSHTKGIWMWCVPHPKKPEHTLVLLDTEGLGDVKKGDNQNDSWIFTLAV
SEG    ............................................................
PRD    ccccccccccccccceeeeeecccccccceeeeeeccccccccccccccchhhhhhh
COILS  ............................................................
MEM    ............................................................

SEQ    LLSSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDSADFVSFFPDFVWTL
SEG    ............................................................
PRD    hhhhheeeccccchhhhhhhhhhhhhhhhhhhhhcccccccccccccceeeecccceeeeh
COILS  ............................................................
MEM    ............................................................

SEQ    RDFSLDLEADGQPLTPDEYLEYSLKLTQGNRKLAQLEKLQDEELDPEFVQQVADFCSYIF
SEG    ............................................................
PRD    hhhhhhhhcccccccccchhhhhhhhhcccchhhhhhhhhhhhhccccchhhhhhhhhhhc
COILS  ............................................................
```

```
MEM     ............................................................

SEQ     SNSKTKTLSGGIKVNGPCLESLVLTYINAISRGDLPCMENAVLALAQIENSAAVQKAIAH
SEG     ............................................................
PRD     ccccceeecccccccccccchhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhh
COILS   ............................................................
MEM     ............................................................

SEQ     YDQQMGQKVQLPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQLDKKRDD
SEG     ............................................................
PRD     hhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhh
COILS   ............................................................
MEM     ............................................................

SEQ     FCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGGYCLFIQKLQDLEKKYYEEPRKG
SEG     ............................................................
PRD     hhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhccccccccccceeehhhhhhhhhhhhhccccc
COILS   ............................................................
MEM     ............................................................

SEQ     IQAEEILQTYLKSKESVTDAILQTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQ
SEG     ............................xxxxxxxxxxxxxx..................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   ............................................................
MEM     ............................................................

SEQ     QMMEEKEKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKERCQGESTQLQN
SEG     .....................xxxxxxxxxxxx...........................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccchhhhhhhh
COILS   CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC........CCCCCCCCCCCCCCCCCCCCCC
MEM     ............................................................

SEQ     EIQKLQKTLKKKTKRYMSHKLKI
SEG     ..xxxxxxxxxxxx.........
PRD     hhhhhhhhhhhhhhhhhhhhccc
COILS   CCCCCCC................
MEM     .......................
```

Prosite for DKFZphfbr2_78c24.3

PS00016	272->275	RGD	PDOC00016
PS00017	45->53	ATP_GTP_A	PDOC00017

(No Pfam data available for DKFZphfbr2_78c24.3)

DKFZphfbr2_78d13
----

group: brain derived

DKFZphfbr2_78d13 encodes a novel 259 amino acid protein with similarity to C. elegans putative protein from cosmid K08B12.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to C.elegans K08B12.3

Sequenced by MediGenomix

Locus: /map="338.4 cR from top of Chr18 linkage group"

Insert length: 2195 bp
Poly A stretch at pos. 2175, polyadenylation signal at pos. 2156

```
   1 CGTCCGTCGG GCAGCAGCGG GGCTGTCTAT CCCGGCTGAG GACCCGCGGC
  51 CAGTGCGGGT GGCTGGCTTT GCCATTAGCG GGGGCCTTTC CTGAGGACGG
 101 CGTACGGAGT GTGGGGAATG AAGGATGGCA GCATGCCGTG CATTAAAAGC
 151 TGTTTTGGTA GATCTCAGTG GCACACTTCA CATTGAAGAT GCAGCTGTGC
 201 CAGGCGCACA GGAAGCTCTT AAAAGGTTAC GTGGTGCTTC TGTAATCATT
 251 AGGTTTGTGA CCAATACAAC CAAAGAGAGC AAGCAAGACC TGTTAGAAAG
 301 GTTGAGAAAA TTGGAATTTG ATATCTCTGA AGATGAAATA TTCACATCTC
 351 TGACTGCAGC CAGAAGTTTA CTAGAGCGGA AACAAGTCAG ACCCATGCTG
 401 CTAGTTGATG ATCGGGCACT ACCTGATTTC AAAGGAATAC AAACAAGTGA
 451 TCCTAATGCT GTGGTCATGG GATTGGCACC AGAACATTTT CATTATCAAA
 501 TTCTGAATCA AGCATTCCGG TTACTCCTGG ATGGAGCACC TCTGATAGCA
 551 ATCCACAAAG CCAGGTATTA CAAGAGGAAA GATGGCTTAG CCCTGGGGCC
 601 TGGACCATTT GTGACTGCTT TAGAGTATGC CACAGATACC AAAGCCACAG
 651 TCGTGGGGAA ACCAGAGAAG ACGTTCTTTT TGGAAGCATT GCGGGGCACT
 701 GGCTGTGAAC CTGAGGAGGC TGTCATGATA GGAGATGATT GCAGGGATGA
 751 TGTTGGTGGG GCTCAAGATG TCGGCATGCT GGGCATCTTA GTAAAGACTG
 801 GGAAATATCG AGCATCAGAT GAAGAAAAAA TTAATCCACC TCCTTACTTA
 851 ACTTGTGAGA GTTTCCCTCA TGCTGTGGAC CACATTCTGC AGCACCTATT
 901 GTGAAGCAAT GTGTGCATCT GAAGCAACTT GAAATGCAGC TTCTTATTGT
 951 CTGGAATGAA TCCCTTACCA ACTCAGTGCC AGCATCGGTA GACACCAGTC
1001 AGTGCTGATC GCTTTTTAAC CCTCTTTTGT TGTGCATTAA TTAGAAAGAA
1051 AGGTATTGAA TTGCGGCTAG CCAGTAAGCC TTGCTAATCT CTTTTATTTT
1101 GTAACTGAAG ATGAGACCCA AAGAAAGGGA AAGCTGAGAT TTTGTGCCAT
1151 TCCTTTTAAA ATATTCATCA GGTTAGGTGG GGCTGTGGGG GAAAAGCTAC
1201 TACAGGGAAG AGTGTTCTCT GCTGTCTCTT CACTGGAAAA CAGGGAGGGG
1251 GGATTTCAGA CTGTGAAGAA AGTTGAATGG TGGTTTTTAA ATTATAAAGT
1301 AATGTATTAA AAGGTGCATT AGGCTGTAGT TCTAATATTG AGTTCAACTG
1351 TGAAATCCAT CAGATGTGCC AAATGGAGAA GACAGAAAGC AACAAAGTGA
1401 ATTGTTCTTT AGCCCAAGTG GTACAGTGAA TTTGCTTTAA CAGATGTTGA
1451 AAACTAAATT TTCTACTGTA TTCCCAGCAC GGGTGACTTC TTTTTCTCTT
1501 CATTAGCCAG AGATGACTAA TTTAAATTTA GAACCAGATT TTAATTTAAA
1551 TTAATATTTC CATTAATAAC CTACTCATTG CAGATACCTA TTATACTGTG
1601 TAACAGTTGT TTTGGAAATT TTATGTAAAA TTAAAACTAT CAGTATTTTA
1651 CAGATGTTTT AATTAGACAT TGTTATTAAC AGGAACAGTG CAGAAACTAG
1701 AATCAAGCCT TATAATATCT TATAGACCAT GCATTTTTGA AGTTAGTGTC
1751 CACTAGGGTC CTATTAACTG TACATTTGCA AGATTTCATT ATTTTTGCCT
1801 CTGACACTAT GGGAAAAATT TTTTAGAAGC TATTGGGACA GATTCAAGCT
1851 TTTATGCACT TGGTTACTAC AGCTGTAAAA TGAAATCTCG TCTTGTAGCA
1901 TGGATTATTC TTCTCATGTT AAACCCACCA AAATAAAGGG GACTAAATAG
1951 GTAATGATTT TCCTAGTGCA TTTGCATACT GTGATAATCC TGGGCCTTGC
2001 AATAGTTCTA CAGGGCTCTT GGGCATTGAA TTATTAGGAT GTAATTGTAC
2051 ATCATTGTAG TGTTCACCTT ATTGAAGCTC ACTCTGATGT TAATGAGCTT
2101 CGGGTTTTGA TGCTTGTTTA GAGATCAGCA GTCTTGGATG GGAGGGAACA
2151 AAGCTAAATA AATGTTAGTT TGGTGAAAAA AAAAAAAAAA AAAAA
```

BLAST Results

Entry HS599355 from database EMBL:
human STS WI-13484.
Score = 1262, P = 3.6e-52, identities = 274/289

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 125 bp to 901 bp; peptide length: 259
Category: similarity to unknown protein
Classification: no clue

```
  1 MAACRALKAV LVDLSGTLHI EDAAVPGAQE ALKRLRGASV IIRFVTNTTK
 51 ESKQDLLERL RKLEFDISED EIFTSLTAAR SLLERKQVRP MLLVDDRALP
101 DFKGIQTSDP NAVVMGLAPE HFHYQILNQA FRLLLDGAPL IAIHKARYYK
151 RKDGLALGPG PFVTALEYAT DTKATVVGKP EKTFFLEALR GTGCEPEEAV
201 MIGDDCRDDV GGAQDVGMLG ILVKTGKYRA SDEEKINPPP YLTCESFPHA
251 VDHILQHLL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78d13, frame 2

TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid K08B12., N = 1, Score = 609, P = 2.2e-59

TREMBL:CEC13C4_5 gene: "C13C4.4"; Caenorhabditis elegans cosmid C13C4, N = 1, Score = 408, P = 4.4e-38

```
>TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid
     K08B12.
            Length = 257

  HSPs:

 Score = 609 (91.4 bits), Expect = 2.2e-59, P = 2.2e-59
 Identities = 132/251 (52%), Positives = 172/251 (68%)

Query:     7 LKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIRFVTNTTKESKQDLLERLRKLEFD 66
             + +VL+DLSGT+HIE+ A+PGAQ AL+ LR  + + +FVTNTTKESK+ L +RL    F
Sbjct:     4 ISSVLIDLSGTIHIEEFAIPGAQTALELLRQHAKV-KFVTNTTKESKRLLHQRLINCGFK 62

Query:    67 ISEDEIFTSLTAARSLLERKQVRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQI 126
             + ++EIFTSLTAAR L+ + Q RP  +VDDRA+ DF+GI T DPNAVV+GLAPE F+
Sbjct:    63 VEKEEIFTSLTAARDLIVKNQYRPFFIVDDRAMEDFEGISTDDPNAVVIGLAPEKFNDTT 122

Query:   127 LNQAFRLLLDG-APLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKATVVGKPEKTFF 185
             L  AFRL+ +  A LIAI+K RY++   GL LGPG +V  LEY+   +AT+VGKP K FF
Sbjct:   123 LTHAFRLIKEKKASLIAINKGRYHQTNAGLCLGPGTYVAGLEYSAGVEATIVGKPNKLFF 182

Query:   186 LEALRGTG--CEPEEAVMIGDDCRDDVGGAQDVGMLGILVKTGKYRASDEEKINPPPYLT 243
              AL+       +  AVMIGDD  DD  GA  +GM  ILVKTGK+R  DE K+
Sbjct:   183 ESALQSLNENVDFSSAVMIGDDVNDDALGAIKIGMRAILVKTGKFRDGDELKVKN----V 238

Query:   244 CESFPHAVDHILQH 257
               SF  AV+ I+++
Sbjct:   239 ANSFVDAVNMIIEN 252
```

Pedant information for DKFZphfbr2_78d13, frame 2

Report for DKFZphfbr2_78d13.2

```
[LENGTH]     259
[MW]         28536.04
[pI]         5.84
[HOMOL]      TREMBL:CEUK08B12_1 gene: "K08B12.3"; Caenorhabditis elegans cosmid K08B12. 3e-
62
[FUNCAT]     r general function prediction       [M. jannaschii, MJ1437] 3e-05
[SUPFAM]     nagD protein 4e-18
[KW]         Alpha_Beta
```

```
SEQ     MAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIRFVTNTTKESKQDLLERL
PRD     cccccccceeeeeeccccceeeecccccchhhhhhhhhhccceeeeeeeccccchhhhhhhh

SEQ     RKLEFDISEDEIFTSLTAARSLLERKQVRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPE
PRD     hhhccccccceeeehhhhhhhhhhhhccceeeeeechhhhhhcccccccccceeeeecccc

SEQ     HFHYQILNQAFRLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKATVVGKP
PRD     chhhhhhhhhhhhhhccceeeeeecccccccccccccccccchhhhhhhhccceeeeccc

SEQ     EKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGMLGILVKTGKYRASDEEKINPPP
PRD     cchhhhhhhhhhcccccceeeeecccchhhhhhhhhhccceeeeeeecccccccccccccc

SEQ     YLTCESFPHAVDHILQHLL
PRD     ccccccchhhhhhhhhhccc
```

(No Prosite data available for DKFZphfbr2_78d13.2)

(No Pfam data available for DKFZphfbr2_78d13.2)

DKFZphfbr2_78k24
----

group: metabolism

DKFZphfbr2_78k24 encodes a novel 372 amino acid protein with similarity to Mus musculus ubiquitin specific protease UBP43.

The novel protein contains a Prosite ubiquitin carboxyl-terminal hydrolases family 2 signature 2. Ubiquitin carboxyl-terminal hydrolases (EC 3.1.2.15) (UCH) (deubiquitinating enzymes) are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquinated proteins.

The new protein can find application in modulation of protein stability/degradation in cells.

Ubiquitin carboxyl-terminal hydrolases family 2 signature 2.

strong similarity to mouse ubiquitin specific protease UBP43

Sequenced by MediGenomix

Locus: unknown

Insert length: 1874 bp
Poly A stretch at pos. 1852, polyadenylation signal at pos. 1836

```
   1 AGTCCCGACG TGGAACTCAG CAGCGGAGGC TGGACGCTTG CATGGCGCTT
  51 GAGAGATTCC ATCGTGCCTG GCTCACATAA GCGCTTCCTG GAAGTGAAGT
 101 CGTGCTGTCC TGAACGCGGG CCAGGCAGCT GCGGCCTGGG GGTTTTGGAG
 151 TGATCACGAA TGAGCAAGGC GTTTGGGCTC CTGAGGCAAA TCTGTCAGTC
 201 CATCCTGGCT GAGTCCTCGC AGTCCCCGGC AGATCTTGAA GAAAAGAAGG
 251 AAGAAGACAG CAACATGAAG AGAGAGCAGC CCAGAGAGCG TCCCAGGGCC
 301 TGGGACTACC CTCATGGCCT GGTTGGTTTA CACAACATTG GACAGACCTG
 351 CTGCCTTAAC TCCTTGATTC AGGTGTTCGT AATGAATGTG GACTTCACCA
 401 GGATATTGAA GAGGATCACG GTGCCCAGGG GAGCTGACGA GCAGAGGAGA
 451 AGCGTCCCTT TCCAGATGCT TCTGCTGCTG GAGAAGATGC AGGACAGCCG
 501 GCAGAAAGCA GTGCGGCCCC TGGAGCTGGC CTACTGCCTG CAGAAGTGCA
 551 ACGTGCCCTT GTTTGTCCAA CATGATGCTG CCCAACTGTA CCTCAAACTC
 601 TGGAACCTGA TTAAGGACCA GATCACTGAT GTGCACTTGG TGGAGAGACT
 651 GCAGGCCCTG TATACGATCC GGGTGAAGGA CTCCTTGATT TGCGTTGACT
 701 GTGCCATGGA GAGTAGCAGA AACAGCAGCA TGCTCACCCT CCCACTTTCT
 751 CTTTTTGATG TGGACTCAAA GCCCCTGAAG ACACTGGAGG ACGCCCTGCA
 801 CTGCTTCTTC CAGCCCAGGG AGTTATCAAG CAAAAGCAAG TGCTTCTGTG
 851 AGAACTGTGG GAAGAAGACC CGTGGGAAAC AGGTCTTGAA GCTGACCCAT
 901 TTGCCCCAGA CCCTGACAAT CCACCTCATG CGATTCTCCA TCAGGAATTC
 951 ACAGACGAGA AAGATCTGCC ACTCCCTGTA CTTCCCCCAG AGCTTGGATT
1001 TCAGCCAGAT CCTTCCAATG AAGCGAGAGT CTTGTGATGC TGAGGAGCAG
1051 TCTGGAGGGC AGTATGAGCT TTTTGCTGTG ATTGCGCACG TGGGAATGGC
1101 AGACTCCGGT CATTACTGTG TCTACATCCG GAATGCTGTG GATGGAAAAT
1151 GGTTCTGCTT CAATGACTCC AATATTTGCT TGGTGTCCTG GGAAGACATC
1201 CAGTGTACCT ACGGAAATCC TAACTACCAC TGGCAGGAAA CTGCATATCT
1251 TCTGGTTTAC ATGAAGATGG AGTGCTAATG GAAATGCCCA AAACCTTCAG
1301 AGATTGACAC GCTGTCATTT TCCATTTCCG TTCCTGGATC TACGGAGTCT
1351 TCTAAGAGAT TTTGCAATGA GGAGAAGCAT TGTTTTCAAA CTATATAACT
1401 GAGCCTTATT TATAATTAGG GATATTATCA AAATATGTAA CCATGAGGCC
1451 CCTCAGGTCC TGATCAGTCA GAATGGATGC TTTCACCAGC AGACCCGGCC
1501 ATGTGGCTGC TCGGTCCTGG GTGCTCGCTG CTGTGCAAGA CATTAGCCCT
1551 TTAGTTATGA GCCTGTGGGA ACTTCAGGGG TTCCCAGTGG GGAGAGCAGT
1601 GGCAGTGGGA GGCATCTGGG GGCCAAAGGT CAGTGGCAGG GGGTATTTCA
1651 GTATTATACA ACTGCTGTGA CCAGACTTGT ATACTGGCTG AATATCAGTG
1701 CTGTTTGTAA TTTTTCACTT TGAGAACCAA CATTAATTCC ATATGAATCA
1751 AGTGTTTTGT AACTGCTATT CATTTATTCA GCAAATATTT ATTGATCATC
1801 TCTTCTCCAT AAGATAGTGT GATAAACACA GTCATGAATA AAGTTATTTT
1851 CCACAAAAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry AC005500 from database EMBL:
, complete sequence.
Score = 859, P = 5.7e-143, identities = 175/179
8 exons matching Bp 317-1230

Medline entries

99182491:
A novel ubiquitin-specific protease, UBP43, cloned from leukemia fusion protein AML1-ETO-expressing mice, functions in hematopoietic cell differentiation.

Peptide information for frame 1

ORF from 160 bp to 1275 bp; peptide length: 372
Category: strong similarity to known protein
Classification: Protein management
Prosite motifs: UCH_2_2 (302-320)

```
  1 MSKAFGLLRQ ICQSILAESS QSPADLEEKK EEDSNMKREQ PRERPRAWDY
 51 PHGLVGLHNI GQTCCLNSLI QVFVMNVDFT RILKRITVPR GADEQRRSVP
101 FQMLLLLEKM QDSRQKAVRP LELAYCLQKC NVPLFVQHDA AQLYLKLWNL
151 IKDQITDVHL VERLQALYTI RVKDSLICVD CAMESSRNSS MLTLPLSLFD
201 VDSKPLKTLE DALHCFFQPR ELSSKSKCFC ENCGKKTRGK QVLKLTHLPQ
251 TLTIHLMRFS IRNSQTRKIC HSLYFPQSLD FSQILPMKRE SCDAEEQSGG
301 QYELFAVIAH VGMADSGHYC VYIRNAVDGK WFCFNDSNIC LVSWEDIQCT
351 YGNPNYHWQE TAYLLVYMKM EC
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78k24, frame 1

TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus musculus ubiquitin specific protease UBP43 mRNA, complete cds., N = 1, Score = 1367, P = 1e-139

SWISSPROT:UBPE_DROME UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)., N = 2, Score = 248, P = 5.3e-33

```
>TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus
     musculus ubiquitin specific protease UBP43 mRNA, complete cds.
            Length = 368

  HSPs:

 Score = 1367 (205.1 bits), Expect = 1.0e-139, P = 1.0e-139
 Identities = 262/369 (71%), Positives = 295/369 (79%)

Query:     1 MSKAFGLLRQICQSILAESSQSPADLEEKKEEDSNMKREQPRERPRAWDYPHGLVGLHNI 60
             M K FGLLR+ CQS++AE  Q  A LEE  E     KR  R+  AWD PHGLVGLHNI
Sbjct:     1 MGKGFGLLRKPCQSVVAEPQQYSA-LEE--ERTMKRKRVLSRDLCSAWDSPHGLVGLHNI 57

Query:    61 GQTCCLNSLIQVFVMNVDFTRILKRITVPRGADEQRRSVPFQMLLLLEKMQDSRQKAVRP 120
             GQTCCLNSL+QVF+MN+DF  ILKRITVPR A+E++RSVPFQ+LLLLEKMQDSRQKA+ P
Sbjct:    58 GQTCCLNSLLQVFMMNMDFRMILKRITVPRSAEERKRSVPFQLLLLLEKMQDSRQKALLP 117

Query:   121 LELAYCLQKCNVPLFVQHDAAQLYLKLWNLIKDQITDVHLVERLQALYTIRVKDSLICVD 180
              EL  CLQK NVPLFVQHDAAQLYL +WNL KDQITD  L ERLQ L+TI  ++SLICV
Sbjct:   118 TELVQCLQKYNVPLFVQHDAAQLYLTIWNLTKDQITDTDLTERLQGLFTIWTQESLICVG 177

Query:   181 CAMESSRNSSMLTLPLSLFDVDSKPLKTLEDALHCFFQPRELSSKSKCFCENCGKKTRGK 240
             C  ESSR S +LTL L LFD D+KPLKTLEDAL CF QP+EL+S   C CE CG+KT  K
Sbjct:   178 CTAESSRRSKLLTLSLPLFDKDAKPLKTLEDALRCFVQPKELASSDMC-CETCGEKTPWK 236

Query:   241 QVLKLTHLPQTLTIHLMRFSIRNSQTRKICHSLYFPQSLDFSQILPMKRESCDAEEQSGG 300
             QVLKLTHLPQTLTIHLMRFS RNS+T KICHS+ FPQSLDFSQ+LP + +  D +EQS
Sbjct:   237 QVLKLTHLPQTLTIHLMRFSARNSRTEKICHSVNFPQSLDFSQVLPTEEDLGDTKEQSEI 296

Query:   301 QYELFAVIAHVGMADSGHYCVYIRNAVDGKWFCFNDSNICLVSWEDIQCTYGNPNYHWQE 360
              YELFAVIAHVGMAD GHYC YIRN VDGKWFCFNDS++C V+W+D+QCTYGN  Y W+E
Sbjct:   297 HYELFAVIAHVGMADFGHYCAYIRNPVDGKWFCFNDSHVCWVTWKDVQCTYGNHRYRWRE 356

Query:   361 TAYLLVYMK 369
```

```
         TAYLLVY K
Sbjct:   357 TAYLLVYTK 365
```

Pedant information for DKFZphfbr2_78k24, frame 1

Report for DKFZphfbr2_78k24.1

```
[LENGTH]      372
[MW]          43011.12
[pI]          8.05
[HOMOL]       TREMBLNEW:AF069502_1 product: "ubiquitin specific protease UBP43"; Mus musculus
ubiquitin specific protease UBP43 mRNA, complete cds. 1e-151
[FUNCAT]      06.13 proteolysis     [S. cerevisiae, YMR304w] 3e-19
[FUNCAT]      06.13.01 cytoplasmic degradation     [S. cerevisiae, YJL197w] 3e-16
[FUNCAT]      06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)     [S. cerevisiae, YMR223w] 1e-15
[FUNCAT]      04.05.01.04 transcriptional control   [S. cerevisiae, YNL186w] 6e-12
[FUNCAT]      03.10 sporulation and germination    [S. cerevisiae, YDR069c] 9e-11
[FUNCAT]      10.03.99 other osmosensing activities      [S. cerevisiae, YDR069c] 9e-11
[FUNCAT]      30.10 nuclear organization    [S. cerevisiae, YDR069c] 9e-11
[FUNCAT]      30.03 organization of cytoplasm      [S. cerevisiae, YDR069c] 9e-11
[FUNCAT]      09.25 vacuolar and lysosomal biogenesis      [S. cerevisiae, YDR069c] 9e-11
[BLOCKS]      BL00582A Ribosomal protein L33 proteins
[BLOCKS]      BL00972E
[BLOCKS]      BL00972D
[BLOCKS]      BL00972A
[EC]          2.4.2.29 Queuine tRNA-ribosyltransferase 1e-06
[PIRKW]       pentosyltransferase 1e-06
[PIRKW]       glycosyltransferase 1e-06
[PIRKW]       tRNA modification 1e-06
[PIRKW]       alternative splicing 7e-11
[PIRKW]       hydrolase 7e-06
[SUPFAM]      deubiquinating enzyme SSV7 2e-09
[PROSITE]     UCH_2_2 1
[PFAM]        Ubiquitin carboxyl-terminal hydrolases family 2
[PFAM]        Ubiquitin carboxyl-terminal hydrolases family 2
[KW]          Alpha_Beta

SEQ     MSKAFGLLRQICQSILAESSQSPADLEEKKEEDSNMKREQPRERPRAWDYPHGLVGLHNI
PRD     ccccceeechhhhhhhhcccccccchhhhhhhhccccccccccccccccccccccccccc

SEQ     GQTCCLNSLIQVFVMNVDFTRILKRITVPRGADEQRRSVPFQMLLLLEKMQDSRQKAVRP
PRD     cceeehhhhhhhhhhccccchhhhhhhcccccccccchhhhhhhhhhhhhhhhhhccccc

SEQ     LELAYCLQKCNVPLFVQHDAAQLYLKLWNLIKDQITDVHLVERLQALYTIRVKDSLICVD
PRD     hhhhhcccccccccchhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhheeeee

SEQ     CAMESSRNSSMLTLPLSLFDVDSKPLKTLEDALHCFFQPRELSSKSKCFCENCGKKTRGK
PRD     cccccccccccccccccccccccchhhhhhhhhhhhcccccccceeeccccccccccc

SEQ     QVLKLTHLPQTLTIHLMRFSIRNSQTRKICHSLYFPQSLDFSQILPMKRESCDAEEQSGG
PRD     cceeeecccchhhhhhhhhhhcchhhhhcccccccccccccccccccccccccccccccc

SEQ     QYELFAVIAHVGMADSGHYCVYIRNAVDGKWFCFNDSNICLVSWEDIQCTYGNPNYHWQE
PRD     eeeeeeeeeeccccccceeeeeecccccceeeecccceeeeeecccccccccccccchhh

SEQ     TAYLLVYMKMEC
PRD     hhhhhhhhhccc
```

Prosite for DKFZphfbr2_78k24.1

```
PS00973     302->320    UCH_2_2             PDOC00750
```

Pfam for DKFZphfbr2_78k24.1

```
HMM_NAME      Ubiquitin carboxyl-terminal hydrolases family 2

HMM              *GIqNlGNTCYMNSIIQCL*
                  G+ N+G TC +NS+IQ+
Query         56  GLHNIGQTCCLNSLIQVF     73
```

```
HMM_NAME     Ubiquitin carboxyl-terminal hydrolases family 2

HMM                *YdLYgVICHYGntldyGHYWaYVKNenhHRWkWYYFDDEtV*
                    Y+L++VI H G   D+GHY +Y++N     ++KW++F+D+++
Query        302    YELFAVIAHVG-MADSGHYCVYIRNAV--DGKWFCFNDSNI      339
```

DKFZphfbr2_78n23
----

group: brain derived

DKFZphfbr2_78n23 encodes a novel 329 amino acid protein with similarity to A.thaliana F26P21.80 protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A.thaliana F26P21.80

Sequenced by MediGenomix

Locus: /map="89.1 cR from top of Chr19 linkage group"

Insert length: 1447 bp
Poly A stretch at pos. 1374, polyadenylation signal at pos. 1353

```
   1 TACAACTTCC GGCTGTAAAG ATGGCGGCTT CCTAGTGAGT CGGCGGCTGA
  51 CTTAGAAGGA GGTTCAGGCT ACGGTGAGCC GAAGCCACAC AGGAGCCATG
 101 GAAGTGGCAG AGCCCAGCAG CCCCACTGAA GAGGAGGAGG AGGAAGAGGA
 151 GCACTCGGCA GAGCCTCGGC CCCGCACTCG CTCCAATCCT GAAGGGGCTG
 201 AGGACCGGGC AGTAGGGGCA CAGGCCAGCG TGGGCAGCCG CAGCGAGGGT
 251 GAGGGTGAGG CCGCCAGTGC TGATGATGGG AGCCTCAACA CTTCAGGAGC
 301 CGGCCCTAAG TCCTGGCAGG TGCCCCCGCC AGCCCCTGAG GTCCAAATTC
 351 GGACACCAAG GGTCAACTGT CCAGAGAAAG TGATTATCTG CCTGGACCTG
 401 TCAGAGGAAA TGTCACTGCC AAAGCTGGAG TCGTTCAACG GCTCCAAAAC
 451 CAACGCCCTC AATGTCTCTC AGAAGATGAT TGAGATGTTC GTGCGGACAA
 501 AACACAAGAT CGACAAAAGC CACGAGTTTG CACTGGTGGT GGTGAACGAT
 551 GACACGGCCT GGCTGTCTGG CCTGACCTCC GACCCCCGCG AGCTCTGTAG
 601 CTGCCTCTAT GATCTGGAGA CGGCCTCCTG TTCCACCTTC AATCTGGAAG
 651 GACTTTTCAG CCTCATCCAG CAGAAAACTG AGCTTCCGGT CACAGAGAAC
 701 GTGCAGACGA TTCCCCCGCC ATATGTGGTC CGCACCATCC TTGTCTACAG
 751 CCGTCCACCT TGCCAGCCCC AGTTCTCCTT GACGGAGCCC ATGAAGAAAA
 801 TGTTCCAGTG CCCATATTTC TTCTTTGACG TTGTTTACAT CCACAATGGC
 851 ACTGAGGAGA AGGAGGAGGA GATGAGTTGG AAGGATATGT TTGCCTTCAT
 901 GGGCAGCCTG GATACCAAGG GTACCAGCTA CAAGTATGAG GTGGCACTGG
 951 CTGGGCCAGC CCTGGAGTTG CACAACTGCA TGGCGAAACT GTTGGCCCAC
1001 CCCCTGCAGC GGCCTTGCCA GAGCCATGCT TCCTACAGCC TGCTGGAGGA
1051 GGAGGATGAA GCCATTGAGG TTGAGGCCAC TGTCTGAACC ATCCCTGTAC
1101 ATCTGCACCT TCTTGTGCAA GGAAGTCCTT GGCCTAAAGC CTTGGTTCTC
1151 AAACTGGGTT CCTTGGGACC TCCGGGGTGG GGGGGTTCCA GGAGGCACGT
1201 AGGGTACCTT GCAGGGTCCT AGGAGGGAAA CCCAGGATTC CAGGAGGGAT
1251 CCCAGGAACT GTGGGCACCC ATTTTCTGTG TCTCCCAGCC CATTTCCACT
1301 CCTAGTTTGT CATGGATAAT TTTTGTTCTT CCCTGTGTGA TTTTTGCCAT
1351 CAAAATAAAA ATTTGAGACT CGTTAAAAAA AAAAAAAAAA AAAAAAAAAA
1401 AAAAAAAAAA AAAAAAAAAA AAAAAAGAAA AAAAAAAAAA AAAAAAA
```

BLAST Results

Entry HS806352 from database EMBL:
human STS EST192543.
Score = 1285, P = 2.5e-51, identities = 263/266

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 98 bp to 1084 bp; peptide length: 329
Category: similarity to unknown protein
Classification: no clue

```
   1 MEVAEPSSPT EEEEEEEEHS AEPRPRTRSN PEGAEDRAVG AQASVGSRSE
```

```
 51 GEGEAASADD GSLNTSGAGP KSWQVPPPAP EVQIRTPRVN CPEKVIICLD
101 LSEEMSLPKL ESFNGSKTNA LNVSQKMIEM FVRTKHKIDK SHEFALVVVN
151 DDTAWLSGLT SDPRELCSCL YDLETASCST FNLEGLFSLI QQKTELPVTE
201 NVQTIPPPYV VRTILVYSRP PCQPQFSLTE PMKKMFQCPY FFFDVVYIHN
251 GTEEKEEEMS WKDMFAFMGS LDTKGTSYKY EVALAGPALE LHNCMAKLLA
301 HPLQRPCQSH ASYSLLEEED EAIEVEATV
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_78n23, frame 2

PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana, N = 1, Score = 142, P = 1.5e-07

```
>PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana
            Length = 264

  HSPs:

 Score = 142 (21.3 bits), Expect = 1.5e-07, P = 1.5e-07
 Identities = 56/216 (25%), Positives = 97/216 (44%)

Query:    93 EKVIICLDL-SEEMSLPKLESFNGSKTNALNVSQKMIEMFVRTKHKIDKSHEFALVVVND 151
             E ++IC+D+ +E M   K    NG     +   ++ I +F+  K  I+  H FA   +
Sbjct:    26 EDILICIDVDAESMVEMKTTGTNGRPLIRMECVKQAIILFIHNKLSINPDHRFAFATLAK 85

Query:   152 DTAWLSG-LTSDPRELCSCLYDLE-TASCSTFNLEGLFSLIQQKTELPVTENVQTIPPPY 209
               AWL    TSD      + L  L    S S  +L  LF    Q+ ++   +N
Sbjct:    86 SAAWLKKEFTSDAESAVASLRGLSGNKSSSRADLTLLFRAAAQEAKVSRAQN-------R 138

Query:   210 VVRTILVYSRPPCQPQFSLTEPMKKMFQCPYFFFDVVYIHNGTEEKEEEMSWKDMF-AFM 268
             + R IL+Y R   +P      P+ +        F  DV+Y+H    ++    +    +D++ + +
Sbjct:   139 IFRVILIYCRSSMRPTHEW--PLNQKL----FTLDVMYLH---DKPSPDNCPQDVYDSLV 189

Query:   269 GSLD--TKGTSYKYEVALAGPALELHNCMAKLLAHPLQRPCQ 308
              +++  ++    Y +E    G A  +    M+ LL HP QR  Q
Sbjct:   190 DAVEHVSEYEGYIFESG-QGLARSVFKPMSMLLTHPQQRCAQ 230
```

Pedant information for DKFZphfbr2_78n23, frame 2

Report for DKFZphfbr2_78n23.2

```
[LENGTH]      329
[MW]          36560.10
[pI]          4.60
[HOMOL]       PIR:T05304 hypothetical protein F26P21.80 - Arabidopsis thaliana 7e-07
[KW]          Alpha_Beta
[KW]          LOW_COMPLEXITY      9.73 %

SEQ    MEVAEPSSPTEEEEEEEEEHSAEPRPRTRSNPEGAEDRAVGAQASVGSRSEGEGEAASADD
SEG    .xxxxxxxxxxxxxxxxxxxxxx......................................
PRD    ccccccccchhhhhhhhhhhcccccccccccccchhhhhhhhhhcccccccccccccc

SEQ    GSLNTSGAGPKSWQVPPPAPEVQIRTPRVNCPEKVIICLDLSEEMSLPKLESFNGSKTNA
SEG    ............................................................
PRD    cccccccccccccccccccceeeccccccccccceeeeecccccccccccccccccccee

SEQ    LNVSQKMIEMFVRTKHKIDKSHEFALVVVNDDTAWLSGLTSDPRELCSCLYDLETASCST
SEG    ............................................................
PRD    ehhhhhhhhhhhhhhhhccccccceeeeeeccchhhhhccccchhhhhhhhhcccccccc

SEQ    FNLEGLFSLIQQKTELPVTENVQTIPPPYVVRTILVYSRPPCQPQFSLTEPMKKMFQCPY
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhcccccccccceeeeeeeccccccccccccchhhhhheeee

SEQ    FFFDVVYIHNGTEEKEEEMSWKDMFAFMGSLDTKGTSYKYEVALAGPALELHNCMAKLLA
SEG    ............................................................
PRD    eeeeeeeeccccchhhhhhhhhhhhhhhhcccccccccceeeeeccccchhhhhhhhhhhh

SEQ    HPLQRPCQSHASYSLLEEEDEAIEVEATV
SEG    ................xxxxxxxxxx...
PRD    hccccccccccchhhhhhhhhhhhhhhccc
```

(No Prosite data available for DKFZphfbr2_78n23.2)

(No Pfam data available for DKFZphfbr2_78n23.2)

DKFZphfbr2_7a24
----

group: brain derived

DKFZphfbr2_7a24 encodes a novel 142 amino acid protein with similarity to the C-terminal part of transforming growth factor-beta activated kinases.

The novel protein shows only similarity to the C-terminus of such kinases; no kinase domain is present.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to C-terminus of TGF-beta-activated kinase

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1697 bp
No poly A stretch found, no polyadenylation signal found

```
   1 GGGGAGAGAG GGGTTGTGAA GGGAAGCGGA AGGGAAGGGA AGGGAGGTCC
  51 CGTGGGACGC TGGGGTCTGG GGTAGAGCAG GTAGCAGCGT GCTGCCCTGA
 101 CAGCTGTCTC CGCTCCTCAG ATTGTCAGTG GCTGCTATGC AGCAGGTGCA
 151 GCCTGGTCTC TCACTGAGTC TCTACTCCAC AAAGGCAACG ACTGGCCAAG
 201 GCAGTGGCTG GCTCTGGGTT ACACAAGTGC AGACACTCAA CTAAGTGAGC
 251 TGGAAGACCC AGGAGAAGGC GGAGGCTCAG GTGCCCACAT GATCAGCACA
 301 GCCAGGGTAC CTGCTGACAA GCCTGTACGC ATCGCCTTTA GCCTCAATGA
 351 CGCCTCAGAT GATACACCCC CTGAAGACTC CATTCCTTTG GTCTTTCCAG
 401 AATTAGACCA GCAGCTACAG CCCCTGCCGC CTTGTCATGA CTCCGAGGAA
 451 TCCATGGAGG TGTTCAGACA GCACTGCCAA ATAGCAGAAG AATACCTTGA
 501 GGTCAAAAAG GAAATCACCC TGCTTGAGCA AAGGAAGAAG GAGCTCATTG
 551 CCAAGTTAGA TCAGGCAGAA GAGGAGAAGG TGGATGCTGC TGAGCTGGTT
 601 CGGGAATTCG AGGCTCTGAC GGAGGAGAAT CGGACGTTGA GGTTGGCCCA
 651 GTCTCAATGT GTGGAACAAC TGGAGAAACT TCGAATACAG TATCAGAAGA
 701 GGCAGGGCTC GTCCTAACTT TAAATTTTTC AGTGTGAGCA TACGAGGCTG
 751 ATGACTGCCC TGTGCTGGCC AAAAGATTTT TATTTTAAAT GAATAGTGAG
 801 TCAGATCTAT TGCTTCTCTG TATTACCCAC ATGACAACTG TCTATAATGA
 851 GTTTACTGCT TGCCAGCTTC TAGCTTGAGA GAAGGGATAT TTTAAATGAG
 901 ATCATTAACG TGAAACTATT ACTAGTATAT GTTTTTGGAG ATCAGAATTC
 951 TTTTCCAAAG ATATATGTTT TTTTCTTTTT TAGGAAGATA TGATCATGCT
1001 GTACAACAGG GTAGAAAATG GTAAAAATAG ACTATTGACT GACCCAGCTA
1051 AGAATCGCGG GCTGAGCAGA GTTAAACCAT GGGACAAACC CATAACATGT
1101 TCACCATAGT TTCACGTATG TGTATTTTTA AATTTCATGC CTTTAATATT
1151 TCAAATATGC TCAAATTTAA ACTGTCAGAA ACTTCTCTGC ATGTATTTAT
1201 ATTTGCCAGA GTATAAACTT TTATACTCTG ATTTTTATCC TTCAATGATT
1251 GATTATACTA AGAATAAATG GTCACATATC CTAAAAGCTT CTTCATGAAA
1301 TTATTAGCAG AAACCATGTT TGAAACCAAA GCACATTTGC CAATGCTAAC
1351 TGGCTGTTGT AATAATAAAC AGATAAGGCT GCATTTGCTT CATGCCATGT
1401 GACCTCACAG TAAACATCTC TGCCTTTGCC TGTGTGTGTT CTGGGGGAGG
1451 GGGGACATGG AAAAATATTG TTTGGACATT ACTTGGGTGA GTGCCCATGA
1501 AGACATCAGT GAACTTGTAA CTATTGTTTT GTTTTGGATT TAAGGAGATG
1551 TTTTAGATCA GTAACAGCTA ATAGGAATAT GCGAGTAAAT TCAGAATTGA
1601 AACAATTTCT CCTTGTTCTA CCTATCACCA CATTTTCTCA AATTGAACTC
1651 TTTGTTATAT GTCCATTTCT ATTCATGTAA CTTCTTTTTC ATTAAAC
```

BLAST Results

No BLAST result

Medline entries

98130593:
Role of TAK1 and TAB1 in BMP signaling in early Xenopus development.

Peptide information for frame 1

```
ORF from 289 bp to 714 bp; peptide length: 142
Category: similarity to known protein


    1 MISTARVPAD KPVRIAFSLN DASDDTPPED SIPLVFPELD QQLQPLPPCH
   51 DSEESMEVFR QHCQIAEEYL EVKKEITLLE QRKKELIAKL DQAEEEKVDA
  101 AELVREFEAL TEENRTLRLA QSQCVEQLEK LRIQYQKRQG SS
```

BLASTP hits

```
Entry U92030_1 from database TREMBL:
product: "TAK1"; Xenopus laevis TGF-beta-activated kinase TAK1 mRNA,
complete cds.
Score = 343, P = 1.3e-30, identities = 69/143, positives = 104/143

Entry AB009356_1 from database TREMBL:
product: "TGF-beta activated kinase 1a"; Homo sapiens mRNA for
TGF-beta activated kinase 1a, complete cds.
Score = 339, P = 2.6e-30, identities = 67/143, positives = 104/143

Entry MMPK_1 from database TREMBL:
product: "TAK1 (TGF-beta-activated kinase)"; Mouse mRNA for TAK1
(TGF-beta-activated kinase), complete cds.
Score = 339, P = 2.6e-30, identities = 67/143, positives = 104/143

Entry AB009357_1 from database TREMBL:
product: "TGF-beta activated kinase 1b"; Homo sapiens mRNA for
TGF-beta activated kinase 1b, complete cds.
Score = 339, P = 3.2e-30, identities = 67/143, positives = 104/143

Entry AB009358_1 from database TREMBL:
product: "TGF-beta activated kinase 1c"; Homo sapiens mRNA for
TGF-beta activated kinase 1c, complete cds.
Score = 144, P = 3.8e-09, identities = 30/67, positives = 47/67
```

Alert BLASTP hits for DKFZphfbr2_7a24, frame 1

```
PIR:JC5955 transforming growth factor-beta activated kinase (EC
-.-.-.-) 1a - Human, N = 1, Score = 339, P = 3e-30


>PIR:JC5955 transforming growth factor-beta activated kinase (EC -.-.-.-) 1a
     - Human
            Length = 579

  HSPs:

 Score = 339 (50.9 bits), Expect = 3.0e-30, P = 3.0e-30
 Identities = 67/143 (46%), Positives = 104/143 (72%)

Query:     1 MISTARVPADKPVRI-AFSLNDASDDTPPEDSIPLVFPELDQQLQPLPPCHDSEESMEVF 59
             MI+T+    ++KP R   ++ +D++D    ++SIP+ +  LD QLQPL PC +S+ESM VF
Sbjct:   437 MITTSGPTSEKPTRSHPWTPDDSTDTNGSDNSIPMAYLTLDHQLQPLAPCPNSKESMAVF 496

Query:    60 RQHCQIAEEYLEVKKEITLLEQRKKELIAKLDQAEEEKVDAAELVREFEALTEENRTLRL 119
              QHC++A+EY++V+ EI LL QRK+EL+A+LDQ E+++ + + LV+E + L +EN++L
Sbjct:   497 EQHCKMAQEYMKVQTEIALLLQRKQELVAELDQDEKDQQNTSRLVQEHKKLLDENKSLST 556

Query:   120 AQSQCVEQLEKLRIQYQKRQGSS 142
                QC +QLE +R Q QKRQG+S
Sbjct:   557 YYQQCKKQLEVIRSQQQKRQGTS 579
```

Pedant information for DKFZphfbr2_7a24, frame 1

Report for DKFZphfbr2_7a24.1

```
[LENGTH]       142
[MW]           16377.53
[pI]           4.64
[HOMOL]        TREMBL:U92030_1 product: "TAK1"; Xenopus laevis TGF-beta-activated kinase TAK1
mRNA, complete cds. 6e-26
[PROSITE]      CK2_PHOSPHO_SITE       3
```

```
[PROSITE]     PKC_PHOSPHO_SITE       2
[PROSITE]     ASN_GLYCOSYLATION      1
[PFAM]        TNFR/NGFR cysteine-rich region
[KW]          All_Alpha
[KW]          LOW_COMPLEXITY      7.04 %
[KW]          COILED_COIL        33.10 %

SEQ    MISTARVPADKPVRIAFSLNDASDDTPPEDSIPLVFPELDQQLQPLPPCHDSEESMEVFR
SEG    .....................................xxxxxxxxxx............
PRD    cccccccccccccccccccccccccccccccccccchhhhhhhhccccccccccchhhhhhh
COILS  ............................................................

SEQ    QHCQIAEEYLEVKKEITLLEQRKKELIAKLDQAEEEKVDAAELVREFEALTEENRTLRLA
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcchhhhh
COILS  ...CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC..........

SEQ    QSQCVEQLEKLRIQYQKRQGSS
SEG    ......................
PRD    hhhhhhhhhhhhhhhhhhhccc
COILS  ......................
```

Prosite for DKFZphfbr2_7a24.1

PS00001	114->118	ASN_GLYCOSYLATION	PDOC00001
PS00005	4->7	PKC_PHOSPHO_SITE	PDOC00005
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00006	18->22	CK2_PHOSPHO_SITE	PDOC00006
PS00006	26->30	CK2_PHOSPHO_SITE	PDOC00006
PS00006	77->81	CK2_PHOSPHO_SITE	PDOC00006

Pfam for DKFZphfbr2_7a24.1

```
HMM_NAME      TNFR/NGFR cysteine-rich region

HMM              *CpeGtYtDWNHvpqClpCtrCePEMGQYMvqPCTwTQNTVC*
                  C++++ + +    +Q   C++ E+    ++++++ T   + ++
Query         49  CHDSEESMEVF-RQH--CQIAEE--YLEVKKEITLLEQRKK      84
```

DKFZphfbr2_7e22
----

group: brain derived

DKFZphfbr2_7e22.2 encodes a novel 286 amino acid protein similar to b561 cytochromes

The new protein shows strong similarity to B561 cytochromes, but contains no heme binding site. In addition, a myc-type, helix-loop-helix dimerization domain domain is present. This helix-loop-helix domain mediates protein dimerization and has been found in proteins such as the myc family of cellular oncogenes, proteins involved in myogenesis and vertebrate proteins that bind specific DNA sequences in various immunoglobulin chains enhancers.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

strong similarity to cytochrome b561

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 4254 bp
Poly A stretch at pos. 4234, polyadenylation signal at pos. 4217

```
   1 GGGGACTACC CAGAGGGCTG CCGCCGCCTC TCCAAGTTCT TGTGGCCCCC
  51 GCGGTGCGGA GTATGGGGCG CTGATGGCCA TGGAGGGCTA CCGGCGCTTC
 101 CTGGCGCTGC TGGGGTCGGC ACTGCTCGTC GGCTTCCTGT CGGTGATCTT
 151 CGCCCTCGTC TGGGTCCTCC ACTACCGAGA GGGGCTTGGC TGGGATGGGA
 201 GCGCACTAGA GTTTAACTGG CACCCAGTGC TCATGGTCAC CGGCTTCGTC
 251 TTCATCCAGG GCATCGCCAT CATCGTCTAC AGACTGCCGT GGACCTGGAA
 301 ATGCAGCAAG CTCCTGATGA AATCCATCCA TGCAGGGTTA AATGCAGTTG
 351 CTGCCATTCT TGCAATTATC TCTGTGGTGG CCGTGTTTGA GAACCACAAT
 401 GTTAACAATA TAGCCAATAT GTACAGTCTG CACAGCTGGG TTGGACTGAT
 451 AGCTGTCATA TGCTATTTGT TACAGCTTCT TTCAGGTTTT TCAGTCTTTC
 501 TGCTTCCATG GGCTCCGCTT TCTCTCCGAG CATTTCTCAT GCCCATACAT
 551 GTTTATTCTG GAATTGTCAT CTTTGGAACA GTGATTGCAA CAGCACTTAT
 601 GGGATTGACA GAGAAACTGA TTTTTTCCCT GAGAGATCCT GCATACAGTA
 651 CATTCCCGCC AGAAGGTGTT TTCGTAAATA CGCTTGGCCT TCTGATCCTG
 701 GTGTTCGGGG CCCTCATTTT TTGGATAGTC ACCAGACCGC AATGGAAACG
 751 TCCTAAGGAG CCAAATTCTA CCATTCTTCA TCCAAATGGA GGCACTGAAC
 801 AGGGAGCAAG AGGTTCCATG CCAGCCTACT CTGGCAACAA CATGGACAAA
 851 TCAGATTCAG AGTTAAACAA TGAAGTAGCA GCAAGGAAAA GAAACTTAGC
 901 TCTGGATGAG GCTGGGCAGA GATCTACCAT GTAAAATGTT GTAGAGATAG
 951 AGCCATATAA CGTCACGTTT CAAAACTAGC TCTACAGTTT TGCTTCTCCT
1001 ATTAGCCATA TGATAATTGG GCTATGTAGT ATCAATATTT ACTTTAATCA
1051 CAAAGGATGG TTTCTTGAAA TAATTTGTAT TGATTGAGGC CTATGAACTG
1101 ACCTGAATTG GAAAGGATGT GATTAATATA AATAATAGCA GATATAAATT
1151 GTGGTTATGT TACCTTTATC TTGTTGAGGA CCACAACATT AGCACGGTGC
1201 CTTGTGCAGA ATAGATACTC AATATGTGAA TATGTGTCTA CTAGTAGTTA
1251 ATTGGATAAA CTGGCAGCAT CCCTGGCCTG TTGTCATGCA GTCATTTCCT
1301 GTTAATTCTG GGAGACAATG ATTTCACAAC TAGAGGGAAG CAGTCCTAAA
1351 AGTTTAAAAT CCGATAAGGA ATATCTGGGA CAGGGTTTAG ATCATGACTC
1401 TACACAGATA CCATGATGAG AGTATATTAA AGAAATTTAG GAAAGCACCT
1451 GGTTCCTTTC TCCCCATGCC TGCCTTCTGC TCCCTCCCCA GCTGGTTTGG
1501 GCTCAAATTG TCCCTGGAGA CTAGGGTTTA TGTTAGGGTA TTGATAGATT
1551 AGAGCAGGTG GTTGAAGAGA TCTTCTCTGG TCAGACTTGG AAGAATTTCC
1601 AAAAGTGAAG TTAGCCCCAA GACTTCCCTA GGGTTGATGT ACTTTATGAT
1651 CCAGATGCTA AACTTCTTAG AATGAAAATA TGCTTCAACA CTTAAGTAGC
1701 ATACACTGCC CTACAAACCT CAGAGAGCAC TTTTCCCCAA GTTCTTGTTT
1751 TTATTTTTGA AAGTACTCAC ACAGCACTTA CTATGCTCCA AACACTCCTC
1801 TAAGCACTTT ACACATATTA GCTCATTCAG TCCCCAGACA GACGGGATGA
1851 AGTAGGTATT GTTACTGTTC CCATTTTACA GGTGAGAGAT TTGAAGCCTG
1901 GGGAGGCTAG TAACTCACCC CAAGGTCACA CGGCTCATAC ATGGTGGGAC
1951 TGAGACTCAG ATGCAGGCAG TCTGGCACCT CAGTCTGGAT TCTAACCATT
2001 TCACTAAGCT ATTTTTGTCT TGTACTACTT TGACCCACCC CTGAATAAAC
2051 CTCAATTGCT GGAGTGGGGT GTAGTTATTA AAGGGATGCT TTTTACCTTT
2101 TGCTGTCTGC TGTGGCAGAT TCCCCAGATA ACCAAGGAAA AGGGGCCACC
2151 CATACCTGGA AATAGGCCAT AGGGCCCCTA CTACTGCCAA CAAGCCATGG
2201 CCTACCTTGA CACTTGTTTG ATCTTAAAAT TGTGTCTTGG TAACAAAAGA
2251 TTTGGACAGG CATATCTGTA GCTTTCAAGT TAATTAATTG CAATATTTTT
2301 TTCTTCAGGA TTTTAGCTGC TGAACAACTT TCAGTTTGGA GCTAAAAGAG
2351 ACCTGTCTCA TGGTCTGCCC TTCCCTGGGG CAATAGCTAG GGTCTTTCCT
2401 GATTTTTATG GAATTTTAGG GGATATTTTG AGCTTTGGGT TCTCAGTAGT
```

```
2451 GAATTGAGAC TTGGAGGTGA CTTTTCATGT TTGGAGTATC ATCTCTGTCT
2501 GGGCTCTGGG CTGACAAATT AAAACCTAGA GTAGTGCTTA TGCTGAAATG
2551 ATACTTTTCA TTTTTTGGTT GATTTTTTTG CCTTCCCTTC AATTTTAAAC
2601 TGAAGCATTT TAATGTGGGT AGAAACTCTA CACCAAATAC ACTAAACATT
2651 TTGGTGCTTA GTGGATTTCT TTTTAGGTAA CTGGTACTTA CTTCCAAAGA
2701 CTGAATACAA GCCACACTCC ATCATATCCC TTAAACTTCA TGAAAAACCA
2751 TTCAAGATCC CCTTGCTGCA ACACTGTTCT CTTCTTCTCT ACTAAATTCT
2801 ATTTCCAAAA TTGGTAATAG AGCCAGAAGG ATCCCCAGTA CCCAGCCCTC
2851 TGCCTGGCAC AAAGTGGTAG CACAATTAAA TTCAGTATGG GTGGAGCATG
2901 GTACAGTCTT GGTGCCATAG AAGGAGTAGT TGCATAGTCA CACATCATTT
2951 GATAAGTTGG ATGTTCCATT ACATAGAGGA ACACAAAATT CCAGGGTTTT
3001 TGGAGGAAGG GATTAGATAG CGACTAAGCC GCCAGAATTG AGGTGGCCAT
3051 TCCTTTTTGT ATAGGCTAAG AAACAGGTTA TCAGTGAAAA GTTAATTATG
3101 GCTTTGGCAC TAGAATAGCA CTGTTGCAAA GTATTTAAGC ACCCCCCATC
3151 TCAGCCCTTT ATTTTATCTT TCATGTGGGC TAATGTGAGG ATAATCTTAC
3201 AGATATTATA GGAATTTCTT TTCTATCTTT ATGAAAACAA CGTATATAAA
3251 ATATATCTAG AAAACCTTTG TTTGAGACTC TTATTTAATG GGCTTTTGAT
3301 TCTAATGATA ATTGTACCTT TATCTTTCAA AAGCTGATAT TTCCTACCTA
3351 AGCATCTCCC GAGAAAAATA TCTCATTAAA AAGCCCATAA ATAATAGGGG
3401 AGAAGAAAGC CTTAGGTATC AATTCCAAAA CAGTGATTGA AATTTCCCAA
3451 AATAATTATG GCTTCTGTCA TCTCCAGAGA TAATCTGGCT TGGTTTACCC
3501 CATAATCTAA TTTCAGAAAA GAAAGCTTTA TTTTAACACT CATCTGAATC
3551 AACATTAAAG CCTTTTCTCT CAAAGCGTTT ATTGAGAAAC TCAAATGAAT
3601 ATACTTTTTG AATTACTGTC ATCAAAAGTG TACGGCTTCC TGTGCTGCTT
3651 GTGTCAAATG GAACCTGCCC TCTAAAGCAC TTTCTTTCCT TTACTTGCGT
3701 GGTTTCATGT AAGCTGTGCT GTTTAGAAAC AACATCTCAG ACTTTACAAA
3751 GAAATGACAA AGAAGGCAAT TGCACTTTTT AAGGGATATC GACAAGCAGT
3801 TTCTGTTTTC TAAAGGACAA AATACAGAGT GTGTGTCATT TTTAATTAGA
3851 TTCTTTCCCC TGCTGAGTTG GAAATTCCAG TGCAGCACTG ATTGACCACA
3901 GTTGCCAATC TAAAAGCACA AAGACAGAAG TAAAGCTTTA TGCTAATTTT
3951 ATTTCAATAT GATAGAAAAT TTATCTTGGT ATGTCCTTTT TTAGATAACT
4001 CCAGCAGGAA ACTGTAACTG CTATGTCTTT AGGAAAACGT AGAAGAAAGA
4051 ACATTATTAT TCTTTAATTC CTACAAGGTA CTTGAAAACC TTAAGTGAAA
4101 AAGATTTCTA TCTTTTTATC TTGGCGCATT TATGGAAAAA ATATTAACTG
4151 TCCTGAATAT TTTATAATTT TGTAGGAAAA ATATGCATCT ATTTTTTCTT
4201 GACTTCTTTT ATATAGTAAT AAAAGTTATT TTGGAAAAAA AAAAAAAAAA
4251 AAAA
```

BLAST Results

Entry HSG20626 from database EMBL:
human STS A005Z27.
Score = 860, P = 3.0e-32, identities = 176/181

Medline entries

89030633:
The structure of cytochrome b561, a secretory vesicle-specific electron transport protein.

Peptide information for frame 2

ORF from 74 bp to 931 bp; peptide length: 286
Category: strong similarity to known protein
Classification: unset

```
  1 MAMEGYRRFL ALLGSALLVG FLSVIFALVW VLHYREGLGW DGSALEFNWH
 51 PVLMVTGFVF IQGIAIIVYR LPWTWKCSKL LMKSIHAGLN AVAAILAIIS
101 VVAVFENHNV NNIANMYSLH SWVGLIAVIC YLLQLLSGFS VFLLPWAPLS
151 LRAFLMPIHV YSGIVIFGTV IATALMGLTE KLIFSLRDPA YSTFPPEGVF
201 VNTLGLLILV FGALIFWIVT RPQWKRPKEP NSTILHPNGG TEQGARGSMP
251 AYSGNNMDKS DSELNNEVAA RKRNLALDEA GQRSTM
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_7e22, frame 2

SWISSPROT:C561_SHEEP CYTOCHROME B561 (CYTOCHROME B-561)., N = 1, Score

= 460, P = 1.3e-43

PIR:S01167 cytochrome b561 - bovine, N = 1, Score = 457, P = 2.7e-43

SWISSPROT:C561_PIG CYTOCHROME B561 (CYTOCHROME B-561)., N = 1, Score = 452, P = 9.1e-43

PIR:S53321 cytochrome B561 - human, N = 1, Score = 451, P = 1.2e-42

```
>SWISSPROT:C561_SHEEP CYTOCHROME B561 (CYTOCHROME B-561).
            Length = 252

  HSPs:

 Score = 460 (69.0 bits), Expect = 1.3e-43, P = 1.3e-43
 Identities = 96/218 (44%), Positives = 131/218 (60%)

Query:    18 LVGFLSVIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVFIQGIAIIVYRLPWTWKC 77
             L+G   V     W+  YR G+ W+ SAL+FN HP+ MV G VF+QG A++VYR+
Sbjct:    23 LLGLTVVAMTGAWLGMYRGGIAWE-SALQFNVHPLCMVIGLVFLQGDALLVYRV--FRNE 79

Query:    78 SKLLMKSIHAGLNAVAAILAIISVVAVFENHNVNNIANMYSLHSWVGLIAVICYLLQLLS 137
             +K   K +H  L+  A ++A++ +VAVFE+H       A++YSLHSW G++    +  Q L
Sbjct:    80 AKRTTKVLHGLLHVFAFVIALVGLVAVFEHHRKKGYADLYSLHSWCGILVFALFFAQWLV 139

Query:   138 GFSVFLLPWAPLSLRAFLMPIHVYSGIVIFGTVIATALMGLTEKLIFSLRDPAYSTFPPE 197
             GFS FL P A  SLR+   P HV+ G  IF   +ATAL+GL E L+F L     YSTF PE
Sbjct:   140 GFSFFLFPGASFSLRSRYRPQHVFFGAAIFLLSVATALLGLKEALLFEL-GTKYSTFEPE 198

Query:   198 GVFVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTIL 235
             GV  N LGLL+  F   ++ +I+TR  WKRP +      L
Sbjct:   199 GVLANVLGLLLAAFATVVLYILTRADWKRPLQAEEQAL 236
```

Pedant information for DKFZphfbr2_7e22, frame 2

Report for DKFZphfbr2_7e22.2

```
[LENGTH]      286
[MW]          31638.58
[pI]          9.12
[HOMOL]       SWISSPROT:C561_SHEEP CYTOCHROME B561 (CYTOCHROME B-561). 4e-40
[PIRKW]       transmembrane protein 9e-40
[KW]          SIGNAL_PEPTIDE 40
[KW]          TRANSMEMBRANE  5
[KW]          LOW_COMPLEXITY     4.90 %

SEQ      MAMEGYRRFLALLGSALLVGFLSVIFALVWVLHYREGLGWDGSALEFNWHPVLMVTGFVF
SEG      ............................................................
PRD      cchhhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhccccccccccccccccchhhhhhhhh
MEM      ...............................................MMMMMMMMMMMMM

SEQ      IQGIAIIVYRLPWTWKCSKLLMKSIHAGLNAVAAILAIISVVAVFENHNVNNIANMYSLH
SEG      ...............................xxxxxxxxxxxxxx................
PRD      cccceeeeecccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccceeecc
MEM      MMMMMMMMMMMMM........MMMMMMMMMMMMMMMMMMMMMMMMMM.............

SEQ      SWVGLIAVICYLLQLLSGFSVFLLPWAPLSLRAFLMPIHVYSGIVIFGTVIATALMGLTE
SEG      ............................................................
PRD      ccchhhhhhhhhhhhhhhheeeecccccccccccccccceeeeeeeeeeehhhhhhhhhh
MEM      ....MMMMMMMMMMMMMMMMMMMMM...........MMMMMMMMMMMMMMMMMMMMM...

SEQ      KLIFSLRDPAYSTFPPEGVFVNTLGLLILVFGALIFWIVTRPQWKRPKEPNSTILHPNGG
SEG      ............................................................
PRD      hhhhhhhcccccccccccchhhhhhhhhhhhhhhhhheeeeeecccccccccccccccccccc
MEM      ................MMMMMMMMMMMMMMMMMMMMMMMMMMMMMM...............

SEQ      TEQGARGSMPAYSGNNMDKSDSELNNEVAARKRNLALDEAGQRSTM
SEG      ..............................................
PRD      ccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhcccc
MEM      ..............................................
```

(No Prosite data available for DKFZphfbr2_7e22.2)

(No Pfam data available for DKFZphfbr2_7e22.2)

DKFZphfbr2_7j4
----

group: brain derived

DKFZphfbr2_7j4 encodes a novel 233 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

unknown

complete cDNA, complete cds, 1 EST hit

Sequenced by GBF

Locus: unknown

Insert length: 1050 bp
Poly A stretch at pos. 1027, polyadenylation signal at pos. 1007

```
   1 GGGGACACAA AGGGGTGGTC ACCCTGCCCT CACCTTGACC TGTAAGTTGC
  51 CTAGGACAGT GGCCTGGTCC CAGGGGCTGT TGTGGGGAGT TGAAGAACAC
 101 CCTGGCCTCC TCCATCATGT CGGCCAAGAG GGCAGAATTG AAGAAAAACAC
 151 ATCTGTGCAA GAACTACAAG GCAGTTTGCC TGGAATTGAA GCCAGAGCCG
 201 ACCAAAACAT TTGATTACAA AGCAGTTAAA CAAGAAGGGC GGTTTACCAA
 251 AGCAGGAGTG ACACAGGACC TAAAGAATGA ACTCAGGGAA GTGAGAGAAG
 301 AGCTCAAGGA GAAAATGGAG GAGATAAAAC AGATAAAGGA TCTAATGGAC
 351 AAGGATTTTG ATAAACTTCA CGAATTTGTG GAAATTATGA AGGAAATGCA
 401 GAAAGATATG GATGAGAAGA TGGACATTTT AATAAATACA CAGAAGAACT
 451 ATAAGCTTCC CCTTAGAAGA GCACCAAAGG AGCAGCAGGA ACTCAGGCTG
 501 ATGGGAAAGA CTCACAGAGA ACCACAGCTC AGGCCCAAGA AAATGGATGG
 551 AGCCAGTGGA GTCAATGGAG CACCCTGTGC TCTTCACAAG AAGACGATGG
 601 CACCACAAAA AACAAAACAG GGCTCACTGG ATCCCCTTCA TCACTGTGGG
 651 ACCTGCTGCG AGAAATGTTT GTTGTGTGCT CTAAAGAACA ACTACAATCG
 701 GGGGAACATT CCTTCAGAGG CCTCAGGCCT TTACAAAGGT GGAGAGGAGC
 751 CAGTGACCAC CCAACCTTCT GTGGGCCACG CTGTGCCTGC CCCAAAGTCC
 801 CAGACTGAGG GAAGGTGAAG CTTAACTGCC AGCTTGAAAT GAGAGTAAAG
 851 AAGATACAGA GCAAACAGTG TTTCAGAAAC TGTCCTGCCC TGGGTGTGAT
 901 TCTTTGGCTT CAATTTGAAG GAGGAGGAAT GATGGGATTT CATATTTTAT
 951 TTCACACCAG TTCCTCCTTG TTTCATCTCT TTGCTAAGCT GGCTGCTTCT
1001 ACCATCTAAT AAATAATTGG CCAAGTTAAA AAAAAAAAAA AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 117 bp to 815 bp; peptide length: 233
Category: putative protein

```
   1 MSAKRAELKK THLCKNYKAV CLELKPEPTK TFDYKAVKQE GRFTKAGVTQ
  51 DLKNELREVR EELKEKMEEI KQIKDLMDKD FDKLHEFVEI MKEMQKDMDE
 101 KMDILINTQK NYKLPLRRAP KEQQELRLMG KTHREPQLRP KKMDGASGVN
 151 GAPCALHKKT MAPQKTKQGS LDPLHHCGTC CEKCLLCALK NNYNRGNIPS
 201 EASGLYKGGE EPVTTQPSVG HAVPAPKSQT EGR
```

BLASTP hits

Entry JC2223 from database PIR:
major surface glycoprotein 3 - Pneumocystis carinii (fragment)
Score = 109, P = 3.5e-04, identities = 41/136, positives = 67/136

Alert BLASTP hits for DKFZphfbr2_7j4, frame 3

TREMBLNEW:PCP115C_1 product: "P115C"; Pneumocystis carinii mRNA for P115C, partial sequence., N = 1, Score = 109, P = 0.00024

```
>TREMBLNEW:PCP115C_1 product: "P115C"; Pneumocystis carinii mRNA for P115C,
     partial sequence.
            Length = 196

  HSPs:

 Score = 109 (16.4 bits), Expect = 2.4e-04, P = 2.4e-04
 Identities = 41/134 (30%), Positives = 67/134 (50%)

Query:    14 CKN-YKAVCLELKPEPTKTFDYKAVKQEGRFTKA-GVTQDLKNELREVREELKEKMEEIK 71
             CK   K C ELK       + K VK+    TK  G  ++LK+++++  E  KE++E  K
Sbjct:    22 CKTELKKYCEELKEADGLKVNDK-VKEICDDTKRDGKCKELKDKVKKELETFKEELE--K 78

Query:    72 QIKDLMDKDFDKLHEFVEIMKEMQKDMDEKMDILINTQKNYKLPLRRAPKEQQELRLMGK 131
              +KD+ D++ +K  E   +++E   D D K + +   +  YKL  +R   E   LR +GK
Sbjct:    79 ALKDIKDENCEKYEEKCILLEETNHD-DVKKNCVKLREGCYKLKRKRVA-EDLLLRALGK 136

Query:   132 THREPQLRPKKMDGAS 147
              +  +     K  D  S
Sbjct:   137 DVKNGECEKKMKDVCS 152
```

Pedant information for DKFZphfbr2_7j4, frame 3

Report for DKFZphfbr2_7j4.3

```
[LENGTH]       233
[MW]           26533.95
[pI]           9.18
[PROSITE]      MYRISTYL        3
[PROSITE]      CK2_PHOSPHO_SITE       3
[PROSITE]      PKC_PHOSPHO_SITE       3
[KW]           All_Alpha
[KW]           LOW_COMPLEXITY    14.59 %
[KW]           COILED_COIL       13.73 %

SEQ    MSAKRAELKKTHLCKNYKAVCLELKPEPTKTFDYKAVKQEGRFTKAGVTQDLKNELREVR
SEG    ...................................................xxxxxxxxx
PRD    cchhhhhhhhhhhcccchhhhhhhcccccccccccceeeccccccccccccchhhhhhhhh
COILS  .................................................CCCCCCCCCCC

SEQ    EELKEKMEEIKQIKDLMDKDFDKLHEFVEIMKEMQKDMDEKMDILINTQKNYKLPLRRAP
SEG    xxxxxxxxx...................xxxxxxxxxxxxxxxx................
PRD    hhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhchhhhhhhhhcccccccccccc
COILS  CCCCCCCCCCCCCCCCCCCC........................................

SEQ    KEQQELRLMGKTHREPQLRPKKMDGASGVNGAPCALHKKTMAPQKTKQGSLDPLHHCGTC
SEG    ............................................................
PRD    hhhhhhhhhcccccccccccccccccccccccccchhhhhhcccccccccccccccccccc
COILS  ............................................................

SEQ    CEKCLLCALKNNYNRGNIPSEASGLYKGGEEPVTTQPSVGHAVPAPKSQTEGR
SEG    .....................................................
PRD    chhhhhhhcccccccccccccccccccccccccccccccccccccccccccc
COILS  .....................................................
```

Prosite for DKFZphfbr2_7j4.3

PS00005	2->5	PKC_PHOSPHO_SITE	PDOC00005
PS00005	108->111	PKC_PHOSPHO_SITE	PDOC00005
PS00005	132->135	PKC_PHOSPHO_SITE	PDOC00005
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	179->183	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00008	151->157	MYRISTYL	PDOC00008
PS00008	196->202	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_7j4.3)

DKFZphfbr2_82c20
----

group: transmembrane protein

DKFZphfbr2_82c20 encodes a novel 492 amino acid protein with very weak similarity to C. elegans cosmid D1007.

The novel protein contains 7 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans D1007.5 ;
membrane regions: 7
Summary DKFZphfbr2_82c20 encodes a novel 492 amino acid protein with similarity to a hypothetical C.elegans protein.

similarity to C.elegans D1007.5

complete cDNA (Bp 1-100 GC ritch), complete cds,
potential start at Bp 128 matches Kozak consensus PyNNatgG,
EST hits, localisation? primer B of STS doesn't match perfect!
TRANSMEMBRANE 7

Sequenced by DKFZ

Locus: /map="109.9 cR from top of Chrl linkage group"???

Insert length: 1804 bp
Poly A stretch at pos. 1794, no polyadenylation signal found

```
   1 CGGCGGGAGC GCGCGGCTGA TACCCGGGAC TGGGCTGCGG CGGTTAGTCC
  51 TCTCCCGGCC GCCGTCGCCT CCGACATATT GCTCGCAGGA GCTGCGGCGG
 101 CGAAGCGGAG AGCACCGGGG GGAGGAGATG GGAGGACGAA GAGGTCCCAA
 151 CAGGACATCT TACTGTCGAA ATCCGCTCTG TGAGCCGGGA TCCTCGGGGG
 201 GCTCTAGTGG AAGCCACACT TCCAGTGCAT CGGTGACCAG TGTTCGTTCC
 251 CGCACCAGGA GCAGTTCTGG AACAGGCCTC TCCAGCCCTC CTCTGGCCAC
 301 CCAAACTGTT GTGCCTCTAC AGCACTGCAA GATCCCCGAG CTGCCAGTCC
 351 AGGCCAGCAT TCTGTTTGAG TTGCAGCTCT TCTTCTGCCA GCTCATAGCA
 401 CTCTTCGTCC ACTACATCAA CATCTACAAG ACAGTGTGGT GGTATCCACC
 451 TTCCCACCCA CCCTCCCACA CCTCCCTGAA CTTCCATCTG ATCGACTTCA
 501 ACTTGCTGAT GGTGACCACC ATCGTTCTGG GCCGCCGCTT CATTGGGTCC
 551 ATCGTGAAGG AGGCCTCTCA GAGGGGGAAG GTCTCCCTCT TTCGCTCCAT
 601 CCTGCTGTTC CTCACTCGCT TCACCGTTCT CACGGCAACA GGCTGGAGTC
 651 TGTGCCGATC CCTCATCCAC CTCTTCAGGA CCTACTCCTT CCTGAACCTC
 701 CTGTTCCTCT GCTATCCGTT TGGGATGTAC ATTCCGTTCC TGCAGCTGAA
 751 TTGCGACCTC CGCAAGACAA GCCTCTTCAA CCACATGGCC TCCATGGGGC
 801 CCCGGGAGGC GGTCAGTGGC CTGGCAAAGA GCCGGGACTA CCTCCTGACA
 851 CTGCGGGAGA CGTGGAAGCA GCACACAAGA CAGCTGTATG GCCCGGACGC
 901 CATGCCCACC CATGCCTGCT GCCTGTCACC CAGCCTCATC CGCAGTGAGG
 951 TGGAGTTCCT CAAGATGGAC TTCAACTGGC GCATGAAGGA AGTGCTCGTC
1001 AGCTCCATGC TGAGCGCCTA CTATGTGGCC TTTGTGCCTG TCTGGTTCGT
1051 GAAGAACACA CATTACTATG ACAAGCGCTG GTCCTGTGAA CTCTTCCTGC
1101 TGGTGTCCAT CAGCACCTCC GTGATCCTCA TGCAGCACCT GCTGCCTGCC
1151 AGCTACTGTG ACCTGCTGCA CAAGGCCGCC GCCCATCTGG GCTGTTGGCA
1201 GAAGGTGGAC CCAGCGCTGT GCTCCAACGT GCTGCAGCAC CCGTGGACTG
1251 AAGAATGCAT GTGGCCGCAG GGCGTGCTGG TGAAGCACAG CAAGAACGTC
1301 TACAAAGCCG TAGGCCACTA CAACGTGGCT ATCCCCTCTG ACGTCTCCCA
1351 CTTCCGCTTC CATTTCTTTT TCAGCAAACC TCTGCGGATC CTCAACATCC
1401 TCCTGCTGCT GGAGGGCGCT GTCATTGTCT ATCAGCTGTA CTCCCTAATG
1451 TCCTCTGAAA AGTGGCACCA GACCATCTCG CTGGCCCTCA TCCTCTTCAG
1501 CAACTACTAT GCCTTCTTCA AGCTGCTCCG GGACCGCTTG GTATTGGGCA
1551 AGGCCTACTC ATACTCTGCT AGCCCCCAGA GAGACCTGGA CCACCGTTTC
1601 TCCTGAGCCC TGGGGTCACC TCAGGGACAG CGTCCAGGCT TCAGCCAAGG
1651 GCTCCCTGGC AAGGGGCTGT TGGGTAGAAG TGGTGGTGGG GGGGACAAAA
1701 GACAAAAAAA TCCACCAGAG CTTTGTATTT TTGTTACGTA CTGTTTCTTT
1751 GATAATTGAT GTGATAAGGA AAAAAGTCCT ATTTTTATAC TCCCAAAAAA
1801 AAAA
```

BLAST Results

Entry HS285343 from database EMBL:
human STS WI-17488.

```
 Score = 1225, P = 1.3e-50, identities = 263/281
```

Medline entries

No Medline entry

Peptide information for frame 2

```
      1 MGGRRGPNRT SYCRNPLCEP GSSGGSSGSH TSSASVTSVR SRTRSSSGTG
     51 LSSPPLATQT VVPLQHCKIP ELPVQASILF ELQLFFCQLI ALFVHYINIY
    101 KTVWWYPPSH PPSHTSLNFH LIDFNLLMVT TIVLGRRFIG SIVKEASQRG
    151 KVSLFRSILL FLTRFTVLTA TGWSLCRSLI HLFRTYSFLN LLFLCYPFGM
    201 YIPFLQLNCD LRKTSLFNHM ASMGPREAVS GLAKSRDYLL TLRETWKQHT
    251 RQLYGPDAMP THACCLSPSL IRSEVEFLKM DFNWRMKEVL VSSMLSAYYV
    301 AFVPVWFVKN THYYDKRWSC ELFLLVSIST SVILMQHLLP ASYCDLLHKA
    351 AAHLGCWQKV DPALCSNVLQ HPWTEECMWP QGVLVKHSKN VYKAVGHYNV
    401 AIPSDVSHFR FHFFFSKPLR ILNILLLLEG AVIVYQLYSL MSSEKWHQTI
    451 SLALILFSNY YAFFKLLRDR LVLGKAYSYS ASPQRDLDHR FS

ORF from 128 bp to 1603 bp; peptide length: 492
Category: similarity to unknown protein
Prosite motifs: LEUCINE_ZIPPER  (210-232)
LEUCINE_ZIPPER  (210-232)
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82c20, frame 2

```
TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid
D1007., N = 2, Score = 247, P = 4.6e-29


>TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid D1007.
            Length = 512

  HSPs:

 Score = 247 (37.1 bits), Expect = 4.6e-29, Sum P(2) = 4.6e-29
 Identities = 58/204 (28%), Positives = 102/204 (50%)

Query:   291 VSSMLSAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLLPASYCDLLHKA 350
             +S ML   +V F     +       ++ W C+L ++V ++    + + +L P +Y DLLH+A
Sbjct:   299 LSIMLPCIFVPFKTSQGIPQKILINEVWECQLAIVVGLTAFSLYVAYLSPLNYLDLLHRA 358

Query:   351 AAHLGCWQKVD-PAL----CSNVLQHPWTEECMWPQGVLVKHSKN-VYKAVGHYNV---- 400
             A HLG W +++ P +         +    PW+E C++  G  V+       Y+A    ++
Sbjct:   359 AIHLGSWHQIEGPRIGHTGSMSSAPTPWSEFCLYNDGETVQMPDGRCYRAKSSNSIRTVA 418

Query:   401 AIPSDVSHFRFHFFFSKPLRILNILLLLEGAVIVYQLYSLMSSEKWHQTISLALILFSNY 460
             A P     H  F     KP  ++NI+    E  +I  Q + L+ +  W   ++  L++F+NY
Sbjct:   419 AHPESSRHNTFFKVLRKPNNLINIMCSFEFLLIFIQFWMLVLTNDWQHIVTFVLLMFANY 478

Query:   461 YAFFKLLRDRLVLGKAYSYSASPQRDL 487
               F KL +D+++L + Y  S   Q DL
Sbjct:   479 LLFAKLFKDKIILSRIYEPS---QEDL 502

 Score = 178 (26.7 bits), Expect = 4.3e-21, Sum P(2) = 4.3e-21
 Identities = 50/179 (27%), Positives = 90/179 (50%)

Query:   262 HACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSMLSAYYVAFVPVWFV--KNTHYYDKR-- 317
             H C  SP+ IR E++ L  D   R+K+ + + + +A+    +P  FV  K +    ++
Sbjct:   262 HMCSDSPAQIREEIQVLIDDLVLRVKKSIFAGVSTAFLSIMLPCIFVPFKTSQGIPQKIL 321

Query:   318 ----WSCELFLLVSISTSVILMQHLLPASYCDLLHKAAAHLGCWQKVD-PAL----CSNV 368
                 W C+L ++V ++    + + +L P +Y DLLH+AA HLG W +++ P +       +
Sbjct:   322 INEVWECQLAIVVGLTAFSLYVAYLSPLNYLDLLHRAAIHLGSWHQIEGPRIGHTGSMSS 381

Query:   369 LQHPWTEECMWPQGVLVKHSKN-VYKAVGHYNV-AIPSDVSHFRFHFFFSKPLRILNILL 426
                PW+E C++  G  V+       Y+A    ++  + +       R + FF K LR  N L+
Sbjct:   382 APTPWSEFCLYNDGETVQMPDGRCYRAKSSNSIRTVAAHPESSRHNTFF-KVLRKPNNLI 440
```

```
 Score = 146 (21.9 bits), Expect = 4.6e-29, Sum P(2) = 4.6e-29
 Identities = 34/86 (39%), Positives = 50/86 (58%)

Query:    52 SSPPLATQTVVPLQHCKIPELP-VQASILFELQLFFCQLIALFVHYINIYKTVWWYPPSH 110
             +S P A+    + + H   P++   Q  + FE  LF   ++ALF+ Y+NIYKT+WW P S+
Sbjct:    19 ASIPRASGVTLSV-HPIWPDIQFTQGELFFECTLFLYSVLALFLQYLNIYKTLWWLPKSY 77

Query:   111 PPSHTSLNFHLIDFNLLMVTTIVLGRR 137
               H SL FHLI+   L    ++LG R
Sbjct:    78 --WHYSLKFHLINPYFLSCVGLLLGWR 102

 Score = 39 (5.9 bits), Expect = 6.8e-18, Sum P(2) = 6.8e-18
 Identities = 12/41 (29%), Positives = 20/41 (48%)

Query:   154 LFRSILLFLTRFTVLTATGWSLCRSLIHLFRTYSFLNLLFL 194
             L+  + LFL ++  +  T W L +S  H    +  +N  FL
Sbjct:    53 LYSVLALFL-QYLNIYKTLWWLPKSYWHYSLKFHLINPYFL 92
```

```
          Pedant information for DKFZphfbr2_82c20, frame 2
          ------------------------------------------------

                  Report for DKFZphfbr2_82c20.2

[LENGTH]       492
[MW]           56274.05
[pI]           9.51
[HOMOL]        TREMBL:CEAF3151_8 gene: "D1007.5"; Caenorhabditis elegans cosmid D1007. 4e-31

[PROSITE]      LEUCINE_ZIPPER 1
[PROSITE]      AMIDATION      2
[PROSITE]      MYRISTYL       5
[PROSITE]      CAMP_PHOSPHO_SITE      2
[PROSITE]      CK2_PHOSPHO_SITE       3
[PROSITE]      GLYCOSAMINOGLYCAN      1
[PROSITE]      PKC_PHOSPHO_SITE       5
[PROSITE]      ASN_GLYCOSYLATION      1
[KW]           TRANSMEMBRANE  7
[KW]           LOW_COMPLEXITY     8.74 %
```

```
SEQ     MGGRRGPNRTSYCRNPLCEPGSSGGSSGSHTSSASVTSVRSRTRSSSGTGLSSPPLATQT
SEG     ....................xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.......
PRD     ccccccccccccccccccccccccccccccccccccceeeccccccccccccccccccee
MEM     ............................................................

SEQ     VVPLQHCKIPELPVQASILFELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFH
SEG     ............................................................
PRD     eeeccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhheeeeecccccccccceeeeee
MEM     .............MMMMMMMMMMMMMMMMMMMMMMMMMMMMM.........MMMMMMMMM

SEQ     LIDFNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTVLTATGWSLCRSLI
SEG     ............................................................
PRD     eeehhhhhhhhhhhhhheeeehhhhhhcccchhhhhhhhhhhhhhhhhhcccchhhhhhhh
MEM     MMMMMMMMMMMMMMMMM.................MMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ     HLFRTYSFLNLLFLCYPFGMYIPFLQLNCDLRKTSLFNHMASMGPREAVSGLAKSRDYLL
SEG     ............................................................
PRD     hhhhhhhheeeeeeecccccceeeecccccchhhhhhhhhhccchhhhhhhhhhhhhhhhh
MEM     ............................................................

SEQ     TLRETWKQHTRQLYGPDAMPTHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSMLSAYYV
SEG     ............................................................
PRD     hhhhhhhhhhhhccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhcchhhhhh
MEM     ...........................................MMMMMMMMMMMMMMMMM

SEQ     AFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMQHLLPASYCDLLHKAAAHLGCWQKV
SEG     ............................................................
PRD     heeeeeeeeccccccchhhhhhhhhhhhcchhhhhhhhhccchhhhhhhhhhhhhhhccc
MEM     MMMMMMMMM.........MMMMMMMMMMMMMMMMMMMMMMMMMMMMMM............

SEQ     DPALCSNVLQHPWTEECMWPQGVLVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLR
SEG     ..........................................................xx
PRD     cccccccccccccccceeecccceeeeeccceeeecccccccccccccceeeeeeeccccch
MEM     ..................................................MMMMMMMMMM

SEQ     ILNILLLLEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRLVLGKAYSYS
SEG     xxxxxxxx....................................................
PRD     hhhhhhhhhheeeeehhhhcccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc
MEM     MMMMMMMMMMMMMMMMMMM......MMMMMMMMMMMMMMMMMMMMM..............
```

SEQ	ASPQRDLDHRFS
SEG	....
PRD	ccchhhhhhccc
MEM	....

Prosite for DKFZphfbr2_82c20.2

PS00001	8->12	ASN_GLYCOSYLATION	PDOC00001
PS00002	47->51	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	212->216	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	316->320	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	38->41	PKC_PHOSPHO_SITE	PDOC00005
PS00005	147->150	PKC_PHOSPHO_SITE	PDOC00005
PS00005	241->244	PKC_PHOSPHO_SITE	PDOC00005
PS00005	245->248	PKC_PHOSPHO_SITE	PDOC00005
PS00005	443->446	PKC_PHOSPHO_SITE	PDOC00005
PS00006	241->245	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	342->346	CK2_PHOSPHO_SITE	PDOC00006
PS00008	21->27	MYRISTYL	PDOC00008
PS00008	24->30	MYRISTYL	PDOC00008
PS00008	28->34	MYRISTYL	PDOC00008
PS00008	48->54	MYRISTYL	PDOC00008
PS00008	231->237	MYRISTYL	PDOC00008
PS00009	2->6	AMIDATION	PDOC00009
PS00009	134->138	AMIDATION	PDOC00009
PS00029	168->190	LEUCINE_ZIPPER	PDOC00029

(No Pfam data available for DKFZphfbr2_82c20.2)

DKFZphfbr2_82e17
----

group: transmembrane protein

DKFZphfbr2_82e17 encodes a novel 311 amino acid protein with very weak similarity to C. elegans cosmid R01B10.

The novel protein contains 6 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

similarity to C.elegans "R01B10.5" ;
membrane regions: 6
Summary DKFZphfbr2_82e17 encodes a novel 311 amino acid protein with similarity to a hypothetical C.elegans protein.

similarity to C.elegans "R01B10.5"

complete cDNA, EST HS763158 extendes the sequence, complete cds, EST hits
six potential transmembrane domains

Sequenced by DKFZ

Locus: /map="779_C_?; 818_A_1; 877_C_1; 734_C_12; 760_E_11; 171.7 cR from top of Chr14 linkage group"

Insert length: 1618 bp
Poly A stretch at pos. 1608, polyadenylation signal at pos. 1588

```
   1 CTGATCTAGT GCTTCTCGAA AAAAACCTTC AGGCGGCCCA TGGCTGTCGA
  51 TATTCAACCA GCATGCCTTG GACTTTATTG TGGGAAGACC CTATTATTTA
 101 AAAATGGCTC AACTGAAATA TATGGAGAAT GTGGGGTATG CCCAAGAGGA
 151 CAGAGAACGA ATGCACAGAA ATATTGTCAG CCTTGCACAG AATCTCCTGA
 201 ACTTTATGAT TGGCTCTATC TTGGATTTAT GGCAATGCTT CCTCTGGTTT
 251 TACATTGGTT CTTCATTGAA TGGTACTCGG GGAAAAAGAG TTCCAGCGCA
 301 CTTTTCCAAC ACATCACTGC ATTATTTGAA TGCAGCATGG CAGCTATTAT
 351 CACCTTACTT GTGAGTGATC CAGTTGGTGT TCTTTATATT CGTTCATGTC
 401 GAGTATTGAT GCTTTCTGAC TGGTACACGA TGCTTTACAA CCCAAGTCCA
 451 GATTACGTTA CCACAGTACA CTGTACTCAT GAAGCCGTCT ACCCACTATA
 501 TACCATTGTA TTTATCTATT ACGCATTCTG CTTGGTATTA ATGATGCTGC
 551 TCCGACCTCT TCTGGTGAAG AAGATTGCAT GTGGGTTAGG GAAATCTGAT
 601 CGATTTAAAA GTATTTATGC TGCACTTTAC TTCTTCCCAA TTTTAACCGT
 651 GCTTCAGGCA GTTGGTGGAG GCCTTTTATA TTACGCCTTC CCATACATTA
 701 TATTAGTGTT ATCTTTGGTT ACTCTGGCTG TGTACATGTC TGCTTCTGAA
 751 ATAGAGAACT GCTATGATCT TCTGGTCAGA AAGAAAAGAC TTATTGTTCT
 801 CTTCAGCCAC TGGTTACTTC ATGCCTATGG AATAATCTCC ATTTCCAGAG
 851 TGGATAAACT TGAGCAAGAT TTGCCCCTTT TGGCTTTGGT ACCTACACCA
 901 GCCCTTTTTT ACTTGTTCAC TGCAAAATTT ACCGAACCTT CAAGGATACT
 951 CTCAGAAGGA GCCAATGGAC ACTGAGTGTA GACATGTGAA ATGCCAAAAA
1001 CCTGAGAAGT GCTCCTAATA AAAAAGTAAA TCAATCTTAA CAGTGTATGA
1051 GAACTATTCT ATCATATATG GGAACAAGAT TGTCAGTATA TCTTAATGTT
1101 TGGGTTTGTC TTTGTTTTGT TTATGGTTAG ACTTACAGAC TTGGAAAATG
1151 CAAAACTCTG TAATACTCTG TTACACAGGG TAATATTATC TGCTACACTG
1201 GAAGGCCGCT AGGAAGCCCT TGCTTCTCTC AACAGTTCAG CTGTTCTTTA
1251 GGGCAAAATC ATGTTTCTGT GTACCTAGCA ATGTGTTCCC ATTTTATTAA
1301 GAAAAGCTTT AACACGTGTA ATCTGCAGTC CTTAACAGTG GCGTAATTGT
1351 ACGTACCTGT TGTGTTTCAG TTTGTTTTTC ACCTATAATG AATTGTAAAA
1401 ACAAACATAC TTGTGGGGTC TGATAGCAAA CATAGAAATG ATGTATATTG
1451 TTTTTTGTTA TCTATTTATT TTCATCAATA CAGTATTTTG ATGTATTGCA
1501 AAAATAGATA ATAATTTATA TAACAGGTTT TCTGTTTATA GATTGGTTCA
1551 AGATTTGTTT GGATTATTGT TCCTGTAAAG AAAACAATAA TAAAAAGCTT
1601 ACCTACATAA AAAAAAAA
```

BLAST Results

Entry HS981146 from database EMBL:
human STS WI-6253.
Length = 208
Minus Strand HSPs:
Score = 1040 (156.0 bits), Expect = 1.9e-40, P = 1.9e-40

Identities = 208/208 (100%), Positives = 208/208 (100%), Strand = Minus / Plus

Entry HSG20716 from database EMBL:
human STS A006D06.
Length = 195
Minus Strand HSPs:
Score = 975 (146.3 bits), Expect = 1.8e-37, P = 1.8e-37
Identities = 195/195 (100%), Positives = 195/195 (100%), Strand = Minus / Plus

Medline entries

No Medline entry

Peptide information for frame 1

```
  1 MAVDIQPACL GLYCGKTLLF KNGSTEIYGE CGVCPRGQRT NAQKYCQPCT
 51 ESPELYDWLY LGFMAMLPLV LHWFFIEWYS GKKSSSALFQ HITALFECSM
101 AAIITLLVSD PVGVLYIRSC RVLMLSDWYT MLYNPSPDYV TTVHCTHEAV
151 YPLYTIVFIY YAFCLVLMML LRPLLVKKIA CGLGKSDRFK SIYAALYFFP
201 ILTVLQAVGG GLLYYAFPYI ILVLSLVTLA VYMSASEIEN CYDLLVRKKR
251 LIVLFSHWLL HAYGIISISR VDKLEQDLPL LALVPTPALF YLFTAKFTEP
301 SRILSEGANG H
```

ORF from 40 bp to 972 bp; peptide length: 311
Category: similarity to unknown protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82e17, frame 1

TREMBL:AF068718_5 gene: "R01B10.5"; Caenorhabditis elegans cosmid R01B10., N = 1, Score = 399, P = 1.4e-36

>TREMBL:AF068718_5 gene: "R01B10.5"; Caenorhabditis elegans cosmid R01B10.
Length = 670

HSPs:

Score = 399 (59.9 bits), Expect = 1.4e-36, P = 1.4e-36
Identities = 95/280 (33%), Positives = 152/280 (54%)

```
Query:    2 AVDIQPACLGLYCGKTLLFKN------------GSTEIYGECGVCPRGQRTNAQKYCQPC 49
              A  IQP+CLG +CG+T+L  N            GST +   CG C  G R NA   C+ C
Sbjct:  292 ASTIQPSCLG-FCGRTVLVGNYSEDVEATTTAAGSTSL-SRCGPCSFGYRNNAMSICESC 349

Query:   50 TESPELYDWLYLGFMAMLPLVLHWFFIEWYSGKKSSSALFQ---HITALFECSMAAIITL 106
                    + YDW+YL F+A+LPL+LH  FI   + K   +  ++    ++  + E  +A +I +
Sbjct:  350 DTPLQPYDWMYLLFIALLPLLLHMQFIR-IARKYCRTRYYEVSEYLCVILENVIACVIAV 408

Query:  107 LVSDPVGVLYIRSCRVLMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV 166
            L+  P     ++  C     + +WY   YNP   Y  T+ CT+E V+PLY+I FI++    +
Sbjct:  409 LIYPPRFTFFLNGCSKTDIKEWYPACYNPRIGYTKTMRCTYEVVFPLYSITFIHHLILIG 468

Query:  167 LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGGGLLYYAFPYIILVLSL 226
             +++LR  L    +    L K+   K  YAA+    PIL V+ AV  G+++Y FPYI+L+ SL
Sbjct:  469 SILVLRSTLYCVL---LYKTYNGKPFYAAIVSVPILAVIHAVLSGVVFYTFPYILLIGSL 525

Query:  227 VTLAVYMSASEIENCYDLLVR----KKRLIVLFSHWLLHAYGIISI 268
             +  +++          +++VR           LI L      L+ ++G+I+I
Sbjct:  526 WAMCFHLALEGKRPLKEMIVRIATSPTHLIFLSITMLMLSFGVIAI 571
```

Pedant information for DKFZphfbr2_82e17, frame 1

Report for DKFZphfbr2_82e17.1

```
[LENGTH]        311
[MW]            35239.14
[pI]            7.91
[HOMOL]         TREMBL:AF068718_5 gene: "R01B10.5"; Caenorhabditis elegans cosmid R01B10. 9e-36

[PROSITE]       AMIDATION       1
[PROSITE]       MYRISTYL        3
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            TRANSMEMBRANE   6
[KW]            LOW_COMPLEXITY      7.72 %

SEQ     MAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVCPRGQRTNAQKYCQPCTESPELYDWLY
SEG     ............................................................
PRD     ccccccccccccccceeeecccccceeeccccccccccccccccceeeccccccccchhhhh
MEM     ......................................................MMMMMM

SEQ     LGFMAMLPLVLHWFFIEWYSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSC
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhcccceeeeeece
MEM     MMMMMMMMMMMMMMMM............MMMMMMMMMMMMMMMMMMMMMMMMMMMMM...

SEQ     RVLMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLVLMMLLRPLLVKKIA
SEG     ............................................xxxxxxxxxxxx....
PRD     eeeeecceeeecccccceeeeeeeeceeeeeeeeeceeeeehhhhhhhhhhhhhhhhhee
MEM     ............................MMMMMMMMMMMMMMMMMMMMMMMMMMMMM...

SEQ     CGLGKSDRFKSIYAALYFFPILTVLQAVGGGLLYYAFPYIILVLSLVTLAVYMSASEIEN
SEG     ............................................................
PRD     eecccccchhhhhhhhhhhhcccccccccccccceeeecceeeeehhhhhhhhhhhhhhhh
MEM     .........MMMMMMMMMMMMMMMMMMMMMMMMMMMMM......................

SEQ     CYDLLVRKKRLIVLFSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFTEP
SEG     .....................................xxxxxxxxxxxx...........
PRD     hhhhhhhhhhhhhhhhhhhhhhcccceeeechhhhhceeeeeecccceeeeeeeeccccc
MEM     .........MMMMMMMMMMMMMMMMMMMMM.........MMMMMMMMMMMMMMMMMMMMM

SEQ     SRILSEGANGH
SEG     ...........
PRD     ceeeeeccccc
MEM     MM.........
```

Prosite for DKFZphfbr2_82e17.1

PS00001	22->26	ASN_GLYCOSYLATION	PDOC00001
PS00004	82->86	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	80->83	PKC_PHOSPHO_SITE	PDOC00005
PS00005	119->122	PKC_PHOSPHO_SITE	PDOC00005
PS00005	186->189	PKC_PHOSPHO_SITE	PDOC00005
PS00005	294->297	PKC_PHOSPHO_SITE	PDOC00005
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	269->273	CK2_PHOSPHO_SITE	PDOC00006
PS00008	11->17	MYRISTYL	PDOC00008
PS00008	37->43	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00009	80->84	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_82e17.1)

DKFZphfbr2_82e4
----

group: signal transduction

DKFZphfbr2_82e4 encodes a novel 473 amino acid protein with strong similarity to the calmodulin-binding proteins.

The novel protein is similar to human and rat Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123), rat calmodulin-binding protein, calmodulin binding protein kinase of Fugu rupies and Rattus norvegicus calcium/calmodulin-dependent protein kinase I. Calmodulin is the archetype of the family of calcium-modulated proteins of which nearly 20 members have been found. Calmodulin is involved in regulation of growth and cell cycle as well as in signal transduction and the synthesis and release of neurotransmitters. The novel protein seems to be involved in calmodulin-mediated pathways in human neuronal cells.

The new protein can find clinical application in modulating/blocking calmodulin-mediated pathways in human neuronal cells.

strong similarity to calmodulin-binding proteins

complete cDNA, complete cds, EST hits
splice variant in comparison to rat I56542
ESTs HSZ54543/HS1141907 define splice variant
see also DKFZphfbr2_82g20 unspliced form

Sequenced by DKFZ

Locus: /map="200.5 cR from top of Chr3 linkage group"

Insert length: 2923 bp
Poly A stretch at pos. 2913, polyadenylation signal at pos. 2890

```
   1 ATGCTGGAGG TTCGCTAGCC GAAGCGGCTG CATCTGGCGC CGCGTCTGCC
  51 CCGCGTGCTC GGAGCGGATT CTGCCCGCCG TCCCCGGAGC CCTCGGCGCC
 101 CCGCTGAGCC CGCGATCACT TCCTCCCTGT GACCAACCGG CGCTGCAGGT
 151 TAGAGCCTGG CAATGCCGTT TGGGTGTGTG ACTCTGGGTG ACAAGAAGAA
 201 CTATAACCAG CCATCGGAGG TGACTGACAG ATATGATTTG GGACAGGTCA
 251 TCAAGACTGA GGAGTTTTGT GAAATCTTCC GGGCCAAGGA CAAGACGACA
 301 GGCAAGCTGC ACACCTGCAA GAAGTTCCAG AAGCGGGACG GCCGCAAGGT
 351 GCGGAAAGCT GCCAAGAACG AGATAGGCAT CCTCAAGATG GTGAAGCATC
 401 CCAACATCCT ACAGCTGGTG GATGTGTTTG TGACCCGCAA GGAGTACTTT
 451 ATCTTCCTGG AGCTGGCCAC GGGGAGGGAG GTGTTTGACT GGATCCTGGA
 501 CCAGGGCTAC TACTCGGAGC GAGACACAAG CAACGTGGTA CGGCAAGTCC
 551 TGGAGGCCGT GGCCTATTTG CACTCACTCA AGATCGTGCA CAGGAATCTC
 601 AAGCTGGAGA ACCTGGTTTA CTACAACCGG CTGAAGAACT CGAAGATTGT
 651 CATCAGTGAC TTCCATCTGG CTAAGCTAGA AAATGGCCTC ATCAAGGAGC
 701 CCTGTGGGAC CCCCGAGTAT CTGGGCAACC CACCTTTCTA TGAGGAGGTG
 751 GAAGAAGATG ATTATGAGAA CCATGATAAG AATCTCTTCC GCAAGATCCT
 801 GGCTGGTGAC TATGAGTTTG ACTCTCCATA TTGGGATGAT ATTTCGCAGG
 851 CAGCCAAAGA CCTGGTCACA AGGCTGATGG AGGTGGAGCA AGACCAGCGG
 901 ATCACTGCAG AAGAGGCCAT CTCCCATGAG TGGATTTCTG GCAATGCTGC
 951 TTCTGATAAG AACATCAAGG ATGGTGTCTG TGCCCAGATT GAAAAGAACT
1001 TTGCCAGGGC CAAGTGGAAG AAGGCTGTCC GAGTGACCAC CCTCATGAAA
1051 CGGCTCCGGG CACCAGAGCA GTCCAGCACG GCTGCAGCCC AGTCGGCCTC
1101 AGCCACAGAC ACTGCCACCC CCGGGGCTGC AGGTGGGGCC ACAGCTGCAG
1151 CTGCGAGTGG AGCTACCTCA GCCCCTGAGG GTGATGCTGC TCGTGCTGCA
1201 AAGAGTGATA ATGTGGCCCC CGCAGACCGT AGTGCCACCC CAGCCACAGA
1251 TGGAAGTGCC ACCCCAGCCA CTGATGGCAG TGTCACCCCA GCCACCGATG
1301 GAAGCATCAC TCCAGCCACT GATGGGAGTG TCACCCCAGC CACTGACAGG
1351 AGCGCTACTC CAGCCACTGA TGGGAGAGCC ACACCAGCCA CAGAAGAGAG
1401 CACTGTGCCC ACCACCCAAA GCAGTGCCAT GCTGGCCACC AAGGCAGCTG
1451 CCACCCCTGA GCCGGCTATG GCCCAGCCGG ACAGCACAGC CCCAGAGGGC
1501 GCCACAGGCC AGGCTCCACC CTCTAGTAAA GGGGAAGAGG CTGCTGGTTA
1551 TGCCCAGGAG TCTCAAAGGG AGGAGGCCAG CTGAGTAGGC AGCCTGGTGA
1601 GGGGGGGCAG GGGATGGGCA GGAGGGTGGG AGAGTGGATG AGGGGCTTCT
1651 CACTGTACAT AGAGTCACTG GCATGATGCC CTCGCTCCCC CATGCCCCCA
1701 CATCCCAGTG GGGCATAACT AGGGGTCACG GGAGAGCAGT CTCGTCTCCT
1751 GTGTGTATGT GTGTGAGTGG TGGGCAGGCC AGTGGCAGGG CCGGCCCCAG
1801 CCCCTGCATG GATTCCTTGT GGCTTTTCTG TCTTTTGCTA GCTTCACCAG
1851 TTTCTGTTCC TTGTGGGATG CTGCTCTAGG GATACTCAGG GGGCTCCTGC
1901 TCTCCTTCCC CTTCCCTTCT TGCCTCACCA TTCCCCTAGG CAGGCCCTGC
1951 AGGTCCCACA CTCTCCCAGG CCCTAAACTT GGGCGGCCTT GCCCTGAGAG
2001 CTGGTCCTCC AGCGAGGCCC TGTCAGCGGT CTTAGGCTCC TGCACATGAA
2051 GGTGTGTGCC TGTGGTGTGT GGGCTGCTCT AGGAGCAGAT ACAGGCTGGT
2101 ATAGAGGATG CAGAAAGGTA GGGCAGTATG TTTAAGTCCA GACTTGGCAC
2151 ATGGCTAGGG ATACTGCTCA CTAGCTGTGG AGGTCCTCAG GAGTGGAGAG
2201 AATGAGTAGG AGGGCAGAAG CTTCCATTTT TGTCCTTCCT AAGACCCTGT
```

```
2251 TATTTGTGTT ATTTCCTGCC TTTCCGAGTC CTGCAGTGGG CTGCCCTGTA
2301 CCCTGAACCT CATGAGCCTC TAAGGGAAAG GAGGAACAAT TAGGACGTGG
2351 CAATGAGACC TGGCAGGGCA GAGTACAAGC CCAGCACCCA GTGTCCCAGC
2401 CTTACTGGGT CCTTACCCTG GGCCAAACAG GGAGGGCTGA TACCTCCTTG
2451 CTCTTCCTAG ATGCCCACCT CCTACAATCT CAGCCCACAA GTCCTCTCCA
2501 CCCTAGGGGG CTTGCTGCAT GGCAATAACT CATAATCTGA TTTGGAGGTT
2551 TGCCCTTTAC AGGGGCAGAT TTTCTGCTCA GTTCAACAAT GAAATGAAGA
2601 GGAACTCCCT CTTTCTACAG CTCACTTCTA TCAGAGGCCC AGGTGCCTCA
2651 GAGCCACATT GAGTTGCTTT TTCTGGGATG AGGAAGTAGG GTTAAACTCC
2701 CCAGTTTCCT GAGGGAGGCT CCTGACAGGT GCCCTTTGTC AGACCCTACC
2751 ACAGCCTGGA TAGGCAGCCA CATTGGTCCT CGCCCTTGCT CGGCACTCCG
2801 TGGTGGTCCT GCCCTTCTCC CTGCATGCCT GTGGGTCTGC TCTGGTGTGT
2851 GAAGGTCGGT GGGTTAACTG TGTGCCTACT GAACCTGGCA AATAAACATC
2901 ACCCTGCAAA GCCAAAAAAA AAA
```

BLAST Results

Entry HS452352 from database EMBL:
human STS WI-15318.
Length = 350
Minus Strand HSPs:
Score = 1547 (232.1 bits), Expect = 5.2e-63, P = 5.2e-63
Identities = 331/348 (95%), Positives = 331/348 (95%), Strand = Minus / Pl

Medline entries

94110847:
J Neurosci 1994 Jan;14(1):1-13
1G5: a calmodulin-binding, vesicle-associated, protein kinase-like protein enriched in forebrain neurites.
Godbout M, Erlander MG, Hasel KW, Danielson PE, Wong KK, Battenberg EL, Foye PE,
Bloom FE, Sutcliffe JG

Peptide information for frame 1

```
  1 MPFGCVTLGD KKNYNQPSEV TDRYDLGQVI KTEEFCEIFR AKDKTTGKLH
 51 TCKKFQKRDG RKVRKAAKNE IGILKMVKHP NILQLVDVFV TRKEYFIFLE
101 LATGREVFDW ILDQGYYSER DTSNVVRQVL EAVAYLHSLK IVHRNLKLEN
151 LVYYNRLKNS KIVISDFHLA KLENGLIKEP CGTPEYLGNP PFYEEVEEDD
201 YENHDKNLFR KILAGDYEFD SPYWDDISQA AKDLVTRLME VEQDQRITAE
251 EAISHEWISG NAASDKNIKD GVCAQIEKNF ARAKWKKAVR VTTLMKRLRA
301 PEQSSTAAAQ SASATDTATP GAAGGATAAA ASGATSAPEG DAARAAKSDN
351 VAPADRSATP ATDGSATPAT DGSVTPATDG SITPATDGSV TPATDRSATP
401 ATDGRATPAT EESTVPTTQS SAMLATKAAA TPEPAMAQPD STAPEGATGQ
451 APPSSKGEEA AGYAQESQRE EAS
```

ORF from 163 bp to 1581 bp; peptide length: 473
Category: strong similarity to known protein

BLASTP hits

Entry S50193 from database PIR:
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
Length = 374
Score = 371 (130.6 bits), Expect = 2.2e-66, Sum P(2) = 2.2e-66
Identities = 74/176 (42%), Positives = 115/176 (65%)

Entry S57347 from database PIR:
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
Length = 370
Score = 369 (129.9 bits), Expect = 4.6e-66, Sum P(2) = 4.6e-66
Identities = 74/176 (42%), Positives = 114/176 (64%)

Alert BLASTP hits for DKFZphfbr2_82e4, frame 1

PIR:I56542 calmodulin-binding protein - rat, N = 2, Score = 1246, P = 4e-228

TREMBLNEW:FRU010348_3 product: "calmodulin binding protein kinase"; Fugu rubripes UBE1-like gene, PRGFR2 gene and gene encoding calmodulin binding protein kinase, clone 168J21, N = 2, Score = 846, P = 2.6e-139

TREMBL:RNPRKI_1 product: "protein kinase I"; Rattus norvegicus calcium/calmodulin-dependent protein kinase I mRNA, complete cds., N = 2, Score = 364, P = 5.1e-63

```
>PIR:I56542 calmodulin-binding protein - rat
           Length = 504

  HSPs:

 Score = 1246 (186.9 bits), Expect = 4.0e-228, Sum P(2) = 4.0e-228
 Identities = 255/289 (88%), Positives = 259/289 (89%)

Query:   188 GNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRI 247
             GNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRI
Sbjct:   216 GNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRI 275

Query:   248 TAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSSTA 307
             TAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQS TA
Sbjct:   276 TAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPEQSGTA 335

Query:   308 AAQSASATDTATPGAAGGATAAAASGATSAPE--------GDAARAAKSDNVAPADRSAT 359
             A      +D ATPGAAGGA AAAA GA  A          GDA  AAKSD++A ADRSAT
Sbjct:   336 AT-----SDAATPGAAGGAVAAAAGGAAPASGASATVGTGGDAGCAAKSDDMASADRSAT 390

Query:   360 PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPTTQ 419
             PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVP  Q
Sbjct:   391 PATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPAAQ 450

Query:   420 SSAMLATKAAATPEPAMAQPDSTAPEGATGQAPPSSKGEEAAGYAQESQREEAS 473
             SSA  A KAAATPEPA+AQPDSTA EGATGQAPPSSKGEEA G AQESQR E S
Sbjct:   451 SSAAPAAKAAATPEPAVAQPDSTALEGATGQAPPSSKGEEATGCAQESQRVETS 504

 Score = 978 (146.7 bits), Expect = 4.0e-228, Sum P(2) = 4.0e-228
 Identities = 186/187 (99%), Positives = 187/187 (100%)

Query:     1 MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 60
             MPFGCVTLGDKKNYNQPSEVTDRYDLGQV+KTEEFCEIFRAKDKTTGKLHTCKKFQKRDG
Sbjct:     1 MPFGCVTLGDKKNYNQPSEVTDRYDLGQVVKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG 60

Query:    61 RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 120
             RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER
Sbjct:    61 RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER 120

Query:   121 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 180
             DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP
Sbjct:   121 DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP 180

Query:   181 CGTPEYL 187
             CGTPEYL
Sbjct:   181 CGTPEYL 187
```

Pedant information for DKFZphfbr2_82e4, frame 1

Report for DKFZphfbr2_82e4.1

[LENGTH]	473
[MW]	51208.89
[pI]	5.30
[HOMOL]	PIR:I56542 calmodulin-binding protein - rat 0.0
[FUNCAT]	30.03 organization of cytoplasm [S. cerevisiae, YFR014c] 4e-30
[FUNCAT]	10.99 other signal-transduction activities [S. cerevisiae, YFR014c] 4e-30
[FUNCAT]	03.01 cell growth [S. cerevisiae, YFR014c] 4e-30
[FUNCAT]	30.10 nuclear organization [S. cerevisiae, YKL101w] 2e-26
[FUNCAT]	03.22 cell cycle control and mitosis [S. cerevisiae, YKL101w] 2e-26
[FUNCAT]	11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YDL101c] 8e-26
[FUNCAT]	98 classification not yet clear-cut [S. cerevisiae, YCL024w] 5e-24
[FUNCAT]	03.25 cytokinesis [S. cerevisiae, YDR507c] 7e-23
[FUNCAT]	03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR507c] 7e-23
[FUNCAT]	03.22.01 cell cycle check point proteins [S. cerevisiae, YPL153c] 1e-21
[FUNCAT]	03.19 recombination and dna repair [S. cerevisiae, YPL153c] 1e-21

[FUNCAT] 11.01 stress response [S. cerevisiae, YDR477w] 3e-19
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YDR477w] 3e-19
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YPL141c] 1e-16
[FUNCAT] 03.16 dna synthesis and replication [S. cerevisiae, YMR001c] 3e-16
[FUNCAT] 03.13 meiosis [S. cerevisiae, YOR351c] 1e-15
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YDR122w] 3e-14
[FUNCAT] 10.03.11 key kinases [S. cerevisiae, YCR073c] 6e-11
[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YNR031c] 8e-11
[FUNCAT] 10.02.11 key kinases [S. cerevisiae, YJL095w] 2e-09
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 10.05.11 key kinases [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 10.04.11 key kinases [S. cerevisiae, YLR362w] 1e-08
[FUNCAT] 02.19 metabolism of energy reserves (glycogen, trehalose) [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 04.05.01.04 transcriptional control [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 01.04.04 regulation of phosphate utilization [S. cerevisiae, YPL031c] 7e-08
[FUNCAT] 06.07 protein modification (glycolsylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YFL033c] 1e-07
[FUNCAT] 04.99 other transcription activities [S. cerevisiae, YFL033c] 1e-07
[FUNCAT] 10.05.09 regulation of g-protein activity [S. cerevisiae, YBL016w] 5e-07
[FUNCAT] 05.07 translational control [S. cerevisiae, YDR283c] 8e-07
[FUNCAT] 01.06.10 regulation of lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YHR079c] 5e-06
[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YHR079c] 5e-06
[FUNCAT] 30.01 organization of cell wall [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 30.90 extracellular/secretion proteins [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 01.05.01 carbohydrate utilization [S. cerevisiae, YIR019c] 1e-05
[FUNCAT] 04.05.01.01 general transcription activities [S. cerevisiae, YDL108w] 1e-05
[FUNCAT] 01.02.04 regulation of nitrogen and sulphur utilization [S. cerevisiae, YNL183c] 8e-05
[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL183c] 8e-05
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YDR523c] 2e-04
[FUNCAT] c energy conversion [M. genitalium, MG109] 3e-04
[BLOCKS] BL00107A Protein kinases ATP-binding region proteins
[BLOCKS] BL00939F
[SCOP] d1gol__ 5.1.1.1.9 MAP kinase Erk2 [rat Rattus norvegicus 3e-62
[SCOP] d1wfc__ 5.1.1.1.8 MAP kinase p38 [human (Homo sapiens) 5e-59
[SCOP] d1koa_2 5.1.1.1.7 (1-350) Twitchin, kinase domain [Caenorhabditi 1e-75
[SCOP] d1koba_ 5.1.1.1.6 Twitchin, kinase domain [california sea har 1e-72
[SCOP] d1phk__ 5.1.1.1.5 gamma-subunit of glycogen phosphorylase kinas 4e-65
[SCOP] d1irk__ 5.1.1.2.4 insulin receptor [Human (Homo sapiens) 2e-56
[SCOP] d1apme_ 5.1.1.1.4 cAMP-dependent PK, catalytic subunit [mouse (Mu 4e-71
[SCOP] d1fgka_ 5.1.1.2.3 Fibroblast growth factor receptor 1 [human (Hom 1e-50
[SCOP] d1ydre_ 5.1.1.1.3 cAMP-dependent PK, catalytic subunit [bovine (Bo 3e-70
[SCOP] d1fmk_3 5.1.1.2.2 (168-437) c-src tyrosine kinase [human (Hom 5e-49
[SCOP] d1cdkb_ 5.1.1.1.2 cAMP-dependent PK, catalytic subunit [pig (Su 2e-72
[SCOP] d2hcka3 5.1.1.2.1 (167-437) Haemopoetic cell kinase Hck [huma 5e-46
[SCOP] d1csn__ 5.1.1.1.11 Casein kinase-1, CK1 [Schizosaccharomyces pombe 9e-42
[SCOP] d1jsua_ 5.1.1.1.1 Cyclin-dependent PK [Human (Homo sapiens) 1e-56
[SCOP] d1ckia_ 5.1.1.1.10 Casein kinase-1, CK1 [rat (Rattus norvegicus) 9e-52
[EC] 2.7.1.38 Phosphorylase kinase 3e-29
[EC] 2.7.1.123 Ca2+/calmodulin-dependent protein kinase 8e-66
[EC] 2.7.1.128 [Acetyl-CoA carboxylase] kinase 2e-17
[EC] 2.7.1.117 Myosin-light-chain kinase 2e-38
[EC] 2.7.1.109 [Hydroxymethylglutaryl-CoA reductase(NADPH)] kinase 2e-17
[EC] 2.7.1.37 Protein kinase 6e-28
[PIRKW] phosphotransferase 8e-66
[PIRKW] nucleus 2e-24
[PIRKW] transferase 8e-30
[PIRKW] calcium 2e-27
[PIRKW] duplication 4e-19
[PIRKW] tandem repeat 2e-31
[PIRKW] phorbol ester binding 1e-16
[PIRKW] zinc 1e-16
[PIRKW] cell cycle control 2e-20
[PIRKW] serine/threonine-specific protein kinase 8e-66
[PIRKW] phospholipid binding 1e-16
[PIRKW] autophosphorylation 8e-66
[PIRKW] brain 1e-14
[PIRKW] heterotetramer 2e-16
[PIRKW] polymer 3e-29
[PIRKW] mitosis 2e-20
[PIRKW] magnesium 7e-22
[PIRKW] ATP 8e-66
[PIRKW] alternative initiators 1e-29

[PIRKW] phosphoprotein 8e-66
[PIRKW] apoptosis 2e-31
[PIRKW] glycoprotein 4e-19
[PIRKW] skeletal muscle 3e-28
[PIRKW] protein kinase 2e-28
[PIRKW] testis 3e-28
[PIRKW] signal transduction 1e-21
[PIRKW] cAMP binding 1e-16
[PIRKW] purine nucleotide binding 5e-25
[PIRKW] structural protein 4e-19
[PIRKW] calcium binding 3e-45
[PIRKW] alternative splicing 3e-45
[PIRKW] P-loop 5e-25
[PIRKW] lipoprotein 2e-16
[PIRKW] cardiac muscle 4e-19
[PIRKW] muscle 3e-28
[PIRKW] myristylation 2e-16
[PIRKW] EF hand 5e-29
[PIRKW] cell division 2e-38
[PIRKW] calmodulin binding 8e-66
[PIRKW] smooth muscle 7e-31
[SUPFAM] fibronectin type III repeat homology 7e-31
[SUPFAM] immunoglobulin homology 7e-31
[SUPFAM] ribosomal protein S6 kinase II 3e-26
[SUPFAM] calcium-dependent protein kinase 5e-29
[SUPFAM] AMP-activated protein kinase 7e-22
[SUPFAM] protein kinase akt 1e-14
[SUPFAM] protein kinase SPK1 3e-20
[SUPFAM] unassigned Ser/Thr or Tyr-specific protein kinases 2e-36
[SUPFAM] Ca2+/calmodulin-dependent protein kinase 3e-45
[SUPFAM] calmodulin repeat homology 5e-29
[SUPFAM] protein kinase DUN1 2e-24
[SUPFAM] Dictyostelium cAMP-dependent protein kinase catalytic chain 1e-14
[SUPFAM] death-associated protein kinase 2e-31
[SUPFAM] myosin-light-chain kinase, nonmuscle 1e-29
[SUPFAM] pleckstrin repeat homology 1e-14
[SUPFAM] ankyrin repeat homology 2e-31
[SUPFAM] protein kinase homology 8e-66
[SUPFAM] Ca2+/calmodulin-dependent protein kinase II 8e-36
[SUPFAM] twitchin 1e-18
[SUPFAM] protein kinase C zinc-binding repeat homology 1e-16
[SUPFAM] titin 4e-19
[SUPFAM] protein kinase cdr1 2e-20
[SUPFAM] kinase-related transforming protein 2e-38
[SUPFAM] Ca2+/calmodulin-dependent protein kinase I 8e-66
[SUPFAM] kinase interaction domain homology 2e-24
[SUPFAM] protein kinase C mu 1e-16
[PROSITE] AMIDATION 1
[PROSITE] MYRISTYL 3
[PROSITE] CK2_PHOSPHO_SITE 10
[PROSITE] TYR_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 11
[PFAM] Eukaryotic protein kinase domain
[KW] All_Alpha
[KW] 3D
[KW] LOW_COMPLEXITY 7.40 %

SEQ MPFGCVTLGDKKNYNQPSEVTDRYDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDG
SEG ....
1a06- .............CEETTTGGGCEEEEEEECBCGGGGGEEEEEEETTTTCEEEEEEEEEC---

SEQ RKVRKAAKNEIGILKMVKHPNILQLVDVFVTRKEYFIFLELATGREVFDWILDQGYYSER
SEG ....
1a06- -------HHHHHHHHHCCTTTBCCEEEEEEEETTEEEEEEECCCCCEEHHHHHHHTTTTBHH

SEQ DTSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAKLENGLIKEP
SEG ....
1a06- HHHHHHHHHHHHHHHHHHHCCCTTTTTTTTEEECCCTTTTCEEECCCTTTTCHHHHHCCC

SEQ CGTPEYLGNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDDISQAAKDLVTRLME
SEG ....
1a06- HHHHHHHCCTTTTTTT--------THHHHHHHHHCCCCCCTTTTTTTTCHHHHHHHHHHCT

SEQ VEQDQRITAEEAISHEWISGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRA
SEG ....
1a06- TTGGGCCCHHHHHHTTTTTTCCCCCCBHHHHHHHHHHHHHCCTTTTTTBTHHHHHHHC..

SEQ PEQSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAAKSDNVAPADRSATP
SEG ..xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.........................
1a06- ....

```
SEQ     ATDGSATPATDGSVTPATDGSITPATDGSVTPATDRSATPATDGRATPATEESTVPTTQS
SEG     ............................................................
1a06-   ............................................................

SEQ     SAMLATKAAATPEPAMAQPDSTAPEGATGQAPPSSKGEEAAGYAQESQREEAS
SEG     .....................................................
1a06-   .....................................................
```

Prosite for DKFZphfbr2_82e4.1

PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	46->49	PKC_PHOSPHO_SITE	PDOC00005
PS00005	51->54	PKC_PHOSPHO_SITE	PDOC00005
PS00005	91->94	PKC_PHOSPHO_SITE	PDOC00005
PS00005	103->106	PKC_PHOSPHO_SITE	PDOC00005
PS00005	118->121	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	264->267	PKC_PHOSPHO_SITE	PDOC00005
PS00005	394->397	PKC_PHOSPHO_SITE	PDOC00005
PS00005	454->457	PKC_PHOSPHO_SITE	PDOC00005
PS00005	467->470	PKC_PHOSPHO_SITE	PDOC00005
PS00006	7->11	CK2_PHOSPHO_SITE	PDOC00006
PS00006	91->95	CK2_PHOSPHO_SITE	PDOC00006
PS00006	103->107	CK2_PHOSPHO_SITE	PDOC00006
PS00006	118->122	CK2_PHOSPHO_SITE	PDOC00006
PS00006	248->252	CK2_PHOSPHO_SITE	PDOC00006
PS00006	313->317	CK2_PHOSPHO_SITE	PDOC00006
PS00006	336->340	CK2_PHOSPHO_SITE	PDOC00006
PS00006	442->446	CK2_PHOSPHO_SITE	PDOC00006
PS00006	455->459	CK2_PHOSPHO_SITE	PDOC00006
PS00006	467->471	CK2_PHOSPHO_SITE	PDOC00006
PS00007	456->464	TYR_PHOSPHO_SITE	PDOC00007
PS00007	127->136	TYR_PHOSPHO_SITE	PDOC00007
PS00008	260->266	MYRISTYL	PDOC00008
PS00008	321->327	MYRISTYL	PDOC00008
PS00008	324->330	MYRISTYL	PDOC00008
PS00009	59->63	AMIDATION	PDOC00009

Pfam for DKFZphfbr2_82e4.1

```
HMM_NAME    Eukaryotic protein kinase domain

HMM            *YeigRiIGeGsFGtVYkCiWr.TGeIVAIKIIkkrsms.....FlREIq
                Y +G++I     F ++++++++ TG++    K++ KR+        + +EI
Query       24  YDLGQVIKTEEFCEIFRAKDKTTGKLHTCKKFQKRDGRKVRKAAKNEIG     72

HMM             IMRrLnHPNIIRFYDwFedddDHIYMIMEYMeGGDLFDYIrrngpMsEwe
                I+++++HPNI+++ D+F   + +++ + +E++ G + FD+I ++G++SE++
Query       73  ILKMVKHPNILQLVDVFV-TRKEYFIFLELATGREVFDWILDQGYYSERD   121

HMM             IrfIMyQILrGMeYLHSMgIIHRDLKPENILIDeN...gqIKIcDFGLAR
                 ++++Q+L++++YLHS +I+HR LK EN+ + ++      I I+DF LA+
Query      122  TSNVVRQVLEAVAYLHSLKIVHRNLKLENLVYYNRLKNSKIVISDFHLAK   171

HMM             qMnnYerMttfCGTPWY*
                + N  ++ +  CGTP+Y
Query      172  LEN--GLIKEPCGTPEY    186

HMM             *GepPFyd...........dnMemImrIiqrfrrpfWpnCSeElyDFMr
                 G PPFY+           + +++I++++++F +P+W+ +S  ++D+++
Query      188   GNPPFYEEVEEDDYENHDKNLFRKILAGDYEFDSPYWDDISQAAKDLVT   236

HMM             wCWnyDPekRPTFrQILnHPWF*
                +++++  ++R+T+++++ H W+
Query      237  RLMEVEQDQRITAEEAISHEWI    258
```

DKFZphfbr2_82g14
----

group: transmembrane protein

DKFZphfbr2_82g14 encodes a novel 208 amino acid proline-rich protein without similarity to known proteins.

The protein contains one transmembrane domain.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes and as a new marker for neuronal cells.

unknown prolin rich protein
membrane regions: 1
Summary DKFZphfbr2_82g14 encodes a novel 208 amino acid protein.

unknown prolin rich protein

complete cDNA, complete cds, EST hits
TRANSMEMBRANE 1

Sequenced by DKFZ

Locus: /map="26.2 cR from top of Chr16 linkage group"

Insert length: 2059 bp
Poly A stretch at pos. 2049, polyadenylation signal at pos. 2024

```
   1 AGAAGTGCGA CTGCCAGCTG CCGAGGCGTT CGGTCCTGCT GTTGCGGCCG
  51 CTGCCCCAGG GCTGCGGGGA CGCTCCCGGA GCCCTGCCTG TCCCCTGTCC
 101 ATCCAGGCCA GCAGCTGAAG GAGCCTCACC TGCCTCCCTT CTCTGAGTAG
 151 CACGGATTTG AGGAGAAGCA GCGAAGATGT CCAGCGAGCC TCCCCCTCCT
 201 TATCCTGGGG GCCCCACAGC CCCACTTCTG GAAGAGAAAA GTGGAGCCCC
 251 GCCCACCCCA GGCCGTTCCT CCCCAGCTGT GATGCAGCCC CCTCCAGGCA
 301 TGCCACTGCC CCCTGCGGAC ATTGGCCCCC CACCCTATGA GCCGCCGGGT
 351 CACCCAATGC CCCAGCCTGG CTTCATCCCA CCACACATGA GTGCAGATGG
 401 CACCTACATG CCTCCGGGTT TCTACCCTCC TCCAGGCCCC CACCCACCCA
 451 TGGGCTACTA CCCCCCAGGG CCCTACACGC CAGGGCCCTA CCCTGGCCCT
 501 GGGGGCCACA CAGCCACAGT CCTGGTCCCT TCAGGAGCTG CCACCACGGT
 551 GACAGTGCTG CAGGGAGAGA TCTTTGAGGG AGCGCCTGTG CAGACGGTGT
 601 GTCCCCACTG CCAGCAGGCC ATCGCCACCA AGATCTCCTA CGAGATTGGC
 651 TTGATGAATT TCGTGCTGGG TTTCTTCTGT TGCTTCATGG GATGTGATCT
 701 GGGCTGCTGC CTGATCCCCT GCCTCATCAA TGACTTCAAG GATGTGACGC
 751 ACACATGCCC CAGCTGCAAA GCCTACATCT ACACGTACAA GCGCCTGTGC
 801 TAACGGAGCT GGGACTCGGG ACTCCCCCGC CTGTCAGTCT GGCCCCCTGT
 851 GCTTTGCTCC CTGCGCTCAG TGGTCACTTT CCCGCTCCCA CTTGGGGCTG
 901 GGAGCCGTGC CACCATCCCC TAGAAGTCCT GTCCTCTTCA CCCTGCCCTA
 951 CCTGAGCCGC TGACTCTTCT GGCAAAAATT CTGTTGGGAT TTAAGGCCAA
1001 GGGTCAGTGG GTGGCAGGGG GCTGGCAATG AGCTTGTGTG TTGTTGGTCT
1051 GCTTGGTGTG TGTGATCGGG AAGATAAGCT GGGAGGGGTC TCCTGCTGGG
1101 GTCCTGATGC CTCTGTTTCC AAACAAGGTA CAGGTTCAGT CCAGACTCTT
1151 TCCCCCTGGG ACCAACAGCA GCCAGAGCAG TTAGCCAGTT AGTCCCCAGG
1201 CCTGTGGCCA CAGGCGTTTC TGACCTGCTG GGCCGAGAAT GGGTAAGTTG
1251 TCTGGAGTCA GGTGGGCCCA CGTAGGACAG GGTCACAAAG CCTGGGTTTG
1301 TTTCTGGGTA CTTTGCGCCT CTGGGGTGCT AGAGGTGGGG CATGGTGGCT
1351 GGAAGTAAAA CTGCCAACTC TGGCCCTCAG AACTCTCAGG TATAGAAGCC
1401 CAGGATGTCT AATACCCTGT CCCAGTGCCC GAGAGCTGCC TGGTGTCAGG
1451 TAGAGAGGAC ACTGTACCTG GGTGAATGAT CAGACCCTGG TAGCTAAGAA
1501 GGAACTTGTC CCTTTGAGTC AGTGTGCAGA CCCCCTTTCA GGCCATGCCT
1551 CTGTGAACCC TGTATTGCTG GGGCCGGAAG GAGCCCCTGA GCCTAGCCCC
1601 TTCCCGTCTG CCCTGTGTCC TCACTGCGTG TGGGTATGAC CTCTGCCTGG
1651 TGGCTGGTGT ATCCCAACTG GGCAAGAGAT GGCAGAGGGT CCCCCTTGTG
1701 GGTGCGCTTG GATGTGCAGA GCCTTCTCCA TGGATTTTCT TCCCTGTAAG
1751 TGCCGGGCCC CCCACCCCAG CTGACAGGCT GTTGCTGTGC CTGCTCACAC
1801 CTGCTCCTGC AGGCACACTG GGCTAGGGAC GAGGAAGGAG CAGCCACAAG
1851 TGGTAGAACT GCCTTGGTGG ACACCAGCCT CGCCCTGTCT TTATTTCCTG
1901 AATGGTTTGT GAACTTGCTC ACCTGGACCA CTGTATCCTG CCACTGTCCT
1951 TCCTGGTCTC GCACTGCCAC TGCATGGCCT CCTGTCACTG TGAATCGTGG
2001 CCCAGTCTCA GTTTGTAGTT TCTCATTAAA TTGGCCCTTT CACTCCCCCA
2051 AAAAAAAAA
```

BLAST Results

Entry HS727347 from database EMBL:
human STS WI-16589.
Length = 275
Plus Strand HSPs:
Score = 1365 (204.8 bits), Expect = 3.0e-55, P = 3.0e-55
Identities = 275/276 (99%), Positives = 275/276 (99%), Strand = Plus /
Pl

Medline entries

No Medline entry

Peptide information for frame 3

```
  1 MSSEPPPPYP GGPTAPLLEE KSGAPPTPGR SSPAVMQPPP GMPLPPADIG
 51 PPPYEPPGHP MPQPGFIPPH MSADGTYMPP GFYPPPGPHP PMGYYPPGPY
101 TPGPYPGPGG HTATVLVPSG AATTVTVLQG EIFEGAPVQT VCPHCQQAIA
151 TKISYEIGLM NFVLGFFCCF MGCDLGCCLI PCLINDFKDV THTCPSCKAY
201 IYTYKRLC
```

ORF from 177 bp to 800 bp; peptide length: 208
Category: similarity to known protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82g14, frame 3

PIR:S57447 HPBRII-7 protein - human, N = 1, Score = 206, P = 8.4e-16

PIR:A47655 spliceosome-associated protein SAP 62 - human, N = 1, Score
= 198, P = 4.3e-15

>PIR:S57447 HPBRII-7 protein - human
Length = 551

HSPs:

Score = 206 (30.9 bits), Expect = 8.4e-16, P = 8.4e-16
Identities = 57/115 (49%), Positives = 62/115 (53%)

```
Query:     5 PPPPYPGGPTAPLLEEKSGAPPTPGRSSPAVMQPPPGMPLPPADIGPP-----PYEP--- 56
             PPPP+P G T P      G P PG   P    PPPG LPP   GPP      P P
Sbjct:   226 PPPPFPAGQTPP--RPPLGPPGPPGPPGP----PPPGQVLPPPLAGPPNRGDRPPPPVLF 279

Query:    57 PGHPMPQP--GFIPPHMSADGTYMP-PGFYPPPGPHPPM-GYYPP-GPYTPGPYPGPGGH 111
             PG P  QP  G +PP      G    P PG+ PPPGP PP  G  PP GP+ P P PGP G
Sbjct:   280 PGQPFGQPPLGPLPP-----GPPPPVPGYGPPPGPPPPQQGPPPPPGPFPPRP-PGPLGP 333

Query:   112 TATVLVP 118
               T+  P
Sbjct:   334 PLTLAPP 340
```

Score = 177 (26.6 bits), Expect = 1.1e-12, P = 1.1e-12
Identities = 55/120 (45%), Positives = 61/120 (50%)

```
Query:     5 PPPPYPGGPTAP--LLEEKSGAPPTPG-RSSPAVM---QP---PPGMPLPPADIGPPPYE 55
             P PP P GP  P  +L       PP  G R  P V+   QP   PP  PLPP   GPPP
Sbjct:   244 PGPPGPPGPPPPGQVLPPPLAGPPNRGDRPPPPVLFPGQPFGQPPLGPLPP---GPPP-P 299

Query:    56 PPGHPMPQPGFIPPHMSADGTYMPPGFYPP--PGP-HPPMGYYPPGPYTPGPYPG---PG 109
              PG+  P PG  PP      G    PPG +PP  PGP  PP+    PP P+ PGP PG    P
Sbjct:   300 VPGYG-PPPGPPPPQQ---GPPPPPGPFPPRPPGPLGPPLTLAPP-PHLPGPPPGAPPPA 354

Query:   110 GHTATVLVP 118
             H      P
Sbjct:   355 PHVNPAFFP 363
```

Score = 168 (25.2 bits), Expect = 1.1e-11, P = 1.1e-11
Identities = 47/118 (39%), Positives = 51/118 (43%)

```
Query:     5 PPPPYPG-GPTAPLLEEKSGAPPTPGRSSPAVMQP--PPGMPLPPADI-GPPPYEPPGHP 60
```

```
                PPPP PG GP       + G PP PG   P    P  PP    PP  + GPPP  PP  P
Sbjct:   296 PPPPVPGYGPPPGPPPPQQGPPPPPGPFPPRPPGPLGPPLTLAPPPHLPGPPPGAPPPAP 355

Query:    61 MPQPGFIPPHMSADGTYMPPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSG 120
                P F PP  ++    MP       P P  P G  PP PY  G Y  PG     T   P
Sbjct:   356 HVNPAFFPPPTNSG---MPTSDSRGPPPTDPYGR-PP-PYDRGDYGPPGREMDTARTPLS 410

Query:   121 AA 122
              A
Sbjct:   411 EA 412

 Score = 156 (23.4 bits), Expect = 2.1e-10, P = 2.1e-10
 Identities = 44/103 (42%), Positives = 50/103 (48%)

Query:     6 PPPYPGGPTAPLLEEKSGAPPT-PGRSSPAVMQPPPGMPLPPADIGPPPYEPPGHPMPQP 64
             P   PGG   P        G PP  P   +P   +PP G P PP   GPPP    PG  +P P
Sbjct:   208 PGAVPGGDRFPGPAGPGGPPPPFPAGQTPP--RPPLGPPGPPGPPGPPP---PGQVLPPP 262

Query:    65 GFIPPHMSADGTYMPPGFYP-PPGPHPPMGYYPPGPYTP----GPYPGP 108
                  PP+   D     PP  +P  P   PP+G  PPGP  P      GP PGP
Sbjct:   263 LAGPPNRG-DRP-PPPVLFPGQPFGQPPLGPLPPGPPPPVPGYGPPPGP 309

 Score = 121 (18.2 bits), Expect = 5.2e-05, P = 5.2e-05
 Identities = 40/90 (44%), Positives = 45/90 (50%)

Query:    23 GAPPTPGRSSPAVMQPP-PGMPLPPAD-IGPP-PYEPPGHPMPQPG-FIPPHMSADGTYM 78
             G     PG + P     PP P      PP     +GPP P  PPG P P PG  +PP ++
Sbjct:   213 GGDRFPGPAGPGGPPPPFPAGQTPPRPPLGPPGPPGPPG-P-PPPGQVLPPPLAG----- 265

Query:    79 PP--GFYPPPG---PHPPMGYYPPGPYTPGPYPG-PG 109
             PP  G   PPP      P P G   P GP   PGP P   PG
Sbjct:   266 PPNRGDRPPPPVLFPGQPFGQPPLGPLPPGPPPPVPG 302
```

Pedant information for DKFZphfbr2_82g14, frame 3

Report for DKFZphfbr2_82g14.3

```
[LENGTH]       208
[MW]           21862.47
[pI]           5.55
[PROSITE]      MYRISTYL       3
[PROSITE]      PKC_PHOSPHO_SITE      2
[KW]           TRANSMEMBRANE  1
[KW]           LOW_COMPLEXITY     39.90 %

SEQ     MSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPAVMQPPPGMPLPPADIGPPPYEPPGHP
SEG     ....xxxxxxxxx...................xxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD     cccccccccccccchhhhhhcccccccccccccccccccccccccccccccccccccccc
MEM     ............................................................

SEQ     MPQPGFIPPHMSADGTYMPPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSG
SEG     xxxxxxxxx.....xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.........
PRD     cccccccccccccccccccccccccccccccccccccccccccccccccceeeeeeecccc
MEM     ............................................................

SEQ     AATTVTVLQGEIFEGAPVQTVCPHCQQAIATKISYEIGLMNFVLGFFCCFMGCDLGCCLI
SEG     ............................................................
PRD     cceeeeeeeeeeeccccceeeeccchhhhhhhhhhhhhhhceeeeeeeeeeecccccceeec
MEM     ...............................................MMMMMMMMMMMMM

SEQ     PCLINDFKDVTHTCPSCKAYIYTYKRLC
SEG     ............................
PRD     eeeecccccccccccccccceeeeeeeccc
MEM     MMMM........................
```

Prosite for DKFZphfbr2_82g14.3

PS00005	196->199	PKC_PHOSPHO_SITE	PDOC00005
PS00005	203->206	PKC_PHOSPHO_SITE	PDOC00005
PS00008	109->115	MYRISTYL	PDOC00008
PS00008	120->126	MYRISTYL	PDOC00008
PS00008	172->178	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_82g14.3)

DKFZphfbr2_82i17
----

group: signal transduction

DKFZphtes2_82i17 encodes a novel 334 amino acid protein with similarity to the plasma membrane substrate for the cAMP-dependent protein kinase.

The novel protein is a transmembrane protein with strong similarity to the phospholemman protein, a membrane substrate for the cAMP-dependent protein kinase. It seems to serve as a chloride channel or as a chloride-channel regulator.

The new protein can find application in modulating/blocking cAMP-dependent protein kinase-dependent pathways.

similarity to plasma membrane substrate for cAMP-dependent protein kinase

complete cDNA, complete cds, EST hits
potential start at Bp 31 matches Kozak consensus PyNNatgG
might be a SODIUM/POTASSIUM-TRANSPORTING ATPASE
TRANSMEMBRANE 1

Sequenced by DKFZ

Locus: /map="11; 920_E_12; 786_(A,H)_11; (797,802)_(E,H)_7"

Insert length: 1647 bp
Poly A stretch at pos. 1637, polyadenylation signal at pos. 1615

```
   1 AGTCTCGGAG GGGACCGGCT GTGCAGACGC CATGGAGTTG GTGCTGGTCT
  51 TCCTCTGCAG CCTGCTGGCC CCCATGGTCC TGGCCAGTGC AGCTGAAAAG
 101 GAGAAGGAAA TGGACCCTTT TCATTATGAT TACCAGACCC TGAGGATTGG
 151 GGGACTGGTG TTCGCTGTGG TTCTCTTCTC GGTTGGGATC CTCCTTATCC
 201 TAAGTCGCAG GTGCAAGTGC AGTTTCAATC AGAAGCCCCG GGCCCCAGGA
 251 GATGAGGAAG CCCAGGTGGA GAACCTCATC ACCGCCAATG CAACAGAGCC
 301 CCAGAAAGCA GAGAACTGAA GTGCAGCCAT CAGGTGGAAG CCTCTGGAAC
 351 CTGAGGCGGC TGCTTGAACC TTTGGATGCA AATGTCGATG CTTAAGAAAA
 401 CCGGCCACTT CAGCAACAGC CCTTTCCCCA GGAGAAGCCA AGAACTTGTG
 451 TGTCCCCCAC CCTATCCCCT CTAACACCAT TCCTCCACCT GATGATGCAA
 501 CTAACACTTG CCTCCCCGCT GCAGCCTGTG GTCCTGCCCA CCTCCCGTGA
 551 TGTGTGTGTG TGTGTGTGTG TGTGTGACTG TGTGTGTTTG CTAACTGTGG
 601 TCTTTGTGGC TACTTGTTTG TGGATGGTAT TGTGTTTGTT AGTGAACTGT
 651 GGACTCGCTT TCCCAGGCAG GGGCTGAGCC ACACGGCCAT CTGCTCCTCC
 701 CTGCCCCCGT GGCCCTCCAT CACCTTCTGC TCCTAGGAGG CTGCTTGTTG
 751 CCCGAGACCA GCCCCCTCCC CTGATTTAGG GATGCGTAGG GTAAGAGCAC
 801 GGGCAGTGGT CTTCAGTCGT CTTGGGACCT GGGAAGGTTT GCAGCACTTT
 851 GTCATCATTC TTCATGGACT CCTTTCACTC CTTTAACAAA AACCTTGCTT
 901 CCTTATCCCA CCTGATCCCA GTCTGAAGGT CTCTTAGCAA CTGGAGATAC
 951 AAAGCAAGGA GCTGGTGAGC CCAGCGTTGA CGTCAGGCAG GCTATGCCCT
1001 TCCGTGGTTA ATTTCTTCCC AGGGGCTTCC ACGAGGAGTC CCCATCTGCC
1051 CCGCCCCTTC ACAGAGCGCC CGGGGATTCC AGGCCCAGGG CTTCTACTCT
1101 GCCCCTGGGG AATGTGTCCC CTGCATATCT TCTCAGCAAT AACTCCATGG
1151 GCTCTGGGAC CCTACCCCTT CCAACCTTCC CTGCTTCTGA GACTTCAATC
1201 TACAGCCCAG CTCATCCAGA TGCAGACTAC AGTCCCTGCA ATTGGGTCTC
1251 TGGCAGGCAA TAGTTGAAGG ACTTCCTGTT CCGTTGGGGC CAGCACACCG
1301 GGATGGATGG AGGGAGAGCA GAGGCCTTTG CTTCTCTGCC TACGTCCCCT
1351 TAGATGGGCA GCAGAGGCAA CTCCCGCATC CTTTGCTCTG CCTGTCAGTG
1401 GTCAGAGCGG TGAGCGAGGT GGGTTGGAGA CTCAGCAGGC TCCGTGCAGC
1451 CCTTGGGAAC AGTGAGAGGT TGAAGGTCAT AACGAGAGTG GGAACTCAAC
1501 CCAGATCCCG CCCCTCCTGT CCTCTGTGTT CCCGCGGAAA CCAACCAAAC
1551 CGTGCGCTGT GACCCATTGC TGTTCTCTGT ATCGTGACCT ATCCTCAACA
1601 ACAACAGAAA AAAGGAATAA AATATCCTTT GTTTCCTAAA AAAAAAA
```

BLAST Results

Entry HS31455 from database EMBL:
human STS WI-2739.
Length = 103
Minus Strand HSPs:
Score = 487 (73.1 bits), Expect = 4.4e-14, P = 4.4e-14
Identities = 101/104 (97%), Positives = 101/104 (97%), Strand = Minus / Plus
frame shift in primer binding site

Medline entries

91250422:
Purification and complete sequence determination of the major plasma membrane substrate
for cAMP-dependent protein kinase and protein kinase C in myocardium.

95091702:
Protein kinase C and cyclic AMP-dependent protein kinase phosphorylate phospholemman,
an insulin and adrenaline-regulated membrane phosphoprotein, at specific sites in the
carboxy terminal domain.

95138184:
Mat-8, a novel phospholemman-like protein expressed in human breast tumors, induces a
chloride conductance in Xenopus oocytes.

Peptide information for frame 2

```
 1 MELVLVFLCS LLAPMVLASA AEKEKEMDPF HYDYQTLRIG GLVFAVVLFS
51 VGILLILSRR CKCSFNQKPR APGDEEAQVE NLITANATEP QKAEN
```

ORF from 32 bp to 316 bp; peptide length: 95
Category: strong similarity to known protein

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfbr2_82i17, frame 2

SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR., N = 1, Score = 196, P = 1.2e-15

TREMBL:AF091390_1 product: "phospholemman precursor"; Mus musculus phospholemman precursor, gene, complete cds., N = 1, Score = 187, P = 1.1e-14

PIR:A40533 cAMP-dependent protein kinase major membrane substrate precursor - dog, N = 1, Score = 189, P = 6.5e-15

SWISSPROT:PLM_RAT PHOSPHOLEMMAN PRECURSOR., N = 1, Score = 185, P = 1.7e-14

>SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR.
Length = 92

HSPs:

Score = 196 (29.4 bits), Expect = 1.2e-15, P = 1.2e-15
Identities = 43/85 (50%), Positives = 56/85 (65%)

```
Query:    4 VLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKC 63
              +LVF   LL       + AE  KE DPF YDYQ+L+IGGLV A +LF +GIL++LSRRC+C
Sbjct:    7 ILVFCVGLLT----MAKAESPKEHDPFTYDYQSLQIGGLVIAGILFILGILIVLSRRCRC 62

Query:   64 SFNQKPRA--PGDEEAQVENLITANAT 88
             FNQ+ R   P +EE     + I   +T
Sbjct:   63 KFNQQQRTGEPDEEEGTFRSSIRRLST 89
```

Pedant information for DKFZphfbr2_82i17, frame 2

Report for DKFZphfbr2_82i17.2

[LENGTH]	95
[MW]	10542.37
[pI]	5.05
[HOMOL]	SWISSPROT:PLM_HUMAN PHOSPHOLEMMAN PRECURSOR. 3e-15
[BLOCKS]	BL01310

[EC]	3.6.1.37 Na+/K+-exchanging ATPase 6e-08
[PIRKW]	transmembrane protein 1e-09
[PIRKW]	hydrolase 6e-08
[PROSITE]	ATP1G1_PLM_MAT8 1
[PROSITE]	MYRISTYL 1
[PROSITE]	CK2_PHOSPHO_SITE 1
[PROSITE]	TYR_PHOSPHO_SITE 1
[PROSITE]	PKC_PHOSPHO_SITE 2
[PROSITE]	ASN_GLYCOSYLATION 1
[KW]	Alpha_Beta
[KW]	SIGNAL_PEPTIDE 19

```
SEQ  MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRR
PRD  ccchhhhhhhhhhcccccccccccccccccccceeeeeccccceeeehhhhhhheeeeehhh

SEQ  CKCSFNQKPRAPGDEEAQVENLITANATEPQKAEN
PRD  hhhccccccccccccchhhhhhhhhhhccccccccc
```

Prosite for DKFZphfbr2_82i17.2

PS00001	86->90	ASN_GLYCOSYLATION	PDOC00001
PS00005	36->39	PKC_PHOSPHO_SITE	PDOC00005
PS00005	58->61	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00007	25->33	TYR_PHOSPHO_SITE	PDOC00007
PS00008	41->47	MYRISTYL	PDOC00008
PS01310	28->42	ATP1G1_PLM_MAT8	PDOC01014

(No Pfam data available for DKFZphfbr2_82i17.2)

DKFZphfbr2_82i24
----

group: nucleic acid management

DKFZphfbr2_82i24 encodes a novel 547 amino acid protein with similarity to DEAD-box superfamily ATP-dependent helicases.

RNA helicases comprise a large family of proteins that are involved in basic biological systems such as nuclear and mitochondrial splicing processes, RNA editing, rRNA processing, translation initiation, nuclear mRNA export, and mRNA degradation. RNA helicases are essential factors in cell development and differentiation, and some of them play a role in transcription and replication of viral single-stranded RNA genomes. The members of the largest subgroup, the DEAD and DEAH box proteins, exhibit a strong dependence of the unwinding activity on ATP hydrolysis.
The novel protein contains a DEAD-box an ATP/GTP-binding site motif A (P-loop, interacting with one of the phophate groups of the nucleotide) and a leucine zipper. Mutations in the closely related Drosophila Hlc gene result in lethality in homozygotes. Therefore the new protein seems to be critical involved in RNA processing in eukariontic c ells.

The new protein can find application in modulating RNA metabolism and gene expression.

strong similarity to DEAD-box subfamily ATP-dependent helicase

complete cDNA, complete cds, EST hits
potential Start at Bp 9 matches Kozak consensus PyNNatgG,
[PFAM] Helicases conserved C-terminal domain
[PFAM] DEAD and DEAH box helicases

Sequenced by DKFZ

Locus: /map="720_A_3; 758_H_4; 772_E_3; 804_A_5; 175.5 cR from topFT of Chr7 linkage group"

Insert length: 1860 bp
Poly A stretch at pos. 1850, polyadenylation signal at pos. 1829

```
   1 AGCAGCGCCA TGGAGGACTC TGAAGCACTG GGCTTCGAAC ACATGGGCCT
  51 CGATCCCCGG CTCCTTCAGG CTGTCACCGA TCTGGGCTGG TCGCGACCTA
 101 CGCTGATCCA GGAGAAGGCC ATCCCACTGG CCCTAGAAGG GAAGGACCTC
 151 CTGGCTCGGG CCCGCACGGG CTCCGGGAAG ACGGCCGCTT ATGCTATTCC
 201 GATGCTGCAG CTGTTGCTCC ATAGGAAGGC GACAGGTCCG GTGGTAGAAC
 251 AGGCAGTGAG AGGCCTTGTT CTTGTTCCTA CCAAGGAGCT GGCACGGCAA
 301 GCACAGTCCA TGATTCAGCA GCTGGCTACC TACTGTGCTC GGGATGTCCG
 351 AGTGGCCAAT GTCTCAGCTG CTGAAGACTC AGTCTCTCAG AGAGCTGTGC
 401 TGATGGAGAA GCCAGATGTG GTAGTAGGGA CCCCATCTCG CATATTAAGC
 451 CACTTGCAGC AAGACAGCCT GAAACTTCGT GACTCCCTGG AGCTTTTGGT
 501 GGTGGACGAA GCTGACCTTC TTTTTTCCTT TGGCTTTGAA GAAGAGCTCA
 551 AGAGTCTCCT CTGTCACTTG CCCCGGATTT ACCAGGCTTT TCTCATGTCA
 601 GCTACTTTTA ACGAGGACGT ACAAGCACTC AAGGAGCTGA TATTACATAA
 651 CCCGGTTACC CTTAAGTTAC AGGAGTCCCA GCTGCCTGGG CCAGACCAGT
 701 TACAGCAGTT TCAGGTGGTC TGTGAGACTG AGGAAGACAA ATTCCTCCTG
 751 CTGTATGCCC TGCTCAAGCT GTCATTGATT CGGGGCAAGT CTCTGCTCTT
 801 TGTCAACACT CTAGAACGGA GTTACCGGCT ACGCCTGTTC TTGGAACAGT
 851 TCAGCATCCC CACCTGTGTG CTCAATGGAG AGCTTCCACT GCGCTCCAGG
 901 TGCCACATCA TCTCACAGTT CAACCAAGGC TTCTACGACT GTGTCATAGC
 951 AACTGATGCT GAAGTCCTGG GGGCCCCAGT CAAGGGCAAG CGTCGGGGCC
1001 GAGGGCCCAA AGGGGACAAG GCCTCTGATC CGGAAGCAGG TGTGGCCCGG
1051 GGCATAGACT TCCACCATGT GTCTGCTGTG CTCAACTTTG ATCTTCCCCC
1101 AACCCCTGAG GCCTACATCC ATCGAGCTGG CAGGACAGCA CGCGCTAACA
1151 ACCCAGGCAT AGTCTTAACC TTTGTGCTTC CCACGGAGCA GTTCCACTTA
1201 GGCAAGATTG AGGAGCTTCT CAGTGGAGAG AACAGGGGCC CCATTCTGCT
1251 CCCCTACCAG TTCCGGATGG AGGAGATCGA GGGCTTCCGC TATCGCTGCA
1301 GGGATGCCAT GCGCTCAGTG ACTAAGCAGG CCATTCGGGA GGCAAGATTG
1351 AAGGAGATCA AGGAAGAGCT TCTGCATTCT GAGAAGCTTA AGACATACTT
1401 TGAAGACAAC CCTAGGGACC TCCAGCTGCT GCGGCATGAC CTACCTTTGC
1451 ACCCCGCAGT GGTGAAGCCC CACCTGGGCC ATGTTCCTGA CTACCTGGTT
1501 CCTCCTGCTC TCCGTGGCCT GGTACGCCCT CACAAGAAGC GGAAGAAGCT
1551 GTCTTCCTCT TGTAGGAAGG CCAAGAGAGC AAAGTCCCAG AACCCACTGC
1601 GCAGCTTCAA GCACAAAGGA AAGAAATTCA GACCCACAGC CAAGCCCTCC
1651 TGAGGTTGTT GGGCCTCTCT GGAGCTGAGC ACATTGTGGA GCACAGGCTT
1701 ACACCCTTCG TGGACAGGCG AGGCTCTGGT GCTTACTGCA CAGCCTGAAC
1751 AGACAGTTCT GGGGCCGGCA GTGCTGGGCC CTTTAGCTCC TTGGCACTTC
1801 CAAGCTGGCA TCTTGCCCCT TGACAACAGA ATAAAAATTT TAGCTGCCCC
1851 AAAAAAAAAA
```

BLAST Results

Entry HSG05793 from database EMBL:
human STS WI-6581.
Length = 206
Minus Strand HSPs:
Score = 992 (148.8 bits), Expect = 6.0e-38, P = 6.0e-38
Identities = 204/208 (98%), Positives = 204/208 (98%), Strand = Minus /
Pl

Entry AC004938 from database EMBL:
Homo sapiens clone DJ0971C03; HTGS phase 1, 18 unordered pieces.
Score = 1269, P = 6.5e-202, identities = 269/282
12 exons Bp ~87920-93706 (matching 1-1497)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 10 bp to 1650 bp; peptide length: 547
Category: strong similarity to known protein
Classification: Nucleic acid management
Prosite motifs: ATP_GTP_A (51-59)
LEUCINE_ZIPPER (149-171)

```
  1 MEDSEALGFE HMGLDPRLLQ AVTDLGWSRP TLIQEKAIPL ALEGKDLLAR
 51 ARTGSGKTAA YAIPMLQLLL HRKATGPVVE QAVRGLVLVP TKELARQAQS
101 MIQQLATYCA RDVRVANVSA AEDSVSQRAV LMEKPDVVVG TPSRILSHLQ
151 QDSLKLRDSL ELLVVDEADL LFSFGFEEEL KSLLCHLPRI YQAFLMSATF
201 NEDVQALKEL ILHNPVTLKL QESQLPGPDQ LQQFQVVCET EEDKFLLLYA
251 LLKLSLIRGK SLLFVNTLER SYRLRLFLEQ FSIPTCVLNG ELPLRSRCHI
301 ISQFNQGFYD CVIATDAEVL GAPVKGKRRG RGPKGDKASD PEAGVARGID
351 FHHVSAVLNF DLPPTPEAYI HRAGRTARAN NPGIVLTFVL PTEQFHLGKI
401 EELLSGENRG PILLPYQFRM EEIEGFRYRC RDAMRSVTKQ AIREARLKEI
451 KEELLHSEKL KTYFEDNPRD LQLLRHDLPL HPAVVKPHLG HVPDYLVPPA
501 LRGLVRPHKK RKKLSSSCRK AKRAKSQNPL RSFKHKGKKF RPTAKPS
```

BLASTP hits

No BLASTP hits available
Alert BLASTP hits for DKFZphfbr2_82i24, frame 1

TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; Drosophila melanogaster tweety (tty), flightless (fli), dodo (dod), penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds., N = 1, Score = 1230, P = 3.2e-125

TREMBL:SPCC1494_6 gene: "SPCC1494.06c"; product: "atp dependent helicase"; S.pombe chromosome II cosmid c1494., N = 2, Score = 753, P = 2.5e-113

PIR:S51412 hypothetical protein YLR276c - yeast (Saccharomyces cerevisiae), N = 2, Score = 711, P = 8.2e-117

TREMBL:AF025451_2 gene: "C24H12.4"; Caenorhabditis elegans cosmid C24H12., N = 2, Score = 564, P = 2.7e-99

>TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; Drosophila
melanogaster tweety (tty), flightless (fli), dodo (dod), penguin (pen),
small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox
(bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs)
genes, complete cds.
Length = 560

HSPs:

Score = 1230 (184.5 bits), Expect = 3.2e-125, P = 3.2e-125
Identities = 251/497 (50%), Positives = 344/497 (69%)

```
Query:    9 FEHMGLDPRLLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAAYAIPMLQL 68
            F  + LD R+L+AV  LGW +PTLIQ  AIPL LEGKD++ RARTGSGKTA YA+P++Q
Sbjct:   11 FHELELDQRILKAVAQLGWQQPTLIQSTAIPLLLEGKDVVVRARTGSGKTATYALPLIQK 70

Query:   69 LLHRKATGPVVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVS-AAEDSVSQ 127
            +L+ K      EQ V   +VL PTKEL RQ++ +I+QL   C + VRVA+++ ++ D+V+Q
Sbjct:   71 ILNSKLNAS--EQYVSAVVLAPTKELCRQSRKVIEQLVESCGKVVRVADIADSSNDTVTQ 128

Query:  128 RAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVVDEADLLFSFGFEEELKSLLCHL 187
            R  L E PD+VV TP+ +L++ +  S+     +E LVVDEADL+F++G+E++ K L+ HL
Sbjct:  129 RHALSESPDIVVATPANLLAYAEAGSVVDLKHVETLVVDEADLVFAYGYEKDFKRLIKHL 188

Query:  188 PRIYQAFLMSATFNEDVQALKELILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLL 247
            P IYQA L+SAT  +DV  +K L L+NPVTLKL+E +L   DQL   +++ E E DK  +
Sbjct:  189 PPIYQAVLVSATLTDDVVRMKGLCLNNPVTLKLEEPELVPQDQLSHQRILAE-ENDKPAI 247

Query:  248 LYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSRCHIISQFNQG 307
            LYALLKL LIRGKS++FVN+++R Y++RLFLEQF I  CVLN ELP   R H ISQFN+G
Sbjct:  248 LYALLKLRLIRGKSIIFVNSIDRCYKVRLFLEQFGIRACVLNSELPANIRIHTISQFNKG 307

Query:  308 FYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPE 367
             YD +IA+D    +  P  G +      K  ++ D E+  +RGIDF  V+ V+NFD P
Sbjct:  308 TYDIIIASDEHHMEKP--GGKSATNRKSPRSGDMESSASRGIDFQCVNNVINFDFPRDVT 365

Query:  368 AYIHRAGRTARANNPGIVLTFVLPTEQFHLGKIEELL----SGENRGPILLPYQFRMEEI 423
            +YIHRAGRTAR NN G VL+FV   E      +E+ L    + +    I+  YQF+MEE+
Sbjct:  366 SYIHRAGRTARGNNKGSVLSFVSMKESKVNDSVEKKLCDSFAAQEGEQIIKNYQFKMEEV 425

Query:  424 EGFRYRCRDAMRSVTKQAIREARLKEIKEELLHSEKLKTYFEDNPRDLQLLRHDLPLHPA 483
            E FRYR +D  R+ T+ A+ + R++EIK E+L+ EKLK +FE+N RDLQ LRHD PL
Sbjct:  426 ESFRYRAQDCWRAATRVAVHDTRIREIKIEILNCEKLKAFFEENKRDLQALRHDKPLRAI 485

Query:  484 VVKPHLGHVPDYLVPPALRGLV 505
            V+ HL  +P+Y+VP AL+ +V
Sbjct:  486 KVQSHLSDMPEYIVPKALKRVV 507
```

Pedant information for DKFZphfbr2_82i24, frame 1

Report for DKFZphfbr2_82i24.1

[LENGTH] 547
[MW] 61589.88
[pI] 9.34
[HOMOL] TREMBL:AF017777_10 gene: "hlc"; product: "helicase"; Drosophila melanogaster tweety (tty), flightless (fli), dodo (dod), penguin (pen), small optic lobes (sol), innocent bystander (iby), waclaw (waw), bobby sox (bbx), sluggish (slg), helicase (hlc), misato (mst), and la costa (lcs) genes, complete cds. 1e-121
[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YLR276c] 1e-109
[FUNCAT] j mrna translation and ribosome biogenesis [H. influenzae, HI0231 RNA] 2e-42
[FUNCAT] 04.01.04 rrna processing [S. cerevisiae, YLL008w] 8e-40
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YLL008w] 8e-40
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YLL008w] 8e-40
[FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YKR059w] 3e-39
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YKR059w] 3e-39
[FUNCAT] 04.99 other transcription activities [S. cerevisiae, YDL160c] 3e-35
[FUNCAT] 04.05.03 mrna processing (splicing) [S. cerevisiae, YPL119c] 3e-29
[FUNCAT] 04.05.01.07 chromatin modification [S. cerevisiae, YMR290c] 4e-29
[FUNCAT] 1 genome replication, transcription, recombination and repair [H. influenzae, HI0892] 1e-27
[FUNCAT] 09.01 biogenesis of cell wall [S. cerevisiae, YJL033w] 2e-27
[FUNCAT] 30.16 mitochondrial organization [S. cerevisiae, YDR194c] 4e-21
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YGL064c] 1e-05
[BLOCKS] BL00039D DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS] BL00039C DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS] BL00039B DEAD-box subfamily ATP-dependent helicases proteins
[BLOCKS] BL00039A DEAD-box subfamily ATP-dependent helicases proteins
[PIRKW] nucleus 4e-34
[PIRKW] RNA binding 7e-41
[PIRKW] DEAD box 2e-38
[PIRKW] transmembrane protein 9e-20
[PIRKW] DNA binding 8e-23
[PIRKW] ATP 1e-107
[PIRKW] purine nucleotide binding 2e-38
[PIRKW] P-loop 1e-107
[PIRKW] hydrolase 2e-35
[PIRKW] protein biosynthesis 2e-38
[PIRKW] ATP binding 7e-43

```
[SUPFAM]        WW repeat homology 1e-26
[SUPFAM]        DEAD/H box helicase homology 1e-107
[SUPFAM]        unassigned DEAD/H box helicases 1e-107
[SUPFAM]        ATP-dependent RNA helicase DBP1 3e-31
[SUPFAM]        ATP-dependent RNA helicase DHH1 2e-35
[SUPFAM]        translation initiation factor eIF-4A 2e-38
[SUPFAM]        tobacco ATP-dependent RNA helicase DB10 1e-26
[PROSITE]       ATP_GTP_A       1
[PROSITE]       LEUCINE_ZIPPER  1
[PFAM]          Helicases conserved C-terminal domain
[PFAM]          DEAD and DEAH box helicases
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY      9.87 %

SEQ     MEDSEALGFEHMGLDPRLLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAA
SEG     ............................................................
PRD     ccccccccccccccchhhhhhhhhcccccccccccccccccccccceeeeeecccccccee

SEQ     YAIPMLQLLLHRKATGPVVEQAVRGLVLVPTKELARQAQSMIQQLATYCARDVRVANVSA
SEG     ............................................................
PRD     ehhhhhhhhhhccccccccceeeeeecchhhhhhhhhhhhhhhhhcceeeeeecc

SEQ     AEDSVSQRAVLMEKPDVVVGTPSRILSHLQQDSLKLRDSLELLVVDEADLLFSFGFEEEL
SEG     .......................................xxxxxxxxxxxx.........
PRD     ccchhhhhhhhhcccceeeecccchhhhhhcccccchhhhhhhhhhhhhhhhcchhhh

SEQ     KSLLCHLPRIYQAFLMSATFNEDVQALKELILHNPVTLKLQESQLPGPDQLQQFQVVCET
SEG     ............................................................
PRD     hhhhhhccchhhhhhhhhcchhhhhhhhhhhccccceeeeecccccchhhhhhhhhhh

SEQ     EEDKFLLLYALLKLSLIRGKSLLFVNTLERSYRLRLFLEQFSIPTCVLNGELPLRSRCHI
SEG     .....xxxxxxxxxxx............................................
PRD     hhhhhhhhhhhhhhhhcccceeeeeeehhhhhhhhhhhhhhccccceeeccccchhhhhhhh

SEQ     ISQFNQGFYDCVIATDAEVLGAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNF
SEG     ........................xxxxxxxxxxxxx.......................
PRD     hhhhhccceeeeeeccccccccccccccccccccccccccccccccccceeeeeec

SEQ     DLPPTPEAYIHRAGRTARANNPGIVLTFVLPTEQFHLGKIEELLSGENRGPILLPYQFRM
SEG     ............................................................
PRD     cccccceeeeccccccccccccceeeeeecchhhhhhhhhhhhhhcccccccccccchh

SEQ     EEIEGFRYRCRDAMRSVTKQAIREARLKEIKEELLHSEKLKTYFEDNPRDLQLLRHDLPL
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccchhhhhhhhccc

SEQ     HPAVVKPHLGHVPDYLVPPALRGLVRPHKKRKKLSSSCRKAKRAKSQNPLRSFKHHGKKF
SEG     ............................xxxxxxxxxxxxxxxxxx..............
PRD     cccccccccccccceeeccccccccccccccccccccchhhhhhccccccccccccccccccc

SEQ     RPTAKPS
SEG     .......
PRD     ccccccc
```

Prosite for DKFZphfbr2_82i24.1

```
PS00017       51->59     ATP_GTP_A              PDOC00017
PS00029      149->171    LEUCINE_ZIPPER         PDOC00029
```

Pfam for DKFZphfbr2_82i24.1

```
HMM_NAME        DEAD and DEAH box helicases

HMM                 *gLpPWILRnIyeMGFEkPTPIQQqAIPiILeGRDVMACAQTGSGKTAAF
                     GL+P +L +++++G+++PT IQ++AIP++LEG+D++A+A TGSGKTAA+
Query            13  GLDPRLLQAVTDLGWSRPTLIQEKAIPLALEGKDLLARARTGSGKTAAY     61

HMM                 lIPMLQHIDwdP...WpqpPQdPrALILAPTRELAMQIQEEcRkFgkHMn
                    +IPMLQ +++ +    +  +   +R+L+L+PT ELA+Q Q  +++++ ++
Query            62 AIPMLQLLLHRKATGPVVEQA-VRGLVLVPTKELARQAQSMIQQLATYCA    110

HMM                 g.IRImcIYGGtnMRdQMRmLeRGpPHIVIATPGRLIDHIERgtldLDr.
                      +R++ +    +   Q  +L+++P ++V++TP R++ H+++ +L+L++
Query           111 RDVRVANVSAAEDSVSQRAVLMEKP-DVVVGTPSRILSHLQQDSLKLRDS    159

HMM                 IeMLVMDEADRMLDMGFIDQIRrIMrqIPMpwNRQTMMFSATMPdeIqEL
                    +E LV DEAD +++ GF++++  ++ ++P  +  Q  + SAT+ +++Q L
```

```
Query        160 LELLVVDEADLLFSFGFEEELKSLLCHLP--RIYQAFLMSATFNEDVQAL   207

HMM              ARrFMRNPIRInIdMdElTtnEnIkQwYiyVerEMWKfdcLcrLIe*
                  + +++NP+ + + +++L  +   ++Q+ +++E E++KF +L+ L++
Query        208 KELILHNPVTLKLQESQLPGPDQLQQFQVVCETEEDKFLLLYALLK    253


HMM_NAME        Helicases conserved C-terminal domain

HMM              *EileeWLknlGIrvmYIHGdMpQeERdeIMddFNnGEynVLIcTDV...
                   +L+ +L++  I+++++ G +P + R  I+ +FN+G Y++ I+TD+
Query        272  YRLRLFLEQFSIPTCVLNGELPLRSRCHIISQFNQGFYDCVIATDAEVL   320

HMM              .......................ggRGIDIPdVNHVINYDMPWNPEqYI
                                          +RGID+  V+ V N+D+P +PE YI
Query        321 GAPVKGKRRGRGPKGDKASDPEAGVARGIDFHHVSAVLNFDLPPTPEAYI   370

HMM              QRIGRTgRIG*
                 +R+GRT+R++
Query        371 HRAGRTARAN    380
```

DKFZphfbr2_82m16
----

group: brain derived

DKFZphfbr2_82m16 encodes a novel 289 amino acid protein with very weak similarity to A.thaliana F28A23.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of brain-specific genes.

similarity to A.thaliana F28A23.140

complete cDNA, complete cds, few EST hits
many ATGs in front of the ORF
TRANSMEMBRANE 1

Sequenced by DKFZ

Locus: /map="4"

Insert length: 2715 bp
Poly A stretch at pos. 2705, polyadenylation signal at pos. 2687

```
   1 AGAGGAGGGG AGAGGACTGG GGAGCCGAGC CAGAGCCGGG CTGCCTGCCA
  51 CCCGGCTGCT CGTCCGCTAG CTGGGGAGGA GCGCTCCACC CGCAACTGAC
 101 AAAGGATGGG AGAATGCCCG CGCCCCGGGA TGCCGGCCGC ACGCAGCCTG
 151 GCGGCCGCCT GAGCTACTTC ACCCTCCGCC GGTAAGTGAC TGCAAACATC
 201 ATTCATTCAA TCAGCCTCAC TGGGAGCCCC TTCTCTCCGG CTGGTAGTCC
 251 TGGGCGGCTT GTCCCTGATC CCGAGCGGGG CTTGGCACAG CATCAGCCCT
 301 GGAGGGCAGG CAGCAGGTGC CTTTGCCTGG TGGGTCCACT GGGGAGCGTG
 351 GCTGGGGTTC GCGGCGGGTG CTGCCACCCA ACCTGCGGGC GGCGGGCTCG
 401 CCCAGTAGGC GCCTCTCTGG TGAGAGGAGG CGGCTCCAGC CCGCATCCTG
 451 GGGTAGTTGC TACTATTGGC CCCCAGCGCC CGCTCTGCGC GCGCGCCGTT
 501 TCTGGCGGAT CCCCAGTGCG CGGCGCGCTG TTTACACCGG CGTGGTACTA
 551 GTCACGGAGC CGCACCCCTC GGAAAGCGCG GAGTCGATGA CAGCCACTTC
 601 ACAGGCTCAC GCGCTCCTAG TGTGGGCTTG AAGGGGACGG GGACCGATTA
 651 CCAAAGGAGA GCGCTGAGTA CGGAAGACAC AGGGCAGCCT TTGTCTTGGG
 701 TTTAGCGCTG ATGCGCTCAA CCCTGAGTCG GGTTCACTGC AACTGTTGTG
 751 TCCGATTTCG GTTCCCTGCA ACCGCCCTCC TGGGCGAGAG ATGTCATTGT
 801 GTTCCTGCGG CCAGCGGGAC TGAGAGCTGG GACTTAAGAC GCCAGGAGGG
 851 TCCTGCGCTC ACGGGAAATG TACCCCAAAA GAACTCTGAG AGAATATACT
 901 CAACTGTCCT GCTGTGATTA AACAAGACTG CTGTATTTTA ATTTCAGAAA
 951 TTGAAAAGGG ATAGGAGGAA GGGGAAAATG CTGGGCTGGT GTGAAGCGAT
1001 AGCCCGTAAC CCTCACAGAA TTCCAAACAA CACGCGAACA CCCGAGATCT
1051 CAGGGGATTT GGCTGACGCC TCACAAACCT CCACATTGAA TGAAAAATCC
1101 CCAGGGCGAT CTGCAAGTCG ATCAAGTAAC ATTTCAAAAG CAAGCAGCCC
1151 AACAACAGGG ACAGCTCCCA GGAGCCAGTC AAGGTTGTCT GTCTGTCCAT
1201 CCACTCAGGA CATCTGCAGA ATCTGTCACT GCGAAGGGGA TGAAGAGAGC
1251 CCCCTCATCA CACCCTGTCG CTGCACTGGG ACACTGCGCT TTGTCCACCA
1301 GTCCTGCCTC CACCAGTGGA TAAAGAGCTC AGATACACGC TGCTGTGAGC
1351 TCTGCAAGTA TGACTTCATA ATGGAGACCA AGCTCAAACC CCTCCGGAAG
1401 TGGGAGAAAC TACAGATGAC CACAAGTGAA AGGAGGAAAA TATTCTGCTC
1451 TGTCACATTC CACGTAATCG CGATCACCTG TGTGGTTTGG TCTTTGTATG
1501 TATTGATAGA CCGGACAGCG GAGGAAATCA AGCAAGGCAA TGACAATGGT
1551 GTCCTTGAAT GGCCATTTTG GACAAAACTG GTTGTGGTAG CCATTGGCTT
1601 CACAGGAGGT CTTGTCTTCA TGTACGTACA GTGTAAAGTC TATGTTCAGT
1651 TGTGGCGCAG GCTGAAGGCC TACAACCGTG TGATCTTTGT ACAAAATTGC
1701 CCAGACACTG CCAAAAAACT GGAGAAGAAC TTCTCATGTA ATGTAAACAC
1751 AGACATCAAA GATGCTGTGG TAGTGCCTGT ACCACAAACA GGTGCAAATT
1801 CACTGCCATC TGCAGAGGGT GGCCCCCCTG AAGTTGTATC AGTCTGATGG
1851 AACCTGTTGG GAGTTTCTTC ACCGAAGAAT ATCTTTCTAG CCCTCAGCCA
1901 CTACAAATGA CAGAAGTGAC CTTGAATTAT TTACTCCCTT CAGCTCCTCC
1951 TTTCTCCTAC TGACACATTT TTCCTGACTT TGTTCAAAGA GGAAAGGAGA
2001 AAAACAAACA AACAGACCAA ATGCCCAGGA GCCCATGAAG TAATAGCGTA
2051 AAGTAAAGTA TGATATGGAA ATGTGAAGTT TGCAAGAGAA TGATTTCCAA
2101 GACAATTAAG AACTACTGGG GCAATGAATG CTTTTAGGCA GTAATCAAAG
2151 ATTAAATGGA CCCATGATAC TCTTCTTCAC AGTAACAGGG GAAAAGTTCA
2201 AGAATACAGA CTTGAATTGC GATGTGTATT ACTTCTAGGG CCTTGTAATG
2251 TTAACTGTCT CATCTGGAAA TAATAACTAA CATATTTGGT TTTAAGCCTG
2301 AAATTGTCTG CATTATCCCT AAGTCACATT GGAAGTGAAC TTGGAGGATG
2351 CATATTTTGA TATGCTTTGA CAGCTAACAG ATTTGTATGG TTTAGTGGAG
2401 TCTGGTTATT TTGACAGATG CATGTTTTTT TTAAATAGAT GCAATATACA
2451 TTTGAAGACA TTGATATTTG GAATTAATTA TGTTTGTTTA AGTCACGCAA
2501 AAGATTTTCA GAAAATGTTC GGATATAATT AGCTCTGTTA AATACCCACA
2551 GAACTGTTAT CAGGTCTTAT ATTTATTTTC ATCTGGTTCC TCTAATACAG
```

```
 2601 TGCTGTCCAA TAGAAACACA ACAGCCACAA ATGCAGGCCA CAGATGCAAA
 2651 TATTTAACTT CCCAGTAGCC CTATTTTAAA AAGTAAAAAT AAATGTTTGT
 2701 TTGTTAAAAA AAAAA
```

BLAST Results

Entry G37457 from database EMBLNEW:
SHGC-57357 Human Homo sapiens STS genomic.
Length = 458
Plus Strand HSPs:
Score = 2116 (317.5 bits), Expect = 4.3e-91, P = 4.3e-91
Identities = 444/456 (97%)

Medline entries

No Medline entry

Peptide information for frame 3

```
      1 MLGWCEAIAR NPHRIPNNTR TPEISGDLAD ASQTSTLNEK SPGRSASRSS
     51 NISKASSPTT GTAPRSQSRL SVCPSTQDIC RICHCEGDEE SPLITPCRCT
    101 GTLRFVHQSC LHQWIKSSDT RCCELCKYDF IMETKLKPLR KWEKLQMTTS
    151 ERRKIFCSVT FHVIAITCVV WSLYVLIDRT AEEIKQGNDN GVLEWPFWTK
    201 LVVVAIGFTG GLVFMYVQCK VYVQLWRRLK AYNRVIFVQN CPDTAKKLEK
    251 NFSCNVNTDI KDAVVVPVPQ TGANSLPSAE GGPPEVVSV
```

ORF from 978 bp to 1844 bp; peptide length: 289
Category: similarity to unknown protein

BLASTP hits

Entry AB011169_1 from database TREMBL:
gene: "KIAA0597"; product: "KIAA0597 protein"; Homo sapiens mRNA for KIAA0597 protein, partial cds.
Score = 188, P = 6.0e-12, identities = 30/54, positives = 38/54

Entry SPBC14F5_7 from database TREMBL:
gene: "SPBC14F5.07"; product: "hypothetical protein"; S.pombe chromosome II cosmid c14F5.
Score = 185, P = 1.9e-11, identities = 29/53, positives = 38/53

Entry CEY57A10B_1 from database TREMBL:
gene: "Y57A10B.1"; Caenorhabditis elegans cosmid Y57A10B
Score = 171, P = 2.6e-10, identities = 40/107, positives = 58/107

Alert BLASTP hits for DKFZphfbr2_82m16, frame 3

TREMBL:ATF28A23_14 gene: "F28A23.140"; product: "putative protein"; Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project), N = 1, Score = 198, P = 3.4e-13

```
>TREMBL:ATF28A23_14 gene: "F28A23.140"; product: "putative protein";
     Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)
            Length = 1,051

  HSPs:

 Score = 198 (29.7 bits), Expect = 3.4e-13, P = 3.4e-13
 Identities = 38/103 (36%), Positives = 61/103 (59%)

Query:    28 LADASQTSTLNEKSPGRSASRS-SNISKASSPTTGTAPRSQSRLSVCPSTQDICRICHCE 86
             +++ S +S+ +   SP +++     SN+  A S  TG+              +D+CRIC
Sbjct:    20 VSEPSVSSSSSSSSPNQASPNPFSNMDPAVSTATGSRYVDDDE-----DEEDVCRICRNP 74

Query:    87 GDEESPLITPCRCTGTLRFVHQSCLHQWIKSSDTRCCELCKYDF 130
             GD ++PL   PC C+G+++FVHQ CL QW+  S+ R CE+CK+ F
Sbjct:    75 GDADNPLRYPCACSGSIKFVHQDCLLQWLNHSNARQCEVCKHPF 118
```

Pedant information for DKFZphfbr2_82m16, frame 3

Report for DKFZphfbr2_82m16.3

```
[LENGTH]        289
[MW]            32308.36
[pI]            8.76
[HOMOL]         PIR:T00268 hypothetical protein KIAA0597 - human (fragment) 9e-14
[FUNCAT]        04.99 other transcription activities [S. cerevisiae, YIL030c] 4e-09
[PIRKW]         transmembrane protein 9e-08
[PROSITE]       MYRISTYL        1
[PROSITE]       CK2_PHOSPHO_SITE        4
[PROSITE]       TYR_PHOSPHO_SITE        1
[PROSITE]       PKC_PHOSPHO_SITE        3
[PROSITE]       ASN_GLYCOSYLATION       3
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY      6.57 %
```

```
SEQ   MLGWCEAIARNPHRIPNNTRTPEISGDLADASQTSTLNEKSPGRSASRSSNISKASSPTT
SEG   ......................................xxxxxxxxxxxxxxxxxxx..
PRD   ccchhhhhhccccccccccccccccchhhhhhhhhcccccccccccccccccccccccccc

SEQ   GTAPRSQSRLSVCPSTQDICRICHCEGDEESPLITPCRCTGTLRFVHQSCLHQWIKSSDT
SEG   ............................................................
PRD   ccccccccccccccccceeeeeeecccccccccccccccccceeeeehhhhhhhhhcccc

SEQ   RCCELCKYDFIMETKLKPLRKWEKLQMTTSERRKIFCSVTFHVIAITCVVWSLYVLIDRT
SEG   ............................................................
PRD   ceeeeeeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccc

SEQ   AEEIKQGNDNGVLEWPFWTKLVVVAIGFTGGLVFMYVQCKVYVQLWRRLKAYNRVIFVQN
SEG   ............................................................
PRD   ccccccccccceeehhhhheeeeeeeccccccceeeeehhhhhhhhhhhhhhhheeeeee

SEQ   CPDTAKKLEKNFSCNVNTDIKDAVVVPVPQTGANSLPSAEGGPPEVVSV
SEG   .................................................
PRD   ccchhhhhhcccccccccccceeeeeeecccccccccccccccccccc
```

Prosite for DKFZphfbr2_82m16.3

PS00001	17->21	ASN_GLYCOSYLATION	PDOC00001
PS00001	51->55	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00005	102->105	PKC_PHOSPHO_SITE	PDOC00005
PS00005	150->153	PKC_PHOSPHO_SITE	PDOC00005
PS00005	244->247	PKC_PHOSPHO_SITE	PDOC00005
PS00006	36->40	CK2_PHOSPHO_SITE	PDOC00006
PS00006	75->79	CK2_PHOSPHO_SITE	PDOC00006
PS00006	148->152	CK2_PHOSPHO_SITE	PDOC00006
PS00006	180->184	CK2_PHOSPHO_SITE	PDOC00006
PS00007	121->129	TYR_PHOSPHO_SITE	PDOC00007
PS00008	187->193	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfbr2_82m16.3)

DKFZphfbr2_82m6
----

group: signal transduction

DKFZphfbr2_82m6.3 encodes a novel 654 amino acid protein with similarity to murine sphingosine kinase.

Sphingosine kinase is a new type of lipid kinase, which is regulated by growth factors. The enzyme phosphorylates sphingosine, which subsequently exerts intracellular and extracellular actions. Intracellulary, sphingosine 1-phosphate (SPP) promotes proliferation and inhibits apoptosis. In yeast, survival of cells exposed to heat shock indicates is dependend on SPP. Extracellulary, SPP inhibits cell motility and influences cell morphology, effects that appear to be mediated by the G protein-coupled receptor EDG1.

The new protein can find application in modulating/blocking the shingosine kinase intracellular signal transmission pathway.

strong similarity to mouse "sphingosine kinase"

complete cDNA, complete cds, EST hits,
YLR260w/YOR171c Lcb5p/Lcb4p = long chain base kinases,
involved in biosynthesis of sphingolipids

Sequenced by DKFZ

Locus: unknown

Insert length: 2875 bp
Poly A stretch at pos. 2865, polyadenylation signal at pos. 2838

```
   1 AGTGTTGGAG GTGAGGAGGC GGGGCTGGCA GGGCTAGTCG GGGCATCTGG
  51 AAATTTCCGA CCCCACGCTT CGGGCGTTTC CTTATCAGGT TCACCGCTCC
 101 CTGATCTCGC GCTGCACTTC GTAGGCGCAG CCGCTGCTTG GGAAGTCCTA
 151 CTTAAGAGCT GAAGGTCAGG CCAGGACAGT GAGACCTGAC TCCTTGCTCC
 201 TACCAGCCTA CTATGGCTTA AGACCCAGGG CCAGGGTCCC GTTGATGTAA
 251 CAGAGCAGAG GACCAGCAGA TGAATGGACA CCTTGAAGCA GAGGAGCAGC
 301 AGGACCAGAG GCCAGACCAG GAGCTGACCG GGAGCTGGGG CCACGGGCCT
 351 AGGAGCACCC TGGTCAGGGC TAAGGCCATG GCCCCGCCCC CACCGCCACT
 401 GGCTGCCAGC ACCTCGCTCC TCCATGGCGA GTTTGGCTCC TACCCAGCCC
 451 GAGGCCCACG CTTTGCCCTC ACCCTTACAT CGCAGGCCCT GCACATACAG
 501 CGGCTGCGCC CCAAACCTGA AGCCAGGCCC CGGGGTGGCC TGGTCCCGTT
 551 GGCCGAGGTC TCAGGCTGCT GCACCCTGCG AAGCCGCAGC CCCTCAGACT
 601 CAGCGGCCTA CTTCTGCATC TACACCTACC CTCGGGGCCG GCGCGGGGCC
 651 CGGCGCAGAG CCACTCGCAC CTTCCGGGCA GATGGGGCCG CCACCTACGA
 701 AGAGAACCGT GCCGAGGCCC AGCGCTGGGC CACTGCCCTC ACCTGTCTGC
 751 TCCGAGGACT GCCACTGCCC GGGGATGGGG AGATCACCCC TGACCTGCTA
 801 CCTCGGCCGC CCCGGTTGCT TCTATTGGTC AATCCCTTTG GGGGTCGGGG
 851 CCTGGCCTGG CAGTGGTGTA AGAACCACGT GCTTCCCATG ATCTCTGAAG
 901 CTGGGCTGTC CTTCAACCTC ATCCAGACAG AACGACAGAA CCACGCCCGG
 951 GAGCTGGTCC AGGGGCTGAG CCTGAGTGAG TGGGATGGCA TCGTCACGGT
1001 CTCGGGAGAC GGGCTGCTCC ATGAGGTGCT GAACGGGCTC CTAGATCGCC
1051 CTGACTGGGA GGAAGCTGTG AAGATGCCTG TGGGCATCCT CCCCTGCGGC
1101 TCGGGCAACG CGCTGGCCGG AGCAGTGAAC CAGCACGGGG GATTTGAGCC
1151 AGCCCTGGGC CTCGACCTGT TGCTCAACTG CTCACTGTTG CTGTGCCGGG
1201 GTGGTGGCCA CCCACTGGAC CTGCTCTCCG TGACGCTGGC CTCGGGCTCC
1251 CGCTGTTTCT CCTTCCTGTC TGTGGCCTGG GGCTTCGTGT CAGATGTGGA
1301 TATCCAGAGC GAGCGCTTCA GGGCCTTGGG CAGTGCCCGC TTCACACTGG
1351 GCACGGTGCT GGGCCTCGCC ACACTGCACA CCTACCGCGG ACGCCTCTCC
1401 TACCTCCCCG CCACTGTGGA ACCTGCCTCG CCCACCCCTG CCCATAGCCT
1451 GCCTCGTGCC AAGTCGGAGC TGACCCTAAC CCCAGACCCA GCCCCGCCCA
1501 TGGCCCACTC ACCCCTGCAT CGTTCTGTGT CTGACCTGCC TCTTCCCCTG
1551 CCCCAGCCTG CCCTGGCCTC TCCTGGCTCG CCAGAACCCC TGCCCATCCT
1601 GTCCCTCAAC GGTGGGGGCC CAGAGCTGGC TGGGGACTGG GGTGGGGCTG
1651 GGGATGCTCC GCTGTCCCCG GACCCACTGC TGTCTTCACC TCCTGGCTCT
1701 CCCAAGGCAG CTCTACACTC ACCCGTCTCC GAAGGGGCCC CCGTAATTCC
1751 CCCATCCTCT GGGCTCCCAC TTCCCACCCC TGATGCCCGG GTAGGGGCCT
1801 CCACCTGCGG CCCGCCCGAC CACCTGCTGC CTCCGCTAGG CACCCCGCTG
1851 CCCCCAGACT GGGTGACGCT GGAGGGGGAC TTTGTGCTCA TGTTGGCCAT
1901 CTCGCCCAGC CACCTAGGCG CTGACCTGGT GGCAGCTCCG CATGCGCGCT
1951 TCGACGACGG CCTGGTGCAC CTGTGCTGGG TGCGTAGCGG CATCTCGCGG
2001 GCTGCGCTGC TGCGCCTTTT CTTGGCCATG GAGCGTGGTA GCCACTTCAG
2051 CCTGGGCTGT CCGCAGCTGG GCTACGCCGC GGCCCGTGCC TTCCGCCTAG
2101 AGCCGCTCAC ACCACGCGGC GTGCTCACAG TGGACGGGGA GCAGGTGGAG
2151 TATGGGCCGC TACAGGCACA GATGCACCCT GGCATCGGTA CACTGCTCAC
2201 TGGGCCTCCT GGCTGCCCGG GGCGGGAGCC CTGAAACTAA ACAAGCTTGG
2251 TACCCGCCGG GGGCGGGGCC TACATTCCAA TGGGGCGGAG CCTGAGCTAG
2301 GGGGTGTGGC CTGGCTGCTA GAGTTGTGGT GGCAGGGGCC CTGGCCCCGT
```

```
2351 CTCAGGATTG CGCTCGCTTT CATGGGACCA GACGTGATGC TGGAAGGTGG
2401 GCGTCGTCAC GGTTAAAGAG AAATGGGCTC GTCCCGAGGG TAGTGCCTGA
2451 TCAATGAGGG CGGGGCCTGG CGTCTGATCT GGGGCCGCCC TTACGGGGCA
2501 GGGCTCAGTC CTGACGCTTG CCACCTGCTC CTACCCGGCC AGGATGGCTG
2551 AGGGCGGAGT CTATTTTACG CGTCGCCCAA TGACAGGACC TGGAATGTAC
2601 TGGCTGGGGT AGGCCTCAGT GAGTCGGCCG GTCAGGGCCC GCAGCCTCGC
2651 CCCATCCACT CCGGTGCCTC CATTTAGCTG GCCAATCAGC CCAGGAGGGG
2701 CAGGTTCCCC GGGGCCGGCG CTAGGATTTG CACTAATGTT CCTCTCCCCG
2751 CGGGTGGGGG CGGGGAAATT CATATCCCCT GTTCGTCTCA TGCGCGTCCT
2801 CCGTCCCCAA TCTAAAAAGC AATTGAAAAG GTCTATGCAA TAAAGGCAGT
2851 CGCTTCATTC CTCTCAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

99045661:
Tumor necrosis factor-alpha induces adhesion molecule expression through the sphingosine kinase pathway.

98395082:
Molecular cloning and functional characterization of murine sphingosine kinase.

98241633:
Purification and characterization of rat kidney sphingosine kinase.

99178622:
Sphingosine 1-phosphate: a prototype of a new class of second messengers.

Peptide information for frame 3

```
  1 MNGHLEAEEQ QDQRPDQELT GSWGHGPRST LVRAKAMAPP PPPLAASTSL
 51 LHGEFGSYPA RGPRFALTLT SQALHIQRLR PKPEARPRGG LVPLAEVSGC
101 CTLRSRSPSD SAAYFCIYTY PRGRRGARRR ATRTFRADGA ATYEENRAEA
151 QRWATALTCL LRGLPLPGDG EITPDLLPRP PRLLLLVNPF GGRGLAWQWC
201 KNHVLPMISE AGLSFNLIQT ERQNHARELV QGLSLSEWDG IVTVSGDGLL
251 HEVLNGLLDR PDWEEAVKMP VGILPCGSGN ALAGAVNQHG GFEPALGLDL
301 LLNCSLLLCR GGGHPLDLLS VTLASGSRCF SFLSVAWGFV SDVDIQSERF
351 RALGSARFTL GTVLGLATLH TYRGRLSYLP ATVEPASPTP AHSLPRAKSE
401 LTLTPDPAPP MAHSPLHRSV SDLPLPLPQP ALASPGSPEP LPILSLNGGG
451 PELAGDWGGA GDAPLSPDPL LSSPPGSPKA ALHSPVSEGA PVIPPSSGLP
501 LPTPDARVGA STCGPPDHLL PPLGTPLPPD WVTLEGDFVL MLAISPSHLG
551 ADLVAAPHAR FDDGLVHLCW VRSGISRAAL LRLFLAMERG SHFSLGCPQL
601 GYAAARAFRL EPLTPRGVLT VDGEQVEYGP LQAQMHPGIG TLLTGPPGCP
651 GREP
```

ORF from 270 bp to 2231 bp; peptide length: 654
Category: similarity to known protein

BLASTP hits

Entry SPAC4A8_7 from database TREMBL:
gene: "SPAC4A8.07c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c4A8.
Score = 301, P = 7.9e-32, identities = 68/190, positives = 109/190

Entry CEC34C6_3 from database TREMBLNEW:
product: "C34C6.5"; Caenorhabditis elegans cosmid C34C6
>TREMBL:CEC34C6_3 product: "C34C6.5"; Caenorhabditis elegans cosmid C34C6
Score = 273, P = 9.0e-29, identities = 78/265, positives = 142/265

Entry S67059 from database PIR:
hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae)
>TREMBL:SC55021_9 gene: "O3615"; product: "O3615p"; Saccharomyces cerevisiae cosmid pUOA1258 from chromosome 15R. >TREMBL:SCYOR170W_2 S.cerevisiae chromosome XV reading frame ORF YOR170w

Score = 253, P = 2.0e-25, identities = 70/234, positives = 116/234

Entry S51398 from database PIR:
hypothetical protein YLR260w - yeast (Saccharomyces cerevisiae)
>TREMBL:SCL8479_4 gene: "YLR260W"; product: "Ylr260wp"; Saccharomyces cerevisiae chromosome XII cosmid 8479.
Score = 251, P = 1.0e-24, identities = 62/198, positives = 103/198

Alert BLASTP hits for DKFZphfbr2_82m6, frame 3

TREMBL:AF068749_1 gene: "SPHK1b"; product: "sphingosine kinase"; Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds., N = 2, Score = 615, P = 1.2e-92

TREMBL:AF068748_1 gene: "SPHK1a"; product: "sphingosine kinase"; Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds., N = 2, Score = 616, P = 2e-92

TREMBL:ATF18E5_16 gene: "F18E5.160"; product: "putative protein"; Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project), N = 2, Score = 370, P = 6.8e-33

>TREMBL:AF068748_1 gene: "SPHK1a"; product: "sphingosine kinase"; Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.
Length = 504

HSPs:

Score = 616 (92.4 bits), Expect = 2.0e-92, Sum P(2) = 2.0e-92
Identities = 128/260 (49%), Positives = 173/260 (66%)

```
Query:   154 ATALTCLLRGLPLPGDGEITPDLLPRPPRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGL 213
             A   C       L + E    LLPRP R+L+L+NP GG+G A Q  ++ V P + EA +
Sbjct:   110 APVAPCQREPRDLAMEPECPRGLLPRPCRVLVLLNPQGGKGKALQLFQSRVQPFLEEAEI 169

Query:   214 SFNLIQTERQNHARELVQGLSLSEWDGIVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGI 273
             +F LI TER+NHARELV      L  WD +  +SGDGL+HEV+NGL++RPDWE A++ P+
Sbjct:   170 TFKLILTERKNHARELVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAIQKPLCS 229

Query:   274 LPCGSGNALAGAVNQHGGFEPALGLDLLLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFL 333
             LP GSGNALA +VN + G+E       DLL+NC+LLLCR     P++LLS+  ASG R +S L
Sbjct:   230 LPGGSGNALAASVNHYAGYEQVTNEDLLINCTLLLCRRRLSPMNLLSLHTASGLRLYSVL 289

Query:   334 SVAWGFVSDVDIQSERFRALGSARFTLGTVLGLATLHTYRGRLSYLPA-TVEPASPTPAH 392
             S++WGFV+DVD++SE++R LG  RFT+GT   LA+L  Y+G+L+YLP  TV  AS  PA
Sbjct:   290 SLSWGFVADVDLESEKYRRLGEIRFTVGTFFRLASLRIYQGQLAYLPVGTV--ASKRPAS 347

Query:   393 SL-PRAKSELTLTPDPAPPMAH 413
             +L  +    + L P   P  +H
Sbjct:   348 TLVQKGPVDTHLVPLEEPVPSH 369
```

Score = 324 (48.6 bits), Expect = 2.0e-92, Sum P(2) = 2.0e-92
Identities = 72/160 (45%), Positives = 100/160 (62%)

```
Query:   499 LPLPTPDARVGASTC---GPPDHLLPPLGTPLPPDWVTL-EGDFVLMLAISPSHLGADLV 554
             LP+ T  ++  AST    GP D  L PL  P+P  W  + E DF+L+L +  +HL ++L
Sbjct:   335 LPVGTVASKRPASTLVQKGPVDTHLVPLEEPVPSHWTVVPEQDFLLVLVLLHTHLSSELF 394

Query:   555 AAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSHFSLGCPQLGYAAARAFRLEPLT 614
             AAP  R + G++HL +VR+G+SRAALLRLFLAM++G H  L CP L +    AFRLEP +
Sbjct:   395 AAPMGRCEAGVMHLFYVRAGVSRAALLRLFLAMQKGKHMELDCPYLVHVPVVAFRLEPRS 454

Query:   615 PRGVLTVDGEQVEYGPLQAQMHPGIGTLLTGPPGCP-GRE 653
              RGV +VDGE +    +Q Q+HP     ++ G    P GR+
Sbjct:   455 QRGVFSVDGELMVCEAVQGQVHPNYLWMVCGSRDAPSGRD 494
```

Score = 37 (5.6 bits), Expect = 3.6e-62, Sum P(2) = 3.6e-62
Identities = 8/20 (40%), Positives = 9/20 (45%)

```
Query:   459 GAGDAPLSPDPLLSSPPGSP 478
             G+ DAP   D    PP  P
Sbjct:   485 GSRDAPSGRDSRRGPPPEEP 504
```

Pedant information for DKFZphfbr2_82m6, frame 3

Report for DKFZphfbr2_82m6.3

[LENGTH] 654
[MW] 69207.45
[pI] 6.47
[HOMOL] TREMBL:AF068749_1 gene: "SPHK1b"; product: "sphingosine kinase"; Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds. 2e-50
[FUNCAT] 01.06.01 lipid, fatty-acid and sterol biosynthesis [S. cerevisiae, YLR260w] 4e-20
[PROSITE] AMIDATION 1
[PROSITE] CAMP_PHOSPHO_SITE 1
[PROSITE] MYRISTYL 12
[PROSITE] CK2_PHOSPHO_SITE 6
[PROSITE] TYR_PHOSPHO_SITE 1
[PROSITE] GLYCOSAMINOGLYCAN 1
[PROSITE] PKC_PHOSPHO_SITE 8
[PROSITE] ASN_GLYCOSYLATION 1
[KW] Alpha_Beta
[KW] LOW_COMPLEXITY 20.18 %

```
SEQ    MNGHLEAEEQQDQRPDQELTGSWGHGPRSTLVRAKAMAPPPPPLAASTSLLHGEFGSYPA
SEG    .................................xxxxxxxxxxxxx..............
PRD    ccchhhhhhhcccccceeeccccccccceeehhhhcccccccceeeceeeeccccccccc

SEQ    RGPRFALTLTSQALHIQRLRPKPEARPRGGLVPLAEVSGCCTLRSRSPSDSAAYFCIYTY
SEG    ............................................................
PRD    cccceeehhhhhhhhhhhhcccccccccceeeeeeeceeeeeeeccccccceeeeeeeec

SEQ    PRGRRGARRRATRTFRADGAATYEENRAEAQRWATALTCLLRGLPLPGDEITPDLLPRP
SEG    .xxxxxxxxxxxxxxxxxxxx..................................xxxxx
PRD    ccccchhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccc

SEQ    PRLLLLVNPFGGRGLAWQWCKNHVLPMISEAGLSFNLIQTERQNHARELVQGLSLSEWDG
SEG    xxxxxx......................................................
PRD    ceeeeeeecccccchhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhhhccccce

SEQ    IVTVSGDGLLHEVLNGLLDRPDWEEAVKMPVGILPCGSGNALAGAVNQHGGFEPALGLDL
SEG    .......................................................xxxxx
PRD    eeecccccceeeccccccccccchhhhccceeecccccccccccccccccccchhhhhh

SEQ    LLNCSLLLCRGGGHPLDLLSVTLASGSRCFSFLSVAWGFVSDVDIQSERFRALGSARFTL
SEG    xxxxxxxxxxxxx...............................................
PRD    hhhhhcccccccccccceeeeeecccccceeeeeeeeeccccceeeehhhhhhhhhhhhhc

SEQ    GTVLGLATLHTYRGRLSYLPATVEPASPTPAHSLPRAKSELTLTPDPAPPMAHSPLHRSV
SEG    ............................................................
PRD    hhhhhhhhhhhccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ    SDLPLPLPQPALASPGSPEPLPILSLNGGGPELAGDWGGAGDAPLSPDPLLSSPPGSPKA
SEG    ..xxxxxxxxxxxxxxxx.....................xxxxxxxxxxxxxxxxxxxxx
PRD    cccccccccccccccccccccceeeeccccccccccccccccccccccccccccccccce

SEQ    ALHSPVSEGAPVIPPSSGLPLPTPDARVGASTCGPPDHLLPPLGTPLPPDWVTLEGDFVL
SEG    xx................................xxxxxxxxxxxxxxx...........
PRD    eccccccccccccccccccccccccccccccccccccccccccccccccccccccccccee

SEQ    MLAISPSHLGADLVAAPHARFDDGLVHLCWVRSGISRAALLRLFLAMERGSHFSLGCPQL
SEG    ............................................................
PRD    eeeeccccccccccccccccccccceeeeeeeccchhhhhhhhhhhhhcccceeeccccch

SEQ    GYAAARAFRLEPLTPRGVLTVDGEQVEYGPLQAQMHPGIGTLLTGPPGCPGREP
SEG    ....................................xxxxxxxxxxxxxxx...
PRD    hhhhhhhhhcccccceeeeccceeeccccccccccccccceeecccccccccc
```

Prosite for DKFZphfbr2_82m6.3

PS00001	303->307	ASN_GLYCOSYLATION	PDOC00001
PS00002	245->249	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	129->133	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	102->105	PKC_PHOSPHO_SITE	PDOC00005
PS00005	134->137	PKC_PHOSPHO_SITE	PDOC00005
PS00005	220->223	PKC_PHOSPHO_SITE	PDOC00005
PS00005	347->350	PKC_PHOSPHO_SITE	PDOC00005
PS00005	355->358	PKC_PHOSPHO_SITE	PDOC00005
PS00005	371->374	PKC_PHOSPHO_SITE	PDOC00005
PS00005	477->480	PKC_PHOSPHO_SITE	PDOC00005
PS00005	614->617	PKC_PHOSPHO_SITE	PDOC00005
PS00006	107->111	CK2_PHOSPHO_SITE	PDOC00006

PS00006	142->146	CK2_PHOSPHO_SITE	PDOC00006
PS00006	234->238	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00006	341->345	CK2_PHOSPHO_SITE	PDOC00006
PS00006	419->423	CK2_PHOSPHO_SITE	PDOC00006
PS00007	106->115	TYR_PHOSPHO_SITE	PDOC00007
PS00008	56->62	MYRISTYL	PDOC00008
PS00008	212->218	MYRISTYL	PDOC00008
PS00008	232->238	MYRISTYL	PDOC00008
PS00008	272->278	MYRISTYL	PDOC00008
PS00008	277->283	MYRISTYL	PDOC00008
PS00008	279->285	MYRISTYL	PDOC00008
PS00008	361->367	MYRISTYL	PDOC00008
PS00008	476->482	MYRISTYL	PDOC00008
PS00008	509->515	MYRISTYL	PDOC00008
PS00008	574->580	MYRISTYL	PDOC00008
PS00008	590->596	MYRISTYL	PDOC00008
PS00008	640->646	MYRISTYL	PDOC00008
PS00009	122->126	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfbr2_82m6.3)

DKFZphfkd2_1j9
----

group: kidney derived

DKFZphfkd2_1j9.3 encodes a novel 105 amino acid protein with high similarity to Xenopus laevis XLCL2 protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

strong similarity to XLCL2 protein, African clawed frog

complete cDNA, complete cds, EST hits

Sequenced by LMU

Locus: unknown

Insert length: 2955 bp
Poly A stretch at pos. 2935, polyadenylation signal at pos. 2915

```
   1 GGGGGGGGCT GAGTGCTCAG TGGAGAGCGG GGAGTTGTGT CCACCTTGCC
  51 GACGTCGCTA GCCGTGGGGC TGTCCTGGGA AGGCGGACGG CGAGCGCCCG
 101 GTGTCCGCAC TCGGCCGCCT GCCGTGCCCG TCTGCGCCCG TGTCATCCTC
 151 ACTCGGGACG CAGGGACCGT TTTTAAATCA CAGGGGCGTG TGTCAGCCTG
 201 CCCTAGGACT TCATGTCTAT ATATTTCCCC ATTCACTGCC CCGACTATCT
 251 GAGATCGGCC AAGATGACTG AGGTGATGAT GAACACCCAG CCCATGGAGG
 301 AGATCGGCCT CAGCCCCCGC AAGGATGGCC TTTCCTACCA GATCTTCCCA
 351 GACCCGTCAG ATTTTGACCG CCGCTGCAAA CTGAAGGACC GTCTGCCCTC
 401 CATAGTGGTG GAACCCACAG AAGGGGAGGT GGAGAGCGGG GAGCTCCGGT
 451 GGCCCCCTGA GGAGTTCCTG GTCCAGGAGG ATGAGCAAGA TAACTGCGAA
 501 GAGACAGCGA AAGAAAATAA AGAGCAGTAG AGTCCCTGTG GACTCCCATG
 551 GGTCATACCA GCCAGCATCT GTTCCTGAAC TGTGTTTTTC CCATCATGAC
 601 GGAAGAAGAG AGTGAGCCGC AATTGTTCTG AAAATGTCAA ACGAGGCTTC
 651 TGTTTTGCAC CTGCAGATCA CCGAGTTGGT TTTCTTTTCT TTTCTTGCCT
 701 TTTTTTTTTT TTTGAAATTT GCCGAGCAGT GGAGCCCTCT GACAATTTGC
 751 AAGGCCCTCT GAGAAAGGAA GCTGCTTAGA GCCAGGGGGT TAGTGGGTGA
 801 GGGGAGCGAG TGCTGTTTTT GAGATCATTA TCTGAACTCA GGCAGCCTAG
 851 TAGAGGCAGT GGTGGGATTC CAATGGGTCT TGGTGGGTGG GAGGTGGGGC
 901 ATGTGCAAAG CAAGCAAGGA ACATTTGGGG TAAGAAAACA AACATGAGGC
 951 AAAAGAAAAA ATACATGTTT TTAAGAAAAC ATTGAGCAGA GAACTGCAGC
1001 CAGGATGCGC TCAGCAGACA TTCACTCTGG CCGCTGGGAC ATCAGAAAAC
1051 AAAGTCTTCA TCTCTCTCTC CAGTTTCACC CACCCCACCC TTTGCTTTCA
1101 TTTCAGGTGT GTTGGTCTAT ATGACAGGGA GGAGAGTAAA GGAGAGCAGG
1151 AGCAATTGGC TGCCTGCAAA GCCAGCTGGA GGTGAAGTGC AGGAAAGGAA
1201 AGGTCACCCC ATTCTACTCC ATGGCCTCTC TGCTCCCAGC TGTGGTAGGC
1251 TCACATAGCC AGTGTGATCG GTTTTTAAGA GGCAGTGCTT TTCAGCTTTT
1301 CTCCCTGATA TATCCATTTT GCTTCCCAGC ACTTTTTAGG AGTAGTGAGA
1351 GCACTTCCTG CCCTTGTTGG AAGCCCCAGG GTGGACACTC AGCACGAAGG
1401 TCTCTCCCTT AACTGCTGCC CTTCCAAGAC TTGCTCCCGA GATGGAGTGG
1451 GCGTGGTCTT CCAGGCTGGC CCTTCCTTCT CCTCACCGCC ACCTTCCCTG
1501 CCCCAGCCCC AGCAGCCATG GGTACATGGG TCCCCAGCTC ACCTATGGAT
1551 TCCCGCCAGT CTGCCCAGCT GCAGTACTCA CGCCCCATGG GGGATCTTGG
1601 TCTGTTTTTC TTGTGGGAGC CTAGTGGAGA GCAGACGTGG CTTTTTATGT
1651 GTCTTGTTGG GGAGGTGACT TGCATGGTGG GGACAAGGCT GTCGTGGCAA
1701 CCTTGGGATC GAGTTTGAGA CTAAAGGATG TCATGAGATC CCTGGCTTCT
1751 CCCCATGTTG TTCCCGGACA AGGGCAGAAG GGAGGCATGG CAAGGGACCT
1801 CTGCTGTCCT TACTCAACAG TGGTCCTCAT CCCTCCCCAC CTCCCACTGC
1851 TTCCTGCAAG GGCACCAGTT GTATGAGAAA GTTGGCCTTT GGACTTAGGA
1901 TTTCTTATTG TAGCTAAGAG CCATCTGAAG CAGCAGGTTG CAGGACAAAT
1951 GCTTCAGTCC GCCGAGAGCA GTACCGTGTG GCCAAGAGGT GGACTCAGAG
2001 CCTTCCTTGA GCTAAACTCG GCCAACCAAG GCACGCAGCA TGTCCCCTCA
2051 GGTCTCCAGT CAGTCCAGGT TGACCCTCAG TTCTGGACGT GTGTATATAG
2101 CTGTATTTAA TACCTCAAGG TCATTGTGGC TCTGGGGATG CCAGGGCAGG
2151 AGGACGAGGG TGCGCTGTGG ACACAGCAGT CCGCGGAATT CCGTTCTGGG
2201 AAGCCAATGG TCGCCGGCAC CCCTTGCTTC CTCCCTCTGT TGTCTGCCTG
2251 TGTGACACAC ATCAATGGCA ATAACTTCTT CCAACTCCTC GCAGAAGTGG
2301 GAGAGGCCGG CAGCCTGCAC CGAGAGGGGC TTTCCTCTCT CTTGCTCCCC
2351 GCTTCGTTCT GTTTTGGCTG CAGAGAGTGG TTCATCCATA CTCTCATTCC
2401 CTCGCCTCCC CTTGTGGACG GGGGTCTTGC CTTTTCAATT CCTGTGTTTT
2451 GGTGTCTTCC CTTATCTGCT ACCCTGAATC ACCTGTCCTG GTCTTGCTGT
2501 GTGATGGGAA CATGCTTGTA AACTGCGTAA CAAATCTACT TTGTGTATGT
2551 GTCTGTTTAT GGGGGTGGTT TATTATTTTT GCTGGTCCCT AGACCACTTT
2601 GTATGACCGT TTGCAGTCTG AGCAGGCCAG GGGCTGACAG CTAATGTCAG
2651 GACCCTCAGC GGTGGAGCCT GCTGGGGGGA CCCAGCTGCT CTTGGACAAG
```

```
2701 TGGCTGAGCT CCTATCTGGC CTCCTCTTTT TTTTTTTTTT CAAGTAATTT
2751 GTGTGTATTT CTAACTGATT GTATTGAAAA AATTCCTAGT ATTTCAGTAA
2801 AAATGCCTGT TGTGAGATGA ACCTCCTGTA ACTTCTATCT GTTCTTTTTT
2851 GAGGCTCAGG GAGAAACTAG CATTTTTTTT TTTCCAAACT ACTTTTTGTC
2901 ACTGTGACAG TTGTAAATAA AGTTTGAAAA TGCTCAAAAA AAAAAAAAAA
2951 AAAAC
```

BLAST Results

Entry HSG19750 from database EMBL:
human STS A001X24.
Score = 1050, P = 1.9e-39, identities = 212/213

Entry HSG20267 from database EMBL:
human STS A005C12.
Score = 610, P = 4.1e-19, identities = 122/122

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 213 bp to 527 bp; peptide length: 105
Category: strong similarity to known protein
Classification: unset

```
  1 MSIYFPIHCP DYLRSAKMTE VMMNTQPMEE IGLSPRKDGL SYQIFPDPSD
 51 FDRRCKLKDR LPSIVVEPTE GEVESGELRW PPEEFLVQED EQDNCEETAK
101 ENKEQ
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_1j9, frame 3

PIR:S52241 XLCL2 protein - African clawed frog, N = 1, Score = 443, P = 8e-42

PIR:S52241 XLCL2 protein - African clawed frog, N = 1, Score = 443, P = 8.2e-42

>PIR:S52241 XLCL2 protein - African clawed frog
Length = 102

HSPs:

Score = 443 (66.5 bits), Expect = 8.0e-42, P = 8.0e-42
Identities = 80/104 (76%), Positives = 95/104 (91%)

```
Query:    1 MSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSYQIFPDPSDFDRRCKLKDR 60
            MS+++PIHC DYLRSA+MTEV+MNTQ M+EIGLSPRKD  SYQIFPDPSDF+R CKLKDR
Sbjct:    1 MSVFYPIHCTDYLRSAEMTEVIMNTQSMDEIGLSPRKD--SYQIFPDPSDFERCCKLKDR 58

Query:   61 LPSIVVEPTEGEVESGELRWPPEEFLVQEDEQDNCEETAKENKE 104
            LPSIVVEPTEG+VESGELRWPPEEF+V ED++  C++T KEN++
Sbjct:   59 LPSIVVEPTEGDVESGELRWPPEEFVVDEDKEGTCDQTKKENEQ 102
```

Pedant information for DKFZphfkd2_1j9, frame 3

Report for DKFZphfkd2_1j9.3

[LENGTH]	105
[MW]	12269.78
[pI]	4.40
[HOMOL]	PIR:S52241 XLCL2 protein - African clawed frog 5e-44

```
[KW]          Alpha_Beta

SEQ     MSIYFPIHCPDYLRSAKMTEVMMNTQPMEEIGLSPRKDGLSYQIFPDPSDFDRRCKLKDR
PRD     cccccccccccchhhhhhhhhhhhcccccccccccccccceeeecccccccccchhhhhhc

SEQ     LPSIVVEPTEGEVESGELRWPPEEFLVQEDEQDNCEETAKENKEQ
PRD     ccceeeeccccccccccccccccccceeeccccchhhhhhhhhccc
```

(No Prosite data available for DKFZphfkd2_1j9.3)

(No Pfam data available for DKFZphfkd2_1j9.3)

DKFZphfkd2_24a15
----

group: transmembrane protein

DKFZphfkd2_24a15 encodes a novel amino acid protein with similarity to C. elegans cosmid R07G3.

The novel protein contains 1 transmembrane region.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker for kidney cells.

similarity to C. elegans R07G3.8
membrane regions: 1
Summary DKFZphfkd2_24a15 encodes a novel 323 amino acid protein, with similarity to C. elegans R07G3.8.

similarity to C. elegans R07G3.8

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1513 bp
Poly A stretch at pos. 1494, no polyadenylation signal found

```
   1 GGGGTACTCG GCGGCGGCGG AGCGGGCGGC AGAGCAGGGC GGCGGCGACT
  51 CGCAGGGTAC CACCATCTTA AGGACAGAAA AGCTACAGGA CTCTAGGAGG
 101 CCACCGTCCT GATTTGGGAA GTCCAACTTA CTTTGGCCAG ACAGCAGCTA
 151 AGCTGGTTCA TCCCATCAGC CTGGATTGGT GAAACTGAAT CACAGGAGAT
 201 ATTTCCAGGT TTGCTGGGAT GGGAAACCTG CTCAAAGTCC TTACCAGGGA
 251 AATTGAAAAC TATCCACACT TTTTCCTGGA TTTTGAAAAT GCTCAGCCTA
 301 CAGAAGGAGA GAGAGAAATC TGGAACCAGA TCAGCGCCGT CCTTCAGGAT
 351 TCTGAGAGCA TCCTTGCAGA CCTGCAGGCT TACAAAGGCG CAGGCCCAGA
 401 GATCCGAGAT GCAATTCAAA ATCCCAATGA CATTCAGCTT CAAGAAAAAG
 451 CTTGGAATGC GGTGTGCCCT CTTGTTGTGA GGCTAAAGAG ATTTTACGAG
 501 TTTTCCATTA GACTAGAAAA AGCTCTTCAG AGTTTATTGG AATCTCTGAC
 551 TTGTCCACCC TACACACCAA CCCAACACCT GGAAAGGGAA CAGGCCCTGG
 601 CAAAGGAGTT TGCCGAAATT TTACATTTTA CCCTTCGATT CGATGAGCTG
 651 AAGATGAGGA ACCCGGCTAT TCAGAATGAC TTCAGCTACT ACAGAAGAAC
 701 AATCAGTCGC AACCGCATCA ACAACATGCA CCTAGACATT GAGAATGAAG
 751 TCAATAATGA GATGGCCAAT CGAATGTCCC TCTTCTATGC AGAAGCCACG
 801 CCAATGCTGA AAACCCTTAG CAATGCCACA ATGCACTTTG TCTCTGAAAA
 851 CAAAACTCTG CCAATAGAGA ACACCACAGA CTGCCTCAGC ACAATGACAA
 901 GTGTCTGTAA AGTCATGCTG GAAACTCCGG AGTACAGAAG TAGGTTTACG
 951 AGTGAAGAGA CCCTGATGTT CTGCATGAGG GTGATGGTGG GAGTCATCAT
1001 CCTCTATGAC CATGTCCACC CTGTGGGAGC TTTCTGCAAG ACATCCAAGA
1051 TCGATATGAA AGGCTGCATA AAAGTTTTGA AGGAGCAGGC CCCAGACAGT
1101 GTGGAGGGGC TGCTAAATGC CCTCAGGTTC ACTACAAAGC ACTTGAACGA
1151 TGAATCAACT TCCAAACAGA TTCGAGCAAT GCTTCAGTAG AGCTCTGCTC
1201 AAAGAAGAGG ATCTATGTGC TGACCTCAGA AGATGTATAT GTTTACATAA
1251 TTTAATACAG ATTGATGTTA ATACTTGTGT ATTTACATAA CCGTTTCCTT
1301 CTTGTCACTG AAATATATGG ACCTTAATTT GTATCCTGAC TGACTCAACC
1351 CAGCAGAGCA TAAATTGACT TGAGAGCCTT ACCTTTGATG TCTGAAATGA
1401 AACCCCCTTC TCCAAAGGCA AAATTCGGAG ACTTTGATCT TTGCTACTGG
1451 AGTCCTTTAA CAACATCTAT AACGATAAAA AATTCCTAAT TGTCAAAAAA
1501 AAAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

```
ORF from 219 bp to 1187 bp; peptide length: 323
Category: similarity to unknown protein


  1 MGNLLKVLTR EIENYPHFFL DFENAQPTEG EREIWNQISA VLQDSESILA
 51 DLQAYKGAGP EIRDAIQNPN DIQLQEKAWN AVCPLVVRLK RFYEFSIRLE
101 KALQSLLESL TCPPYTPTQH LEREQALAKE FAEILHFTLR FDELKMRNPA
151 IQNDFSYYRR TISRNRINNM HLDIENEVNN EMANRMSLFY AEATPMLKTL
201 SNATMHFVSE NKTLPIENTT DCLSTMTSVC KVMLETPEYR SRFTSEETLM
251 FCMRVMVGVI ILYDHVHPVG AFCKTSKIDM KGCIKVLKEQ APDSVEGLLN
301 ALRFTTKHLN DESTSKQIRA MLQ
```

BLASTP hits

```
Entry CER07G3_7 from database TREMBL:
gene: "R07G3.8"; Caenorhabditis elegans cosmid R07G3.
Score = 544, P = 1.4e-52, identities = 119/323, positives = 186/323
```

Alert BLASTP hits for DKFZphfkd2_24a15, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_24a15, frame 3

Report for DKFZphfkd2_24a15.3

```
[LENGTH]      323
[MW]          37313.06
[pI]          5.71
[HOMOL]       TREMBL:CER07G3_7 gene: "R07G3.8"; Caenorhabditis elegans cosmid R07G3. 4e-54

[PROSITE]     MYRISTYL       1
[PROSITE]     CK2_PHOSPHO_SITE     4
[PROSITE]     TYR_PHOSPHO_SITE     1
[PROSITE]     PKC_PHOSPHO_SITE     5
[PROSITE]     ASN_GLYCOSYLATION    3
[KW]          TRANSMEMBRANE  1

SEQ  MGNLLKVLTREIENYPHFFLDFENAQPTEGEREIWNQISAVLQDSESILADLQAYKGAGP
PRD  cccccchhhhhhhcccceeecccccccchhhhhhhhhhhhhhcchhhhhhhhhhhccccc
MEM  ............................................................

SEQ  EIRDAIQNPNDIQLQEKAWNAVCPLVVRLKRFYEFSIRLEKALQSLLESLTCPPYTPTQH
PRD  hhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhh
MEM  ............................................................

SEQ  LEREQALAKEFAEILHFTLRFDELKMRNPAIQNDFSYYRRTISRNRINNMHLDIENEVNN
PRD  hhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccchhhhhhcchhhhhhhhhhhhhhhhh
MEM  ............................................................

SEQ  EMANRMSLFYAEATPMLKTLSNATMHFVSENKTLPIENTTDCLSTMTSVCKVMLETPEYR
PRD  hhhhhhhhhhhhcchhhhhhhhceeecccccccccccccceeeeehhhhhhhhcccccc
MEM  ............................................................

SEQ  SRFTSEETLMFCMRVMVGVIILYDHVHPVGAFCKTSKIDMKGCIKVLKEQAPDSVEGLLN
PRD  ccccchhhhhhhhhhhhheeeeeeeccccccccccccccccchhhhhhhhhcccccchhhhhh
MEM  .........MMMMMMMMMMMMMMMMMMMM...............................

SEQ  ALRFTTKHLNDESTSKQIRAMLQ
PRD  hhhhhhccccccccchhhhhhccc
MEM  .......................
```

Prosite for DKFZphfkd2_24a15.3

PS00001	202->206	ASN_GLYCOSYLATION	PDOC00001
PS00001	211->215	ASN_GLYCOSYLATION	PDOC00001
PS00001	218->222	ASN_GLYCOSYLATION	PDOC00001
PS00005	96->99	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	275->278	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005

PS00005	314->317	PKC_PHOSPHO_SITE	PDOC00005
PS00006	28->32	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	276->280	CK2_PHOSPHO_SITE	PDOC00006
PS00007	231->240	TYR_PHOSPHO_SITE	PDOC00007
PS00008	297->303	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfkd2_24a15.3)

DKFZphfkd2_24b15
----

group: metabolism

DKFZphfkd2_24b15 encodes a novel 612 amino acid protein with similarity to bacterial and yeast phosphoglucomutase and phosphomannomutases.

The novel protein contains a phosphoserine signature typical for phosphoglucomutase (EC 5.4.2.2) or phosphomannomutase (EC 5.4.2.8). Thus, the protein seems to be taking part in the conversion of hexose phosphates.

The new protein can find application in modulation of hexose metabolism pathways and as a new enzyme for biotechnologic production processes.

similarity to phosphomannomutases

complete cDNA, complete cds, EST hits
potential start at bp 30 matches kozak consensus PyCNatgG,

Sequenced by GBF

Locus: map="158.8 cR from top of Chr4 linkage group"

Insert length: 2204 bp
Poly A stretch at pos. 2186, no polyadenylation signal found

```
   1 GGGCTCTGCA GCGGTAGCAC AAGCTCAGCG ATGGCGGCTC CAGAAGGCAG
  51 CGGTCTAGGC GAGGACGCCC GGCTGGACCA GGAGACCGCC CAGTGGCTGC
 101 GCTGGGACAA GAATTCCTTA ACTTTGGAGG CAGTGAAACG ACTAATAGCA
 151 GAAGGTAATA AAGAAGAACT ACGAAAATGT TTTGGGGCCC GAATGGAGTT
 201 TGGGACAGCT GGCCTCCGAG CTGCTATGGG ACCTGGAATT TCTCGTATGA
 251 ATGACTTGAC CATCATCCAG ACTACACAGG GATTTTGCAG ATACCTGGAA
 301 AAACAATTCA GTGACTTAAA GCAGAAAGGC ATCGTGATCA GTTTTGACGC
 351 CCGAGCTCAT CCATCCAGTG GGGGTAGCAG CAGAAGGTTT GCCCGACTTG
 401 CTGCAACCAC ATTTATCAGT CAGGGGATTC CTGTGTACCT CTTTTCTGAT
 451 ATAACGCCAA CCCCCTTTGT GCCCTTCACA GTATCACATT TGAAACTTTG
 501 TGCTGGAATC ATGATAACTG CATCTCACAA TCCAAAGCAG GATAATGGTT
 551 ATAAGGTCTA TTGGGATAAT GGAGCTCAGA TCATTTCTCC TCACGATAAA
 601 GGGATTTCTC AAGCTATTGA AGAAAATCTA GAACCGTGGC CTCAAGCTTG
 651 GGACGATTCT TTAATTGATA GCAGTCCACT TCTCCACAAT CCGAGTGCTT
 701 CCATCAATAA TGACTACTTT GAAGACCTTA AAAAGTACTG TTTCCACAGG
 751 AGCGTGAACA GGGAGACAAA GGTGAAGTTT GTGCACACCT CTGTCCATGG
 801 GGTGGGTCAT AGCTTTGTGC AGTCAGCTTT CAAGGCTTTT GACCTTGTTC
 851 CTCCTGAGGC TGTTCCTGAA CAGAGAGATC CGGATCCTGA GTTTCCAACA
 901 GTGAAATACC CGAATCCCGA AGAGGGGAAA GGTGTCTTGA CTTTGTCTTT
 951 TGCTTTGGCT GACAAAACCA AGGCCAGAAT TGTTTTAGCT AACGACCCGG
1001 ATGCTGATAG ACTTGCTGTG GCAGAAAAGC AAGACAGTGG TGAATGGAGG
1051 GTGTTTTCAG GCAATGAGTT GGGGGCCCTC CTGGGCTGGT GGCTTTTTAC
1101 ATCTTGGAAA GAGAAGAACC AGGATCGCAG TGCTCTCAAA GACACGTACA
1151 TGTTGTCCAG CACCGTCTCC TCCAAAATCT TGCGGGCCAT TGCCTTAAAG
1201 GAAGGTTTTC ATTTTGAGGA AACATTAACT GGCTTTAAGT GGATGGGAAA
1251 CAGAGCCAAA CAGCTAATAG ACCAGGGGAA AACTGTTTTA TTTGCATTTG
1301 AAGAAGCTAT TGGATACATG TGCTGCCCTT TTGTTCTGGA CAAAGATGGA
1351 GTCAGTGCCG CTGTCATAAG TGCAGAGTTG GCTAGCTTCC TAGCAACCAA
1401 GAATTTGTCT TTGTCTCAGC AACTAAAGGC CATTTATGTG GAGTATGGCT
1451 ACCATATTAC TAAAGCTTCC TATTTTATCT GCCATGATCA AGAAACCATT
1501 AAGAAATTAT TTGAAAACCT CAGAAACTAC GATGGAAAAA ATAATTATCC
1551 AAAAGCTTGT GGCAAATTTG AAATTTCTGC CATTAGGGAC CTTACAACTG
1601 GCTATGATGA TAGCCAACCT GATAAAAAAG CTGTTCTTCC CACTAGTAAA
1651 AGCAGCCAAA TGATCACCTT CACCTTTGCT AATGGAGGCG TGGCCACCAT
1701 GCGCACCAGT GGGACAGAGC CCAAAATCAA GTACTATGCA GAGCTGTGTG
1751 CCCCACCTGG GAACAGTGAT CCTGAGCAGC TGAAGAAGGA ACTGAATGAA
1801 CTGGTCAGTG CTATTGAAGA ACATTTTTTC CAGCCACAGA AGTACAATCT
1851 GCAGCCAAAA GCAGACTAAA ATAGTCCAGC CTTGGGTATA CTTGCATTTA
1901 CCTACAATTA AGCTGGGTTT AACTTGTTAA GCAATATTTT TAAGGGCCAA
1951 ATGATTCAAA ACATCACAGG TATTTATGTG TTTTACAAAG ACCTACATTC
2001 CTCATTGTTT CATGTTTGAC CTTTAAGGTG AAAAAAGAAA ATGGCCAAAC
2051 CCAACAAACT AACATTCCTA CTAAAAAGTT GAGCTTGGAC ATATTTTGAA
2101 TTTTTGTAAG TGAAGATTTT TAAACTGACT AACTTAAAAA AATAGATTGT
2151 AATTGATGTG CCTTAATTTG CATAAATCAT AAATGTAAAA AAAAAAAAAA
2201 AAAA
```

BLAST Results

Entry HS705145 from database EMBL:

human STS WI-6820.
Score = 1261, P = 3.6e-52, identities = 253/254

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 31 bp to 1866 bp; peptide length: 612
Category: strong similarity to known protein

```
  1 MAAPEGSGLG EDARLDQETA QWLRWDKNSL TLEAVKRLIA EGNKEELRKC
 51 FGARMEFGTA GLRAAMGPGI SRMNDLTIIQ TTQGFCRYLE KQFSDLKQKG
101 IVISFDARAH PSSGGSSRRF ARLAATTFIS QGIPVYLFSD ITPTPFVPFT
151 VSHLKLCAGI MITASHNPKQ DNGYKVYWDN GAQIISPHDK GISQAIEENL
201 EPWPQAWDDS LIDSSPLLHN PSASINNDYF EDLKKYCFHR SVNRETKVKF
251 VHTSVHGVGH SFVQSAFKAF DLVPPEAVPE QRDPDPEFPT VKYPNPEEGK
301 GVLTLSFALA DKTKARIVLA NDPDADRLAV AEKQDSGEWR VFSGNELGAL
351 LGWWLFTSWK EKNQDRSALK DTYMLSSTVS SKILRAIALK EGFHFEETLT
401 GFKWMGNRAK QLIDQGKTVL FAFEEAIGYM CCPFVLDKDG VSAAVISAEL
451 ASFLATKNLS LSQQLKAIYV EYGYHITKAS YFICHDQETI KKLFENLRNY
501 DGKNNYPKAC GKFEISAIRD LTTGYDDSQP DKKAVLPTSK SSQMITFTFA
551 NGGVATMRTS GTEPKIKYYA ELCAPPGNSD PEQLKKELNE LVSAIEEHFF
601 QPQKYNLQPK AD
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24b15, frame 1

TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B, N = 1, Score = 1431, P = 1.6e-146

TREMBL:SPCC1840_5 gene: "SPCC1840.05c"; product: "similarity to phosphomannomutases"; S.pombe chromosome III cosmid c1840., N = 1, Score = 1210, P = 4.2e-123

PIR:S54585 hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae), N = 1, Score = 1046, P = 1e-105

PIR:A71299 probable phosphomannomutase (manB) - syphilis spirochete, N = 1, Score = 697, P = 9.7e-69

>TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B
Length = 595

HSPs:

Score = 1431 (214.7 bits), Expect = 1.6e-146, P = 1.6e-146
Identities = 285/598 (47%), Positives = 393/598 (65%)

```
Query:   13 ARLDQETAQWLRWDKNSLTLEAVKRLIAEGNKEELRKCFGARMEFGTAGLRAAMGPGISR 72
            A+LD++ A WL WDKN       +++L+ E N + L+     R+ FGTAG+R+ M  G  R
Sbjct:    6 AKLDKQVADWLAWDKNDKNRNEIQKLVDEKNVDALKARMDTRLVFGTAGVRSPMQAGFGR 65

Query:   73 MNDLTIIQTTQGFCRYLEKQFSDLKQKGIVISFDARAHPSSGGSSRRFARLAATTFISQG 132
            +NDLTIIQ T GF R++    +   K  G+ I FD R +       SRRFA L+A  F+
Sbjct:   66 LNDLTIIQITHGFARHMLNVYGQPKN-GVAIGFDGRYN------SRRFAELSANVFVRNN 118

Query:  133 IPVYLFSDITPTPFVPFTVSHLKLCAGIMITASHNPKQDNGYKVYWDNGAQIISPHDKGI 192
            IPVYLFS+++PTP V +     L    AG++ITASHNPK+DNGYK YW NGAQII PHD  I
Sbjct:  119 IPVYLFSEVSPTPVVSWATIKLGCDAGLIITASHNPKEDNGYKAYWSNGAQIIGPHDTEI 178

Query:  193 SQAIEENLEPWPQAWDDSLIDSSPLLHNPSASINNDYFEDLKKYCFHRSVNRETKVKFVH 252
             +  E   +P  + WD S + SSPL H+     I+  YFE  K   F R +N  T +KF +
Sbjct:  179 VRIKEAEPQPRDEYWDLSELKSSPLFHSADVVID-PYFEVEKSLNFTREINGSTPLKFTY 237

Query:  253 TSVHGVGHSFVQSAFKAFDLVPPE--AVPEQRDPDPEFPTVKYPNPEEGKGVLTLSFALA 310
            ++ HG+G+ + +  F  F        +V EQ+DP+P+FPT+ +PNPEEG+ VLTL+  A
Sbjct:  238 SAFHGIGYHYTKRMFAEFGFPASSFISVAEQQDPNPDFPTIPFPNPEEGRKVLTLAMETA 297
```

```
Query:  311 DKTKARIVLANDPDADRLAVAEKQDSGEWRVFSGNELGALLGWWLFTSWKEKNQDRSALK 370
            DK  +  ++LANDPDADR+ +AEKQ  GEWRVF+GNE+GAL+ WW++T+W++ N +  A K
Sbjct:  298 DKNGSTVILANDPDADRIQMAEKQKDGEWRVFTGNEMGALITWWIWTNWRKANPNADASK 357

Query:  371 DTYMLSSTVSSKILRAIALKEGFHFEETLTGFKWMGNRAKQLIDQGKTVLFAFEEAIGYM 430
             Y+L+S VSS+I++ IA  EGF  E TLTGFKWMGNRA++L   G  V+ A+EE+IGYM
Sbjct:  358 -VYILNSAVSSQIVKTIADAEGFKNETTLTGFKWMGNRAEELRADGNQVILAWEESIGYM 416

Query:  431 CCP-FVLDKDGVSAAVISAELASFLATKNLSLSQQLKAIYVEYGYHITKASYFICHDQET 489
              P   +DKDGVSAA + AE+A+FL   +  SL  QL A+Y  YG+H+ +++Y++     E
Sbjct:  417 --PGHTMDKDGVSAAAVFAEIAAFLHAEGKSLQDQLYALYNRYGFHLVRSTYWMVPAPEV 474

Query:  490 IKKLFENLRNYDGKNNYPKACGKFEISAIRDLTTGYDDSQPDKKAVLPTSKSSQMITFTF 549
            KKLF  LR  D K  +P   G+ E++++RDLT GYD+S+PD K VLP S SS+M+TF
Sbjct:  475 TKKLFSTLRA-DLK--FPTKIGEAEVASVRDLTIGYDNSKPDNKPVLPLSTSSEMVTFFL 531

Query:  550 ANGGVATMRTSGTEPKIKYYAELCAPPGNS--DPEQLKKELNELVSAIEEHFFQPQKYNL 607
             G V T+R SGTEPKIKYY EL   PG +  D E +  E+++L   +    +PQ++ L
Sbjct:  532 KTGSVTTLRASGTEPKIKYYIELITAPGKTQNDLESVISEMDQLEKDVVATLLRPQQFGL 591

Query:  608 QPK 610
             P+
Sbjct:  592 IPR 594
```

Pedant information for DKFZphfkd2_24b15, frame 1

Report for DKFZphfkd2_24b15.1

[LENGTH]	612
[MW]	68311.58
[pI]	6.28
[HOMOL]	TREMBL:CEY43F4B_5 gene: "Y43F4B.5"; Caenorhabditis elegans cosmid Y43F4B 1e-157
[FUNCAT]	01.05.01 carbohydrate utilization [S. cerevisiae, YMR278w] 1e-111
[FUNCAT]	g carbohydrate metabolism and transport [H. influenzae, HI0740] 3e-66
[FUNCAT]	c energy conversion [M. genitalium, MG053] 4e-50
[FUNCAT]	m outer membrane and cell wall [H. influenzae, HI1463] 2e-04
[BLOCKS]	BL00607D cAMP phosphodiesterases class-II proteins
[BLOCKS]	BL00710 Phosphoglucomutase and phosphomannomutase phosphoserine signa
[EC]	5.4.2.8 Phosphomannomutase 3e-56
[EC]	5.4.2.2 Phosphoglucomutase 1e-09
[PIRKW]	isomerase 3e-56
[PIRKW]	intramolecular transferase 3e-56
[SUPFAM]	Methanobacterium thermoautotrophicum phosphomannomutase 1e-06
[SUPFAM]	probable phosphorylating protein ureC 9e-06
[PROSITE]	PGM_PMM 1
[PROSITE]	MYRISTYL 10
[PROSITE]	LIPOCALIN 2
[PROSITE]	CK2_PHOSPHO_SITE 9
[PROSITE]	GLYCOSAMINOGLYCAN 1
[PROSITE]	PKC_PHOSPHO_SITE 8
[PROSITE]	ASN_GLYCOSYLATION 1
[PFAM]	Phosphoglucomutase and phosphomannomutase phosphoserine
[KW]	Alpha_Beta

```
SEQ   MAAPEGSGLGEDARLDQETAQWLRWDKNSLTLEAVKRLIAEGNKEELRKCFGARMEFGTA
PRD   cccccccccchhhhhhhhhhhhhhhcchhhhhhhhhhhhcchhhhhhhhhhhhccccc

SEQ   GLRAAMGPGISRMNDLTIIQTTQGFCRYLEKQFSDLKQKGIVISFDARAHPSSGGSSRRF
PRD   ccccccccccccceeeeeehhhhhhhhhhhccccccceeeeeeccccccccccccchhhh

SEQ   ARLAATTFISQGIPVYLFSDITPTPFVPFTVSHLKLCAGIMITASHNPKQDNGYKVYWDN
PRD   hhhhhhhhhhcccceeeeecccccccccchhhhhhhccccceeeeeecccccccccceeeeecc

SEQ   GAQIISPHDKGISQAIEENLEPWPQAWDDSLIDSSPLLHNPSASINNDYFEDLKKYCFHR
PRD   cccccccccchhhhhhhhhhhhhcccccccccccccccccccchhhhhhhhhhhhhhhcc

SEQ   SVNRETKVKFVHTSVHGVGHSFVQSAFKAFDLVPPEAVPEQRDPDPEFPTVKYPNPEEGK
PRD   cccccccceeeeeeecccccchhhhhhhhhccccccccccccccccccccccccccccchh

SEQ   GVLTLSFALADKTKARIVLANDPDADRLAVAEKQDSGEWRVFSGNELGALLGWWLFTSWK
PRD   hhhhhhhhhhhhcceeeeecccccccceeeeecccccceeeecccchhhhhhhhhhhhhh

SEQ   EKNQDRSALKDTYMLSSTVSSKILRAIALKEGFHFEETLTGFKWMGNRAKQLIDQGKTVL
PRD   hcccccccccceeeeeeeehhhhhhhhhhccccceeeeecccccchhhhhhhhhhccceee
```

```
SEQ    FAFEEAIGYMCCPFVLDKDGVSAAVISAELASFLATKNLSLSQQLKAIYVEYGYHITKAS
PRD    hhhhhcccccccccccccchhhhhhhhhhhhhhhhhhccchhhhhhhhhhhhcccccccc

SEQ    YFICHDQETIKKLFENLRNYDGKNNYPKACGKFEISAIRDLTTGYDDSQPDKKAVLPTSK
PRD    eeeccchhhhhhhhhhhhhhhccccccccchhhhhhhccccccccccccccccccccccc

SEQ    SSQMITFTFANGGVATMRTSGTEPKIKYYAELCAPPGNSDPEQLKKELNELVSAIEEHFF
PRD    ccceeeeeecccceeeeecccccccceeeeeeccccccchhhhhhhhhhhhhhhhhhhhh

SEQ    QPQKYNLQPKAD
PRD    cccccccccccc
```

Prosite for DKFZphfkd2_24b15.1

PS00001	458->462	ASN_GLYCOSYLATION	PDOC00001
PS00002	7->11	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	116->119	PKC_PHOSPHO_SITE	PDOC00005
PS00005	117->120	PKC_PHOSPHO_SITE	PDOC00005
PS00005	290->293	PKC_PHOSPHO_SITE	PDOC00005
PS00005	358->361	PKC_PHOSPHO_SITE	PDOC00005
PS00005	380->383	PKC_PHOSPHO_SITE	PDOC00005
PS00005	489->492	PKC_PHOSPHO_SITE	PDOC00005
PS00005	538->541	PKC_PHOSPHO_SITE	PDOC00005
PS00005	556->559	PKC_PHOSPHO_SITE	PDOC00005
PS00006	186->190	CK2_PHOSPHO_SITE	PDOC00006
PS00006	210->214	CK2_PHOSPHO_SITE	PDOC00006
PS00006	343->347	CK2_PHOSPHO_SITE	PDOC00006
PS00006	358->362	CK2_PHOSPHO_SITE	PDOC00006
PS00006	523->527	CK2_PHOSPHO_SITE	PDOC00006
PS00006	528->532	CK2_PHOSPHO_SITE	PDOC00006
PS00006	560->564	CK2_PHOSPHO_SITE	PDOC00006
PS00006	579->583	CK2_PHOSPHO_SITE	PDOC00006
PS00006	593->597	CK2_PHOSPHO_SITE	PDOC00006
PS00008	6->12	MYRISTYL	PDOC00008
PS00008	61->67	MYRISTYL	PDOC00008
PS00008	100->106	MYRISTYL	PDOC00008
PS00008	159->165	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00008	257->263	MYRISTYL	PDOC00008
PS00008	344->350	MYRISTYL	PDOC00008
PS00008	348->354	MYRISTYL	PDOC00008
PS00008	440->446	MYRISTYL	PDOC00008
PS00008	552->558	MYRISTYL	PDOC00008
PS00710	159->174	PGM_PMM	PDOC00589
PS00213	346->358	LIPOCALIN	PDOC00187
PS00213	344->358	LIPOCALIN	PDOC00187

Pfam for DKFZphfkd2_24b15.1

```
HMM_NAME    Phosphoglucomutase and phosphomannomutase phosphoserine

HMM             *GvnVIdIGQNGMMPTPMIYFaIRTYKhmcmggGIMITaSHNPGGPDnDN
                 G+ V +     ++PTP + F +    H+++ +GIMITASHNP     DN
Query       132  GIPVYLFS--DITPTPFVPFTVS---HLKLCAGIMITASHNP--KQ-DN   172

HMM             GIK*
                G+K
Query       173 GYK    175
```

DKFZphfkd2_24e23
----

group: kidney derived

DKFZphfkd2_24e23 encodes a novel 198 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

unknown

complete cDNA, complete cds, 1 EST hit,
many ATGs in front of the ORF

Sequenced by GBF

Locus: unknown

Insert length: 1723 bp
Poly A stretch at pos. 1695, no polyadenylation signal found

```
   1 GGGGGATTTT CGATCATGAC AACGATAGCA ATTGATATAC CTTCAAAATA
  51 CGTGTCCAGT GAGTGTTGAT TGTGTGTGGT TTCTCTAGGA GACCGTGTTC
 101 ATGCAACACA GCATTATTTC ACCGCCTTTA CCCCAGCTTC TTCATACACA
 151 TGCACTTGTC AAGGGCTCTT TGGCTGAAGA GAAGTTAGAA GTTTCCAGAT
 201 ATGGAGGGGT ATTTTCAGCA GATATGCCCA CCGCCATGGT TTTGTCAGCT
 251 CTGTAGGGTG GTCTTGCACC CTGCTCACTG CTGGCATCAC CTGAGCCTAT
 301 GGCAGATACC CAGTGCTGCC CGCCACCATG TGAATTCATC AGCTCTGCAG
 351 GCACAGACCT TGCACTAGGA ATGGGCTGGG ACGCCACCCT CTGCCTCTTA
 401 CCATTCACTG GGTTTGGCAA GTGTGCTGGG ATCTGGAATC ACATGGATGA
 451 GGAACCCGAT AATGGTGACG ACCGAGGTAG CAGGCGAACC ACTGGCCAGG
 501 GCAGGAAGTG GGCAGCTCAC GGGACTATGG CTGCACCGCG GGTTCATACC
 551 GACTACCATC CTGGAGGTGG GAGCGCATGC TCATCTGTAA AAGTCCGGTC
 601 CCACGTTGGA CACACCGGGG TCTTCTTCTT TGTTGACCAG GATCCTCTGG
 651 CAGTGTCTTT AACAAGCCAG AGTCTGATCC CACCGCTCAT AAAGCCAGGG
 701 TTGTTGAAAG CTTGGGGCTT CCTCCTCCTC TGTGCGCAGC CCTCAGCAAA
 751 CGGTCACAGC CTGTGCTGTC TGCTGTACAC CGACTTGGTA TCATCCCATG
 801 AACTGTCCCC CTTTCGTGCT CTGTGCTTAG GGCCCTCTGA TGCCCCATCT
 851 GCCTGCGCTT CCTGCAACTG TTTAGCAAGC ACCTATTATC TATAGGGTGC
 901 TGGGGTGCTG GGCGAGGCCA ATCGCTCCTA TTACTTTCTG CCCTGGGGAC
 951 GTCCTGTTTT CCCACCTACC CCTGTAACGC CTCTGCTCTG CCTTCCCATC
1001 TGCGGGGCTA ACGCCATCCC ACAAGGGCTG GGCTGTCCGT TCAGAAGAGA
1051 AACTGGGAAG GGGCCTTGAG GACCTGTGTC CAGGCAGGGT GGACAAGGGC
1101 TTTGTGCAGG GAGCTCCTCT CCCATCTTTG TGTCCTGACA GCCGTGACCG
1151 TGACCCCTCA AAGCAGAGCC AGTAGTGATC AGTATCCTGC TGCTTCAAGC
1201 CTGCACGGTC CTCTTCTCCT CTCCGCACAT CTGCATGCCT GTCAAACCCA
1251 GAGTAGTTTG GGGCCTGGTA AACAGAGGGA AGTTGGCTGG AGGAGGCCAG
1301 TCAGGAGTGC AAGAACCCCG CGTACTCTGT CCCACGTGGA TAAAGTCTCT
1351 AATTCCAGTC TGAGGTGAAT TCTTAGAGAG TGCTTTCATT TAATGTTTGC
1401 TTTATGCATT TCCCCTGCAG CTGTGACTAA TTGTGGAACA GCATACATTT
1451 TGTTTTGAGA CTCTCTTGAG ATTTTTCTGG CAGTGTAAGG TCTACACCAT
1501 TTTCCTCTCA GCATCAGAGA AGGCAGAAAG CAAGAGAAAG GAATGCAATG
1551 TGAGCAAGGC CAGGCACACT TGTGCTACTG CAGTTGGCAA GAATGGAGTC
1601 TAATCCCAGC ACTTTGGGAG GCCGAGGCGG GTGGATCACC TGAGGTCAGG
1651 AATTTGAGAC CAACCTGGCC AACATGTTGA AACCTCGTCT GTACTAAAAA
1701 TACAAAAAAA AAAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

```
ORF from 299 bp to 892 bp; peptide length: 198
Category: putative protein


    1 MADTQCCPPP CEFISSAGTD LALGMGWDAT LCLLPFTGFG KCAGIWNHMD
   51 EEPDNGDDRG SRRTTGQGRK WAAHGTMAAP RVHTDYHPGG GSACSSVKVR
  101 SHVGHTGVFF FVDQDPLAVS LTSQSLIPPL IKPGLLKAWG FLLLCAQPSA
  151 NGHSLCCLLY TDLVSSHELS PFRALCLGPS DAPSACASCN CLASTYYL

                              BLASTP hits

No BLASTP hits available

           Alert BLASTP hits for DKFZphfkd2_24e23, frame 2

No Alert BLASTP hits found

           Pedant information for DKFZphfkd2_24e23, frame 2
           ------------------------------------------------

                   Report for DKFZphfkd2_24e23.2


[LENGTH]       198
[MW]           20948.98
[pI]           6.01
[PROSITE]      MYRISTYL        5
[PROSITE]      AMIDATION       1
[PROSITE]      CAMP_PHOSPHO_SITE      1
[PROSITE]      CK2_PHOSPHO_SITE       1
[PROSITE]      PKC_PHOSPHO_SITE       2
[KW]           All_Beta
[KW]           LOW_COMPLEXITY      6.06 %

SEQ     MADTQCCPPPCEFISSAGTDLALGMGWDATLCLLPFTGFGKCAGIWNHMDEEPDNGDDRG
SEG     ............................................................
PRD     cccccccccccccccccccccccccccccceeeeeccccccceeeecccccccccccccc

SEQ     SRRTTGQGRKWAAHGTMAAPRVHTDYHPGGGSACSSVKVRSHVGHTGVFFFVDQDPLAVS
SEG     ............................................................
PRD     cccccccccccccccccccceeeeecccccccccceeeeeeeccccceeeeeccccceee

SEQ     LTSQSLIPPLIKPGLLKAWGFLLLCAQPSANGHSLCCLLYTDLVSSHELSPFRALCLGPS
SEG     .....xxxxxxxxxxxx...........................................
PRD     ecccccccccccchhhhhhhhhhccccccccceeeeeeeeeccccccccccceeeecccc

SEQ     DAPSACASCNCLASTYYL
SEG     ..................
PRD     cccccccccccccccccc


                   Prosite for DKFZphfkd2_24e23.2

PS00004        62->66    CAMP_PHOSPHO_SITE      PDOC00004
PS00005        61->64    PKC_PHOSPHO_SITE       PDOC00005
PS00005        96->99    PKC_PHOSPHO_SITE       PDOC00005
PS00006       165->169   CK2_PHOSPHO_SITE       PDOC00006
PS00008        18->24    MYRISTYL               PDOC00008
PS00008        60->66    MYRISTYL               PDOC00008
PS00008        89->95    MYRISTYL               PDOC00008
PS00008        91->97    MYRISTYL               PDOC00008
PS00008       134->140   MYRISTYL               PDOC00008
PS00009        67->71    AMIDATION              PDOC00009

(No Pfam data available for DKFZphfkd2_24e23.2)
```

DKFZphfkd2_24n20
----

group: intracellular transport and trafficking

DKFZphfkd2_24n20.3 encodes a novel 366 amino acid protein with similarity to human eps8 binding protein e3B1 and spectrins.

The new protein contains an Src homology domain 3 and is similar to human eps8 SH3 domain binding protein 1 (e3B1) and spectrins. Eps8 is a substrate of receptor tyrosine kinases involved in mitogenic signaling. Spectrin is part of the submembrane cytoskeletal network in the human erythrocyte ghost. Nonerythroid spectrins are proposed to have roles in cell adhesion, establishment of cell polarity, and attachment of other cytoskeletal structures to the plasma membrane. The new protein seems to be part of the signalling pathway between tyrosine kinases and the membrane/cyto skeleton.

The new protein can find application in modulating cell adhesion/motility and membrane/cyto skeleton structure and dynamics.

strong similarity to eps8 binding protein e3B1

complete cDNA, complete cds, few EST hits
potential start at Bp 300, but there are ATGs in other frames in
5' region of the cDNA

Sequenced by GBF

Locus: /map="17"

Insert length: 1719 bp
Poly A stretch at pos. 1699, polyadenylation signal at pos. 1680

```
   1 GGGGACAGCT GCCCCGACCT TGGCTTCCTC TGCTGGGTGG GATTGGGGGC
  51 TGGGCCCCCA AATGGGCCCC TGGCTTCCCC CTTCCTCTGG GCAGGGGACA
 101 GAGAGACACA GGCTCGGGGA GCAGGACTGA CTTCCTCTTG TCCCGGAATG
 151 AGCATGCCTG CCCTTTGCAA GCAGGTTTGG GTCTCACGCA GAGGAAACCA
 201 AAAGCAATAA GAGGGAGGGA AAGCAGAGCA ACCAATCAAG GGCAGGGTGA
 251 GACTCAAAAC GAGCGGGCTC CCTGGGGAGC CAGACAGAGG CTGGGGGTGA
 301 TGGCGGAGCT ACAGCAGCTG CAGGAGTTTG AGATCCCCAC TGGCCGGGAG
 351 GCTCTGAGGG GCAACCACAG TGCCCTGCTG CGGGTCGCTG ACTACTGCGA
 401 GGACAACTAT GTGCAGGCCA CAGACAAGCA GAAGGCGCTG GAGGAGACCA
 451 TGGCCTTCAC TACCCAGGCA CTGGCCAGCG TGGCCTACCA GGTGGGCAAC
 501 CTGGCCGGGC ACACTCTGCG CATGTTGGAC CTGCAGGGGG CCGCCCTGCG
 551 GCAGGTGGAA GCCCGTGTAA GCACGCTGGG CCAGATGGTG AACATGCATA
 601 TGGAGAAGGT GGCCCGAAGG GAGATCGGCA CCTTAGCCAC TGTCCAGCGG
 651 CTGCCCCCCG GCCAGAAGGT CATCGCCCCA GAGAACCTAC CCCCTCTCAC
 701 GCCCTACTGC AGGAGACCCC TCAACTTTGG CTGCCTGGAC GACATTGGCC
 751 ATGGGATCAA GGACCTCAGC ACGCAGCTGT CAAGAACAGG CACCCTGTCT
 801 CGAAAGAGCA TCAAGGCCCC TGCCACACCC GCCTCCGCCA CCTTGGGGAG
 851 ACCGCCCCGG ATTCCCGAGC CAGTGCACCT GCCGGTGGTG CCCGACGGCA
 901 GACTCTCCGC CGCCTCCTCT GCGTCTTCCC TGGCCTCGGC CGGCAGCGCC
 951 GAAGGTGTCG GTGGGGCCCC CACGCCCAAG GGGCAGGCAG CACCTCCAGC
1001 CCCACCTCTC CCCAGCTCCT TGGACCCACC TCCTCCACCA GCAGCCGTCG
1051 AGGTGTTCCA GCGGCCTCCC ACGCTGGAGG AGTTGTCCCC ACCCCCACCG
1101 GACGAAGAGC TGCCCCTGCC ACTGGACCTG CCTCCTCCTC CACCCCTGGA
1151 TGGAGATGAA TTGGGGCTGC CTCCACCCCC ACCAGGATTT GGGCCTGATG
1201 AGCCCAGCTG GGTGCCTGCC TCATACTTGG AGAAAGTGGT GACACTGTAC
1251 CCATACACCA GCCAGAAGGA CAATGAGCTC TCCTTCTCTG AGGGCACTGT
1301 CATCTGTGTC ACTCGCCGCT ACTCCGATGG CTGGTGCGAG GGCGTCAGCT
1351 CGGAGGGGAC TGGATTCTTC CCTGGGAACT ATGTGGAGCC CAGCTGCTGA
1401 CAGCCCAGGG CTCTCTGGGC AGCTGATGTC TGCACTGAGT GGGTTTCATG
1451 AGCCCCAAGC CAAAACCAGC TCCAGTCACA GCTGGACTGG GTCTGCCCAC
1501 CTCTTGGGCT TGTGAGCTGTG TTCTGTCCTT CCTCCCATCG GAGGGAGAAG
1551 GGGTCCTGGG GAGAGAGAAT TTATCCAGAG GCCTGCTGCA GATGGGGAAG
1601 AGCTGGAAAC CAAGAAGTTT GTCAACAGAG GACCCCTACT CCATGCAGGA
1651 CAGGGTCTCC TGCTGCAAGT CCCAACTTTG AATAAAACAG ATGATGTCCA
1701 AAAAAAAAAA AAAAAAAAA
```

BLAST Results

Entry AC004797 from database EMBL:
Homo sapiens chromosome 17, clone hRPC.62_O_9, complete sequence.
Score = 2316, P = 5.9e-255, identities = 464/465
7 exons Bp 93317-110902

Medline entries

97163405:
Isolation and characterization of e3B1, an eps8 binding protein that regulates cell growth.

98256293:
Identification of a candidate human spectrin Src homology 3 domain-binding protein suggests a general mechanism of association of tyrosine kinases with the spectrin-based membrane skeleton.

Peptide information for frame 3

ORF from 300 bp to 1397 bp; peptide length: 366
Category: strong similarity to known protein

```
  1 MAELQQLQEF EIPTGREALR GNHSALLRVA DYCEDNYVQA TDKQKALEET
 51 MAFTTQALAS VAYQVGNLAG HTLRMLDLQG AALRQVEARV STLGQMVNMH
101 MEKVARREIG TLATVQRLPP GQKVIAPENL PPLTPYCRRP LNFGCLDDIG
151 HGIKDLSTQL SRTGTLSRKS IKAPATPASA TLGRPPRIPE PVHLPVVPDG
201 RLSAASSASS LASAGSAEGV GGAPTPKGQA APPAPPLPSS LDPPPPPAAV
251 EVFQRPPTLE ELSPPPPDEE LPLPLDLPPP PPLDGDELGL PPPPPGFGPD
301 EPSWVPASYL EKVVTLYPYT SQKDNELSFS EGTVICVTRR YSDGWCEGVS
351 SEGTGFFPGN YVEPSC
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24n20, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_24n20, frame 3

Report for DKFZphfkd2_24n20.3

```
[LENGTH]        366
[MW]            38947.21
[pI]            4.93
[HOMOL]         TREMBL:U87166_1 gene: "SSH3BP1"; product: "spectrin SH3 domain binding protein
1"; Homo sapiens spectrin SH3 domain binding protein 1 (SSH3BP1) mRNA, complete cds. 3e-48

[FUNCAT]        10.99 other signal-transduction activities   [S. cerevisiae, YGR136w] 9e-06
[FUNCAT]        30.10 nuclear organization     [S. cerevisiae, YGR136w] 9e-06
[FUNCAT]        99 unclassified proteins       [S. cerevisiae, YPR154w] 3e-05
[FUNCAT]        30.04 organization of cytoskeleton    [S. cerevisiae, YDR388w] 2e-04
[FUNCAT]        03.04 budding, cell polarity and filament formation [S. cerevisiae, YDR388w]
2e-04
[FUNCAT]        06.10 assembly of protein complexes   [S. cerevisiae, YDR162c] 4e-04
[BLOCKS]        BL50002B Src homology 3 (SH3) domain proteins profile
[SUPFAM]        SH3 homology 6e-17
[PROSITE]       MYRISTYL        6
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        6
[PROSITE]       PKC_PHOSPHO_SITE        8
[PROSITE]       ASN_GLYCOSYLATION       1
[PFAM]          Src homology domain 3
[KW]            Irregular
[KW]            3D
[KW]            LOW_COMPLEXITY    24.04 %

SEQ    MAELQQLQEFEIPTGREALRGNHSALLRVADYCEDNYVQATDKQKALEETMAFTTQALAS
SEG    ............................................................
1aboA  ............................................................

SEQ    VAYQVGNLAGHTLRMLDLQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPP
SEG    ............................................................
1aboA  ............................................................
```

```
SEQ    GQKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGTLSRKSIKAPATPASA
SEG    ............................................................
1aboA  ............................................................

SEQ    TLGRPPRIPEPVHLPVVPDGRLSAASSASSLASAGSAEGVGGAPTPKGQAAPPAPPLPSS
SEG    ......................xxxxxxxxxxxxxxxxxxxxx......xxxxxxxxxxx
1aboA  ............................................................

SEQ    LDPPPPPAAVEVFQRPPTLEELSPPPPDEELPLPLDLPPPPPLDGDELGLPPPPPGFGPD
SEG    xxxxxxxxx......xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
1aboA  ............................................................

SEQ    EPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRYSDGWCEGVSSEGTGFFPGN
SEG    xx..........................................................
1aboA  .............EECCCBCCCTTTBCCBTTTEEEEEEEEETTTTEEEEEETTEEEEEEGG

SEQ    YVEPSC
SEG    ......
1aboA  GEEE..
```

Prosite for DKFZphfkd2_24n20.3

PS00001	22->26	ASN_GLYCOSYLATION	PDOC00001
PS00004	339->343	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	14->17	PKC_PHOSPHO_SITE	PDOC00005
PS00005	41->44	PKC_PHOSPHO_SITE	PDOC00005
PS00005	72->75	PKC_PHOSPHO_SITE	PDOC00005
PS00005	167->170	PKC_PHOSPHO_SITE	PDOC00005
PS00005	170->173	PKC_PHOSPHO_SITE	PDOC00005
PS00005	225->228	PKC_PHOSPHO_SITE	PDOC00005
PS00005	321->324	PKC_PHOSPHO_SITE	PDOC00005
PS00005	338->341	PKC_PHOSPHO_SITE	PDOC00005
PS00006	14->18	CK2_PHOSPHO_SITE	PDOC00006
PS00006	239->243	CK2_PHOSPHO_SITE	PDOC00006
PS00006	258->262	CK2_PHOSPHO_SITE	PDOC00006
PS00006	308->312	CK2_PHOSPHO_SITE	PDOC00006
PS00006	321->325	CK2_PHOSPHO_SITE	PDOC00006
PS00006	328->332	CK2_PHOSPHO_SITE	PDOC00006
PS00008	21->27	MYRISTYL	PDOC00008
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	94->100	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	215->221	MYRISTYL	PDOC00008
PS00008	332->338	MYRISTYL	PDOC00008

Pfam for DKFZphfkd2_24n20.3

```
HMM_NAME     Src homology domain 3

HMM              *pyVIALYDYqAqdpDELSFkEGDIIiIIEdsDD.WWrgRnnnTNGQEGW
                  ++V+ LY+Y++Q ++ELSF EG +I +   +   D W++G +       +G+
Query        311  EKVVTLYPYTSQKDNELSFSEGTVICVTRRYSDGWCEGVSSE---GTGF    356

HMM              IPSNYVEPi*
                 +P NYVEP
Query        357 FPGNYVEPS    365
```

DKFZphfkd2_24p5
----

group: intracellular transport and trafficking

DKFZphfkd2_24p5 encodes a novel 811 amino acid protein which is a novel splice variant of human ankyrin G.

The ankyrin 3 gene encodes a novel ankyrin, which is expressed in multiple tissues, with very high expression at the axonal initial segment and nodes of Ranvier of neurons in the central and peripheral nervous systems. Ankyrin G shows several tissue-specific alternative mRNA processing. The different ankyrin G proteins participate in maintenance/targeting of ion channels and cell adhesion molecules to nodes of Ranvier and axonal initial segments.

The new protein can find application in modulating the structure and membrane topology of Ranvier nodes and other neuronal cell membranes.

Human ankyrin G (ANK-3) new splice variant

splice variant
potential frame shift at 2720 was checked
see BLASTX

Sequenced by EMBL

Locus: /map="10q21"

Insert length: 3470 bp
Poly A stretch at pos. 3459, no polyadenylation signal found

```
   1 AGCTTTAAAA GGATGTCTGC GAAGTGGTCA AAAGGATCTT AACCTCAATT
  51 AAGTGGGGTT TTTTAAAAAG ATTTTTTGGG GGGCCTGAAA TTTTGAAAAT
 101 CTTCGAACTC TGAGTGGGGA AAGATGTATA ATTCCTCAAT TGCCTACGAG
 151 GATATCAAGA TGCTGAGAGG AATTCAGCGG TGGTGAAGAG AGTGGATACA
 201 AACCAGGGAT TGGTTTCCTT GAGCTGTTTT GGAGGTTGAT TCTAAATCAC
 251 TGCTTAAGGA ATTCCTGGAA ACATCAGGAA AACATTTGAT CATCCAAGCC
 301 TAGTGGAAAT GGCTTTACCG CAGAGTGAAG ATGCAATGAC CGGGGACACA
 351 GACAAATATC TTGGGCCACA GGACCTTAAG GAATTGGGTG ATGATTCCCT
 401 GCCTGCAGAG GGTTACATGG GCTTTAGTCT CGGAGCGCGT TCTGCCAGCC
 451 TCCGCTCCTT CAGTTCGGAT GGGTCTTACA CCTTGAACAG AAGCTCCTAT
 501 GCACGGGACA GCATGATGAT TGAAGAACTC CTCGTGCCAT CCAAAGAGCA
 551 GCATCTAACA TTCACAAGGG AATTTGATTC AGATTCTCTT AGACATTACA
 601 GCTGGGCTGC AGACACCTTA GACAATGTCA ATCTTGTTCC AAGCCCCATT
 651 CATTCTGGGT TTCTGGTTAG CTTTATGGTG GACGCGAGAG GGGGCTCCAT
 701 GAGAGGAAGC CGTCATCACG GGATGAGAAT CATCATTCCT CCACGCAAGT
 751 GTACGGCCCC CACTCGAATC ACCTGCCGTT TGGTAAAGAG ACATAAACTG
 801 GCCAACCCAC CCCCCATGGT GGAAGGAGAG GGATTAGCCA GTAGGCTGGT
 851 AGAAATGGGT CCTGCAGGGG CACAATTTTT AGGCCCTGTC ATAGTGGAAA
 901 TCCCTCACTT TGGGTCCATG AGAGGAAAAG AGAGAGAACT CATTGTTCTT
 951 CGAAGTGAAA ATGGTGAAAC TTGGAAGGAG CATCAGTTTG ACAGCAAAAA
1001 TGAAGATTTA ACCGAGTTAC TTAATGGCAT GGATGAAGAA CTTGATAGCC
1051 CAGAAGAGTT AGGGAAAAAG CGTATCTGCA GGATTATCAC GAAAGATTTC
1101 CCCCAGTATT TTGCAGTGGT TTCCCGGATT AAGCAGGAAA GCAACCAGAT
1151 TGGTCCTGAA GGTGGAATTC TGAGCAGCAC CACAGTGCCC CTTGTTCAAG
1201 CATCTTTCCC AGAGGGTGCC CTAACTAAAA GAATTCGAGT GGGCCTCCAG
1251 GCCCAGCCTG TTCCAGATGA AATTGTGAAA AAGATCCTTG GAAACAAAGC
1301 AACTTTTAGC CCAATTGTCA CTGTGGAACC AAGAAGACGG AAATTCCATA
1351 AACCAATCAC AATGACCATT CCGGTGCCCC CGCCCTCAGG AGAAGGTGTA
1401 TCCAATGGAT ACAAAGGGGA CACTACACCC AATCTGCGTC TTCTCTGTAG
1451 CATTACAGGG GGCACTTCGC CTGCTCAGTG GGAAGACATC ACAGGAACAA
1501 CTCCTTTGAC GTTTATAAAA GATTGTGTCT CCTTTACAAC CAATGTTTCA
1551 GCCAGATTTT GGCTTGCAGA CTGCCATCAA GTTTTAGAAA CTGTGGGGTT
1601 AGCCACGCAA CTGTACAGAG AATTGATATG TGTTCCATAT ATGGCCAAGT
1651 TTGTTGTTTT TGCCAAAATG AATGATCCCG TAGAATCTTC CTTGCGATGT
1701 TTCTGCATGA CAGATGACAA AGTGGACAAA ACTTTAGAGC AACAAGAGAA
1751 TTTTGAGGAA GTCGCAAGAA GCAAAGATAT TGAGGTTCTG GAAGGAAAAC
1801 CTATTTATGT TGATTGTTAT GGAAATTTGG CCCCACTTAC CAAAGGAGGA
1851 CAGCAACTTG TTTTTAACTT TTATTCTTTC AAAGAAAATA GACTGCCATT
1901 TTCCATCAAG ATTAGAGACA CCAGCCAAGA GCCCTGTGGT CGTCTGTCTT
1951 TTCTGAAAGA ACCAAAGACA ACAAAAGGAC TGCCTCAAAC AGCGGTTTGC
2001 AACTTAAATA TCACTCTGCC AGCACATAAA AAGATTGAGA AAACAGATGG
2051 ACGACAGAGC TTCGCATCCT TAGCTTTACG TAAGCGCTAC AGCTACTTGA
2101 CTGAGCCTGG AATGAGTCCA CAGAGTCCAT GTGAACGGAC AGATATCAGG
2151 ATGGCAATAG TAGCCGATCA CCTGGGACTT AGTTGGACAG AACTGGCAAG
2201 GGAACTGAAT TTTTCAGTGG ATGAAATCAA TCAAATACGT GTGGAAAATC
2251 CAAATTCTTT AATTTCTCAG AGCTTCATGT TTTTAAAAAA ATGGGTTACC
2301 AGAGACGGAA AAAATGCCAC AACTGATGCC TTAACTTCGG TCTTGACAAA
2351 AATTAATCGA ATAGATATAG TGACACTGCT AGAAGGACCA ATATTTGATT
```

```
2401 ATGGAAATAT TTCAGGCACC AGAAGTTTTG CAGATGAGAA CAATGTTTTC
2451 CATGACCCTG TTGATGGTTA TCCTTCCCTT CAAGTGGAAC TGGAAACCCC
2501 CACAGGGTTG CACTACACAC CACCTACCCC TTTCCAGCAA GATGATTATT
2551 TTAGTGATAT CTCTAGCATA GAATCTCCCC TTAGAACCCC TAGTAGACTG
2601 AGTGATGGGC TAGTGCCTTC CCAGGGGAAC ATAGAGCATT CCGCAGATGG
2651 ACCTCCAGTC GTAACTGCAG AAGACGCTTC CTTAGAAGAC AGCAAACTGG
2701 AAGACTCAGT GCCTTTAACA GAAATGCCTG AAGCAGTGAT GTAGATGAGA
2751 GCCAGTTGGA GAATGTATGT CTGAGTTGGC AGAATGAGAC ATCAAGTGGA
2801 AACCTAGAGT CCTGCGCTCA AGCTCGAAGA GTAACTGGTG GGTTACTAGA
2851 TCGACTGGAT GACAGCCCTG ACCAGTGTAG AGATTCCATT ACCTCATATC
2901 TCAAAGGAGA AGCTGGCAAA TTTGAAGCAA ATGGAAGCCA TACAGAAATC
2951 ACTCCAGAAG CAAAGACAAA ATCTTACTTT CCAGAATCCC AAAATGATGT
3001 AGGAAAACAG AGTACCAAGG AAACTCTGAA ACCAAAAATA CATGGATCTG
3051 GTCATGTTGA AGAACCAGCA TCACCACTAG CAGCATATCA GAAATCTCTA
3101 GAAGAAACCA GCAAGCTTAT AATAGAAGAG ACTAAACCCT GTGTGCCTGT
3151 CAGTATGAAA AAGATGAGTA GGACTTCTCC AGCAGATGGC AAGCCAAGGC
3201 TTAGCCTCCA TGAAGAAGAG GGGTCCAGTG GGTCTGAGCA AAAGCAGGGA
3251 GAAGGTTTTA AGGTGAAAAC GAAGAAAGAA ATCCGGCATG TGGAAAAGAA
3301 GAGCCACTCG TAACAGCGAA CGGTCAGTCA AGGATCATAA GTTTTTACTG
3351 CCAGTATTGA GAAATTCGTG GAAGAAATGT CAGCAGGAAG TAAAAATTCA
3401 CCGAGAAGTG TGTGTGTGTT CGCTGCTTCC ACACATTAAT GGCATGATTT
3451 TTTTTATGCA AAAAAAAAAA
```

BLAST Results

Entry MMANK3A_1 from database TREMBL:
Ank3"; product: "ankyrin 3"; Mus mu... +3 4022 0.0 2

Entry HS13616 from database EMBL:
Human ankyrin G (ANK-3) mRNA, complete cds.
Length = 14,770
Plus Strand HSPs:
Score = 8505 (1276.1 bits), Expect = 0.0, Sum P(3) = 0.0
Identities = 1799/1873 (96%)

Medline entries

95394457:
Chromosomal localization of the ankyrinG gene
(ANK3/Ank3) to human 10q21 and mouse 10.

95138209:
A new ankyrin gene with neural-specific isoforms localized at the
axonal initial segment and node of Ranvier

Peptide information for frame 3

ORF from 309 bp to 2741 bp; peptide length: 811
Category: known protein
Classification: unset

```
  1 MALPQSEDAM TGDTDKYLGP QDLKELGDDS LPAEGYMGFS LGARSASLRS
 51 FSSDGSYTLN RSSYARDSMM IEELLVPSKE QHLTFTREFD SDSLRHYSWA
101 ADTLDNVNLV PSPIHSGFLV SFMVDARGGS MRGSRHHGMR IIIPPRKCTA
151 PTRITCRLVK RHKLANPPPM VEGEGLASRL VEMGPAGAQF LGPVIVEIPH
201 FGSMRGKERE LIVLRSENGE TWKEHQFDSK NEDLTELLNG MDEELDSPEE
251 LGKKRICRII TKDFPQYFAV VSRIKQESNQ IGPEGGILSS TTVPLVQASF
301 PEGALTKRIR VGLQAQPVPD EIVKKILGNK ATFSPIVTVE PRRRKFHKPI
351 TMTIPVPPPS GEGVSNGYKG DTTPNLRLLC SITGGTSPAQ WEDITGTTPL
401 TFIKDCVSFT TNVSARFWLA DCHQVLETVG LATQLYRELI CVPYMAKFVV
451 FAKMNDPVES SLRCFCMTDD KVDKTLEQQE NFEEVARSKD IEVLEGKPIY
501 VDCYGNLAPL TKGGQQLVFN FYSFKENRLP FSIKIRDTSQ EPCGRLSFLK
551 EPKTTKGLPQ TAVCNLNITL PAHKKIEKTD GRQSFASLAL RKRYSYLTEP
601 GMSPQSPCER TDIRMAIVAD HLGLSWTELA RELNFSVDEI NQIRVENPNS
651 LISQSFMFLK KWVTRDGKNA TTDALTSVLT KINRIDIVTL LEGPIFDYGN
701 ISGTRSFADE NNVFHDPVDG YPSLQVELET PTGLHYTPPT PFQQDDYFSD
751 ISSIESPLRT PSRLSDGLVP SQGNIEHSAD GPPVVTAEDA SLEDSKLEDS
801 VPLTEMPEAV M
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_24p5, frame 3

TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds., N = 1, Score = 4022, P = 0

TREMBL:MMANK3B_3 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (7kb isoform) mRNA, complete cds., N = 1, Score = 4005, P = 0

TREMBL:MMANK3B_4 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial ankyrin 3 (7kb isoform) mRNA, complete cds., N = 1, Score = 4005, P = 0

```
>TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus
     epithelial ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds.
            Length = 1,094

  HSPs:

 Score = 4022 (603.5 bits), Expect = 0.0e+00, P = 0.0e+00
 Identities = 769/805 (95%), Positives = 783/805 (97%)

Query:     1 MALPQSEDAMTGDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASLRSFSSDGSYTLN 60
             MALP SEDA+TGDTDKYLGPQDLKELGDDSLPAEGY+GFSLGARSASLRSFSSD SYTLN
Sbjct:     1 MALPHSEDAITGDTDKYLGPQDLKELGDDSLPAEGYVGFSLGARSASLRSFSSDRSYTLN 60

Query:    61 RSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLVPSPIHSGFLV 120
             RSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLV SP+HSGFLV
Sbjct:    61 RSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLVSSPVHSGFLV 120

Query:   121 SFMVDARGGSMRGSRHHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL 180
             SFMVDARGGSMRGSRHHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL
Sbjct:   121 SFMVDARGGSMRGSRHHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL 180

Query:   181 VEMGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDLTELLNG 240
             VEMGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDL ELLNG
Sbjct:   181 VEMGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDLAELLNG 240

Query:   241 MDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF 300
             MDEELDSPEELG KRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF
Sbjct:   241 MDEELDSPEELGTKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF 300

Query:   301 PEGALTKRIRVGLQAQPVPDEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS 360
             PEGALTKRIRVGLQAQPVP+E VKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS
Sbjct:   301 PEGALTKRIRVGLQAQPVPEETVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS 360

Query:   361 GEGVSNGYKGDTTPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSARFWLA 420
             GEGVSNGYKGD TPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSARFWLA
Sbjct:   361 GEGVSNGYKGDATPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSARFWLA 420

Query:   421 DCHQVLETVGLATQLYRELICVPYMAKFVVFAKMNDPVESSLRCFCMTDDKVDKTLEQQE 480
             DCHQVLETVGLA+QLYRELICVPYMAKFVVFAK NDPVESSLRCFCMTDD+VDKTLEQQE
Sbjct:   421 DCHQVLETVGLASQLYRELICVPYMAKFVVFAKTNDPVESSLRCFCMTDDRVDKTLEQQE 480

Query:   481 NFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ 540
             NFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ
Sbjct:   481 NFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ 540

Query:   541 EPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKKIEKTDGRQSFASLALRKRYSYLTEP 600
             EPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKK EK D RQSFASLALRKRYSYLTEP
Sbjct:   541 EPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKKAEKADRRQSFASLALRKRYSYLTEP 600

Query:   601 GMSPQSPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMFLK 660
              MSPQSPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFM LK
Sbjct:   601 SMSPQSPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMLLK 660

Query:   661 KWVTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDPVDG 720
             KWVTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDPVDG
Sbjct:   661 KWVTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDPVDG 720

Query:   721 YPSLQVELETPTGLHYTPPTPFQQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIEHSAD 780
             +PS QVELETP GL++TPP PFQQDD+FSDISSIESP RTPSRLSDGLVPSQGNIEH
Sbjct:   721 HPSFQVELETPMGLYWTPPNPFQQDDHFSDISSIESPFRTPSRLSDGLVPSQGNIEHPTG 780

Query:   781 GPPVVTAEDASLEDSKLEDSVPLTE 805
             GPPVVTAED SLEDSK++DSV +T+
```

```
Sbjct:   781 GPPVVTAEDTSLEDSKMDDSVTVTD 805
```

Pedant information for DKFZphfkd2_24p5, frame 3

Report for DKFZphfkd2_24p5.3

```
[LENGTH]        811
[MW]            90104.66
[pI]            5.40
[HOMOL]         TREMBL:MMANK3A_1 gene: "Ank3"; product: "ankyrin 3"; Mus musculus epithelial
ankyrin 3 (Ank3) 5kb isoform mRNA, complete cds. 0.0
[BLOCKS]        BL50017B Death domain proteins profile
[PIRKW]         phosphoprotein 0.0
[PIRKW]         alternative splicing 0.0
[PIRKW]         peripheral membrane protein 0.0
[PIRKW]         cytoskeleton 0.0
[SUPFAM]        ankyrin 0.0
[SUPFAM]        ankyrin repeat homology 0.0
[SUPFAM]        unassigned ankyrin repeat proteins 0.0
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY     1.73 %

SEQ    MALPQSEDAMTGDTDKYLGPQDLKELGDDSLPAEGYMGFSLGARSASLRSFSSDGSYTLN
SEG    ............................................................
PRD    cccccccccccccccccccccccccccccccccccccccccccceeeeeccccccccccc
MEM    ............................................................

SEQ    RSSYARDSMMIEELLVPSKEQHLTFTREFDSDSLRHYSWAADTLDNVNLVPSPIHSGFLV
SEG    ............................................................
PRD    ccchhhhhhhhheeeehhhhhhhhhhhccccccccccccccccccccccccccccceee
MEM    ................................................MMMMMMMMMMMM

SEQ    SFMVDARGGSMRGSRHHGMRIIIPPRKCTAPTRITCRLVKRHKLANPPPMVEGEGLASRL
SEG    ......xxxxxxxxxxxxxx........................................
PRD    eeeeeccccccccccccceeeeccccccccccceeeeehhhhcccccccccccccccccee
MEM    MMMMMMMMMMMMMMMM...........................................M

SEQ    VEMGPAGAQFLGPVIVEIPHFGSMRGKERELIVLRSENGETWKEHQFDSKNEDLTELLNG
SEG    ............................................................
PRD    eeccccccceeeceeeeeeccccccccccceeeeeeecccceeeeeeccccccchhhhhhc
MEM    MMMMMMMMMMMMMMMMMMMMMMMMMMMM................................

SEQ    MDEELDSPEELGKKRICRIITKDFPQYFAVVSRIKQESNQIGPEGGILSSTTVPLVQASF
SEG    ............................................................
PRD    ccccchhhhhhhhheeeeeeccccceeeeehhhhhcccccccccccccccceeeeeeeeccc
MEM    ............................................................

SEQ    PEGALTKRIRVGLQAQPVPDEIVKKILGNKATFSPIVTVEPRRRKFHKPITMTIPVPPPS
SEG    ............................................................
PRD    ccchhhhhhhhhhhhhcccccceeeecccccccccccceeeccccccccccccceeeecccccc
MEM    ............................................................

SEQ    GEGVSNGYKGDTTPNLRLLCSITGGTSPAQWEDITGTTPLTFIKDCVSFTTNVSARFWLA
SEG    ............................................................
PRD    cccccccccccccccceeeeeeeecccccccccccccccceeeeeeecccccccccccceeeec
MEM    ............................................................

SEQ    DCHQVLETVGLATQLYRELICVPYMAKFVVFAKMNDPVESSLRCFCMTDDKVDKTLEQQE
SEG    ............................................................
PRD    cchhhhhhhhhhhhhhhhhhhhcchhhhhheeeccccchhhhhhhhccccchhhhhhhhhc
MEM    ............................................................

SEQ    NFEEVARSKDIEVLEGKPIYVDCYGNLAPLTKGGQQLVFNFYSFKENRLPFSIKIRDTSQ
SEG    ............................................................
PRD    cceeeccccceeeeeeecccceeeeeeccccccccchhhhhhhhhchhhhhhhcceeeeeeecccc
MEM    ............................................................

SEQ    EPCGRLSFLKEPKTTKGLPQTAVCNLNITLPAHKKIEKTDGRQSFASLALRKRYSYLTEP
SEG    ............................................................
PRD    cccccceeeeccccccccccccccccccccccccccccccccchhhhhhhhhhhhheeecc
MEM    ............................................................

SEQ    GMSPQSPCERTDIRMAIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMFLK
SEG    ............................................................
PRD    cccccccchhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhhhcceeeeeeccccchhhhhhhhhh
MEM    ............................................................
```

```
SEQ    KWVTRDGKNATTDALTSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDPVDG
SEG    ............................................................
PRD    hhhhcccccccchhhhhhhhhhcceeeeeeeecccccccccccccccccccccccccccc
MEM    ............................................................

SEQ    YPSLQVELETPTGLHYTPPTPFQQDDYFSDISSIESPLRTPSRLSDGLVPSQGNIEHSAD
SEG    ............................................................
PRD    cccceeeeeccccccccccccccccccccceeecccccccccccccccccccccccccccc
MEM    ............................................................

SEQ    GPPVVTAEDASLEDSKLEDSVPLTEMPEAVM
SEG    ...............................
PRD    ccceeeecccccccccccccccccccccccc
MEM    ...............................
```

(No Prosite data available for DKFZphfkd2_24p5.3)

(No Pfam data available for DKFZphfkd2_24p5.3)

DKFZphfkd2_3i13

group: transmembrane protein

DKFZphfkd2_3i13 encodes a novel 406 amino acid protein with C. elegans cosmid Y37D8A and A. thaliana H71412 hypothetical protein.

The novel protein contains 3 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker for kidney cells.

similarity to A.thaliana and C.elegans;
membrane regions: 3

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="17"

Insert length: 2052 bp
Poly A stretch at pos. 2032, no polyadenylation signal found

```
   1 AGTGACGTGA GCGGGTTCCG GTTGTCTGGA GCCCAGCGGC GGGTGTGAGA
  51 GTCCGTAAGG AGCAGCTTCC AGGATCCTGA GATCCGGAGC AGCCGGGGTC
 101 GGAGCGGCTC CTCAAGAGTT ACTGATCTAT GAAATGGCAG AGAATGGAAA
 151 AAATTGTGAC CAGAGACGTG TAGCAATGAA CAAGGAACAT CATAATGGAA
 201 ATTTCACAGA CCCCTCTTCA GTGAATGAAA AGAAGAGGAG GGAGCGGGAA
 251 GAAAGGCAGA ATATTGTCCT GTGGAGACAG CCGCTCATTA CCTTGCAGTA
 301 TTTTTCTCTG GAAATCCTTG TAATCTTGAA GGAATGGACC TCAAAATTAT
 351 GGCATCGTCA AAGCATTGTG GTGTCTTTTT TACTGCTGCT TGCTGTGCTT
 401 ATAGCTACGT ATTATGTTGA AGGAGTGCAT CAACAGTATG TGCAACGTAT
 451 AGAGAAACAG TTTCTTTTGT ATGCCTACTG GATAGGCTTA GGAATTTTGT
 501 CTTCTGTTGG GCTTGGAACA GGGCTGCACA CCTTTCTGCT TTATCTGGGT
 551 CCACATATAG CCTCAGTTAC ATTAGCTGCT TATGAATGCA ATTCAGTTAA
 601 TTTTCCCGAA CCACCCTATC CTGATCAGAT TATTTGTCCA GATGAAGAGG
 651 GCACTGAAGG AACCATTTTT TTGTGGAGTA TCATCTCAAA AGTTAGGATT
 701 GAAGCCTGCA TGTGGGGTAT CGGTACAGCA ATCGGAGAGC TGCCTCCATA
 751 TTTCATGGCC AGAGCAGCTC GCCTCTCAGG TGCTGAACCA GATGATGAAG
 801 AGTATCAGGA ATTTGAAGAG ATGCTGGAAC ATGCAGAGTC TGCACAAGAC
 851 TTTGCCTCCC GGGCCAAACT GGCAGTTCAA AAACTAGTAC AGAAAGTTGG
 901 ATTTTTTGGA ATTTTGGCCT GTGCTTCAAT TCCAAATCCT TTATTTGATC
 951 TGGCTGGAAT AACGTGTGGA CACTTTCTGG TACCTTTTTG GACCTTCTTT
1001 GGTGCAACCC TAATTGGAAA AGCAATAATA AAAATGCATA TCCAGAAAAT
1051 TTTTGTTATA ATAACATTCA GCAAGCACAT AGTGGAGCAA ATGGTGGCTT
1101 TCATTGGTGC TGTCCCCGGC ATAGGTCCAT CTCTGCAGAA GCCATTTCAG
1151 GAGTACCTGG AGGCTCAACG GCAGAAGCTT CACCACAAAA GCGAAATGGG
1201 CACACCACAG GGAGAAAACT GGTTGTCCTG GATGTTTGAA AAGTTGGTCG
1251 TTGTCATGGT GTGTTACTTC ATCCTATCTA TCATTAACTC CATGGCACAA
1301 AGTTATGCCA AACGAATCCA GCAGCGGTTG AACTCAGAGG AGAAAACTAA
1351 ATAAGTAGAG AAAGTTTTAA ACTGCAGAAA TTGGAGTGGA TGGGTTCTGC
1401 CTTAAATTGG GAGGACTCCA AGCCGGGAAG GAAAATTCCC TTTTCCAACC
1451 TGTATCAATT TTTACAACTT TTTTCCTGAA AGCAGTTTAG TCCATACTTT
1501 GCACTGACAT ACTTTTTCCT TCTGTGCTAA GGTAAGGTAT CCACCCTCGA
1551 TGCAATCCAC CTTGTGTTTT CTTAGGGTGG AATGTGATGT TCAGCAGCAA
1601 ACTTGCAACA GACTGGCCTT CTGTTTGTTA CTTTCAAAAG GCCCACATGA
1651 TACAATTAGA GAATTCCCAC CGCACAAAAA AAGTTCCTAA GTATGTTAAA
1701 TATGTCAAGC TTTTTAGGCT TGTCACAAAT GATTGCTTTG TTTTCCTAAG
1751 TCATCAAAAT GTATATAAAT TATCTAGATT GGATAACAGT CTTGCATGTT
1801 TATCATGTTA CAATTTAATA TTCCATCCTG CCCAACCCTT CCTCTCCCAT
1851 CCTCAAAAAA GGGCCATTTT ATGATGCATT GCACACCCTC TGGGGAAATT
1901 GATCTTTAAA TTTTGAGACA GTATAAGGAA AATCTGGTTG GTGTCTTACA
1951 AGTGAGCTGA CACCATTTTT TATTCTGTGT ATTTAGGATG AAGTCTTGAA
2001 AAAAACTTTA TAAAGACATC TTTAATCATT CCAAAAAAAA AAAAAAAAAA
2051 AA
```

BLAST Results

Entry AC004686 from database EMBL:
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone hRPC.1073_F_15; HTGS phase 1, 8 unordered pieces.
Score = 4142, P = 6.1e-199, identities = 830/832

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 134 bp to 1351 bp; peptide length: 406
Category: similarity to unknown protein

```
  1 MAENGKNCDQ RRVAMNKEHH NGNFTDPSSV NEKKRREREE RQNIVLWRQP
 51 LITLQYFSLE ILVILKEWTS KLWHRQSIVV SFLLLLAVLI ATYYVEGVHQ
101 QYVQRIEKQF LLYAYWIGLG ILSSVGLGTG LHTFLLYLGP HIASVTLAAY
151 ECNSVNFPEP PYPDQIICPD EEGTEGTIFL WSIISKVRIE ACMWGIGTAI
201 GELPPYFMAR AARLSGAEPD DEEYQEFEEM LEHAESAQDF ASRAKLAVQK
251 LVQKVGFFGI LACASIPNPL FDLAGITCGH FLVPFWTFFG ATLIGKAIIK
301 MHIQKIFVII TFSKHIVEQM VAFIGAVPGI GPSLQKPFQE YLEAQRQKLH
351 HKSEMGTPQG ENWLSWMFEK LVVVMVCYFI LSIINSMAQS YAKRIQQRLN
401 SEEKTK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_3i13, frame 2

TREMBL:CEY37D8A_20 gene: "Y37D8A.22"; Caenorhabditis elegans cosmid Y37D8A, N = 1, Score = 905, P = 8.8e-91

TREMBL:ATAC98_2 gene: "YUP8H12.2"; Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence., N = 1, Score = 470, P = 1.1e-44

PIR:H71412 hypothetical protein - Arabidopsis thaliana, N = 1, Score = 293, P = 6e-24

```
>TREMBL:CEY37D8A_20 gene: "Y37D8A.22"; Caenorhabditis elegans cosmid
     Y37D8A
            Length = 457

  HSPs:

 Score = 905 (135.8 bits), Expect = 8.8e-91, P = 8.8e-91
 Identities = 167/317 (52%), Positives = 228/317 (71%)

Query:     38 REERQNIVLWRQPLITLQYFSLEILVILKEWTSKLWHRQSIVVSFLLLLAVLIATYYVEG 97
              R ER+ IV WR+P I + Y  +EI  + E   K+  +++++   + + + +  Y+  G
Sbjct:     93 RMERETIVFWRRPHIVIPYALMEIAHLAVELFFKILAHKTVLLLTAISIGLAVYGYHAPG 152

Query:     98 VHQQYVQRIEKQFLLYAYWIGLGILSSVGLGTGLHTFLLYLGPHIASVTLAAYECNSVNF 157
               HQ++VQ IEK  L +++W+ LG+LSS+GLG+GLHTFL+YLGPHIA+VT+AAYEC S++F
Sbjct:    153 AHQEHVQTIEKHILWWSWWVLLGVLSSIGLGSGLHTFLIYLGPHIAAVTMAAYECQSLDF 212

Query:    158 PEPPYPDQIICPDEEGTEGTIFLWSIISKVRIEACMWGIGTAIGELPPYFMARAARLSGA 217
              P+PPYP+ I CP  + +    F W I++KVR+E+ +WG GTA+GELPPYFMARAAR+SG
Sbjct:    213 PQPPYPESIQCPSTKSSIAVTF-WQIVAKVRVESLLWGAGTALGELPPYFMARAARISGQ 271

Query:    218 EPDDEEYQEFEEMLE-HAESAQD----FASRAKLAVQKLVQKVGFFGILACASIPNPLFD 272
              EPDDEEY+EF E++    ES  D       RAK  V+  + ++GF GIL  ASIPNPLFD
Sbjct:    272 EPDDEEYREFLELMNADKESDADQKLSIVERAKSWVEHNIHRLGFPGILLFASIPNPLFD 331

Query:    273 LAGITCGHFLVPFWTFFGATLIGKAIIKMHIQKIFVIITFSKHIVEQMVAFIGAVPGIGP 332
              LAGITCGHFLVPFW+FFGATLIGKA++KMH+Q  FVI+ FS H  E  V  +  +P +GP
Sbjct:    332 LAGITCGHFLVPFWSFFGATLIGKALVKMHVQMGFVILAFSDHHAENFVKILEKIPAVGP 391

Query:    333 SLQKPFQEYLEAQRQKLH 350
               +++P  + LE QR+ LH
Sbjct:    392 YIRQPISDLLEKQRKALH 409
```

Pedant information for DKFZphfkd2_3i13, frame 2

Report for DKFZphfkd2_3i13.2

```
[LENGTH]        406
[MW]            46298.17
[pI]            6.47
[HOMOL]         TREMBL:CEY37D8A_20 gene: "Y37D8A.22"; Caenorhabditis elegans cosmid Y37D8A 1e-
79
[PROSITE]       MYRISTYL        10
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        1
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            TRANSMEMBRANE  3
[KW]            LOW_COMPLEXITY      9.85 %

SEQ   MAENGKNCDQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNIVLWRQPLITLQYFSLE
SEG   ...............................xxxxxxxxxx...................
PRD   ccccccchhhhhhhhhhhccccccccccccchhhhhhhhhhhhcccccchhhhhhhhhhh
MEM   .................................MMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ   ILVILKEWTSKLWHRQSIVVSFLLLAVLIATYYVEGVHQQYVQRIEKQFLLYAYWIGLG
SEG   ........................................................xxxx
PRD   hhhhhhhhhhhhhhhhhhhhhhheeeccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM   MM.....................MMMMMMMMMMMMMMMMMMMMMMMMMMMMM........

SEQ   ILSSVGLGTGLHTFLLYLGPHIASVTLAAYECNSVNFPEPPYPDQIICPDEEGTEGTIFL
SEG   xxxxxxxxxxx.................................................
PRD   hccccccccceeeeeeeecccchhhhhhhhhhcccccccccccccccccccccccceeee
MEM   ............................................................

SEQ   WSIISKVRIEACMWGIGTAIGELPPYFMARAARLSGAEPDDEEYQEFEEMLEHAESAQDF
SEG   .....................................xxxxxxxxxxxxxxx........
PRD   eehhhhhhhhhhhhhccccccccccchhhhhhhcccccchhhhhhhhhhhhhhhhhhhhh
MEM   ............................................................

SEQ   ASRAKLAVQKLVQKVGFFGILACASIPNPLFDLAGITCGHFLVPFWTFFGATLIGKAIIK
SEG   ............................................................
PRD   hhhhhhhhhhhhhhcceeeeeeeecccccccccccccccccceeeeeeehhhhhhhhhhh
MEM   ..........MMMMMMMMMMMMMMMMMMMMM.............................

SEQ   MHIQKIFVIITFSKHIVEQMVAFIGAVPGIGPSLQKPFQEYLEAQRQKLHHKSEMGTPQG
SEG   ............................................................
PRD   hhhheeeeeeechhhhhhhhhhhccccccccccchhhhhhhhhhhhhhhhhhhcccccccc
MEM   ............................................................

SEQ   ENWLSWMFEKLVVVMVCYFILSIINSMAQSYAKRIQQRLNSEEKTK
SEG   ..............................................
PRD   cchhhhhhhhhhhheeehhhhhhhhhhhhhhhhhhhhhhhhhcccc
MEM   ..............................................
```

Prosite for DKFZphfkd2_3i13.2

PS00001	23->27	ASN_GLYCOSYLATION	PDOC00001
PS00005	69->72	PKC_PHOSPHO_SITE	PDOC00005
PS00006	29->33	CK2_PHOSPHO_SITE	PDOC00006
PS00006	215->219	CK2_PHOSPHO_SITE	PDOC00006
PS00006	236->240	CK2_PHOSPHO_SITE	PDOC00006
PS00008	120->126	MYRISTYL	PDOC00008
PS00008	126->132	MYRISTYL	PDOC00008
PS00008	173->179	MYRISTYL	PDOC00008
PS00008	195->201	MYRISTYL	PDOC00008
PS00008	197->203	MYRISTYL	PDOC00008
PS00008	259->265	MYRISTYL	PDOC00008
PS00008	275->281	MYRISTYL	PDOC00008
PS00008	325->331	MYRISTYL	PDOC00008
PS00008	329->335	MYRISTYL	PDOC00008
PS00008	356->362	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfkd2_3i13.2)

DKFZphfkd2_3o17
----

group: metabolism

DKFZphfkd2_3o17 encodes a novel 72 amino acid protein with similarity to bos taurus NADH-ubiquinone oxidoreductase B33 subunit (EC 1.6.5.3) (EC 1.6.99.3).

NADH:ubiquinone oxidoreductase is the first enzyme in the respiratory electron transport chain of mitochondria. It is a a membrane-bound multi-subunit protein. The bovine heart enzyme contains about 40 different polypeptides. The novel protein is the human orthologue of bovine B22.

The new protein can find application in modulation of the respiratory electron transport chain pathways of mitochondria.

strong similarity to bovine NADH-UBIQUINONE OXIDOREDUCTASE B22 subunit

complete cDNA, complete cds, EST hits,
in frame stop codon at ~274 will be checked
ESTs HS1291620/AA883920 show no stop codon at this side

Sequenced by BMFZ

Locus: unknown

Insert length: 693 bp
Poly A stretch at pos. 670, polyadenylation signal at pos. 659

```
  1 CAGCAGGCGT GCAGTTTCCC GGCTCTCCGC GCGGCCGGGG AAGGTCAGCG
 51 CCGTAATGGC GTTCTTGGCG TCGGGACCCT ACCTGACCCA TCAGCAAAAG
101 GTGTTGCGGC TTTATAAGCG GGCGCTACGC CACCTCGAGT CGTGGTGCGT
151 CCAGAGAGAC AAATACCGAT ACTTTGCTTG TTTGATGAGA GCCCGGTTTG
201 AAGAACATAA GAATGAAAAG GATATGGCGA AGGCCACCCA GCTGCTGAAG
251 GAGGCCGAGG AAGAATTCTG GTAACGTCAG CATCCACAGC CATACATCTT
301 CCCTGACTCT CCTGGGGGCA CCTCCTATGA GAGATACGAT TGCTACAAGG
351 TCCCAGAATG GTGCTTAGAT GACTGGCATC CTTCTGAGAA GGCAATGTAT
401 CCTGATTACT TTGCCAAGAG AGAACAGTGG AAGAAACTGC GGAGGGAAAG
451 CTGGGAACGA GAGGTTAAGC AGCTGCAGGA GGAAACGCCA CCTGGTGGTC
501 CTTTAACTGA AGCTTTGCCC CCTGCCCGAA AGGAAGGTGA TTTGCCCCCA
551 CTGTGGTGGT ATATTGTGAC CAGACCCCGG GAGCGGCCCA TGTAGAAAGA
601 GAGAGACCTC ATCTTTCATG CTTGCAAGTG AAATATGTTA CAGAACATGC
651 ACTTGCCCTA ATAAAAAATC AGTAAAAAAA AAAAAAAAAA AAA
```

BLAST Results

Entry S28256 from database PIR:
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine
>TREMBL:MIBTCIB22_1 gene: "cI-B22"; product: "NADH-ubiquinone oxidoreductase complex B22 subunit"; B.taurus mitochondrion cI-B22 mRNA for B22 subunit of the NADH-ubiquinone oxidoreductase complex
Score = 933, P = 5.2e-93, identities = 163/179, positives = 172/179, frame +2

Medline entries

92389317
Sequences of 20 subunits of NADH:ubiquinone oxidoreductase from RT bovine heart mitochondria. Application of a novel strategy for RT sequencing proteins using the polymerase chain reaction

Peptide information for frame 2

ORF from 56 bp to 271 bp; peptide length: 72
Category: strong similarity to known protein

```
  1 MAFLASGPYL THQQKVLRLY KRALRHLESW CVQRDKYRYF ACLMRARFEE
 51 HKNEKDMAKA TQLLKEAEEE FW*RQHPQPY IFPDSPGGTS YERYDCYKVP
101 EWCLDDWHPS EKAMYPDYFA KREQWKKLRR ESWEREVKQL QEETPPGGPL
151 TEALPPARKE GDLPPLWWYI VTRPRERPM
```

BLASTP hits

```
Sequences producing significant alignments:                       (bits) Value

sp|Q02369|NI2M_BOVIN|0D36CE17281FB735 (NDUFB9..)NADH-UBIQUINONE...   141  7e-34
tr|U41534|Q18036|D34BCCB6E8FBCD5F (C16A3.4)SIMILAR TO NADH-UBIQ...    53  3e-07

>sp|Q02369|NI2M_BOVIN|0D36CE17281FB735 (NDUFB9..)NADH-UBIQUINONE
          OXIDOREDUCTASE B22 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3)
          (COMPLEX I-B22) (CI-B22).[BOS TAURUS]
          Length = 178

 Score =  141 bits (351), Expect = 7e-34
 Identities = 63/71 (88%), Positives = 68/71 (95%)

Query: 2  AFLASGPYLTHQQKVLRLYKRALRHLESWCVQRDKYRYFACLMRARFEEHKNEKDMAKAT 61
          AFL+SG YLTHQQKVLRLYKRALRHLESWC+ RDKYRYFACL+RARF+EHKNEKDM KAT
Sbjct: 1  AFLSSGAYLTHQQKVLRLYKRALRHLESWCIHRDKYRYFACLLRARFDEHKNEKDMVKAT 60

Query: 62 QLLKEAEEEFW 72
          QLL+EAEEEFW
Sbjct: 61 QLLREAEEEFW 71


>tr|U41534|Q18036|D34BCCB6E8FBCD5F (C16A3.4)SIMILAR TO
          NADH-UBIQUINONE OXIDOREDUCTASE B22.[CAENORHABDITIS
          ELEGANS]
          Length = 163

 Score = 52.7 bits (124), Expect = 3e-07
 Identities = 25/64 (39%), Positives = 41/64 (64%), Gaps = 1/64 (1%)

Query: 10 LTHQQKVLRLYKRALRHLESWCVQRD-KYRYFACLMRARFEEHKNEKDMAKATQLLKEAE 68
          L+H+QKV RLYKR LR +++W    + + R+  C++RARF+ + +E D  K+  LL +
Sbjct: 12 LSHRQKVTRLYKRCLREVDNWYGGNNLEVRFQKCIIRARFDANADEVDTRKSQILLADGC 71

Query: 69 EEFW 72
           + W
Sbjct: 72 RQLW 75
```

Alert BLASTP hits for DKFZphfkd2_3o17, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_3o17, frame 2

Report for DKFZphfkd2_3o17.2

```
[LENGTH]      72
[MW]          8839.28
[pI]          9.26
[HOMOL]       PIR:S28256 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine
2e-34
[KW]          All_Alpha

SEQ     MAFLASGPYLTHQQKVLRLYKRALRHLESWCVQRDKYRYFACLMRARFEEHKNEKDMAKA
PRD     cccccccccchhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhcchhhhhhh

SEQ     TQLLKEAEEEFW
PRD     hhhhhhhhhccc
```

(No Prosite data available for DKFZphfkd2_3o17.2)

(No Pfam data available for DKFZphfkd2_3o17.2)

DKFZphfkd2_46a6
----

group: kidney derived

DKFZphfkd2_46a6 encodes a novel 315 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="228.6 cR from top of Chr15 linkage group"

Insert length: 2774 bp
Poly A stretch at pos. 2751, polyadenylation signal at pos. 2732

```
   1 CTCGCGAGCG CAGCTATGGC TGCTGGCGTA CCCTGTGCGT TAGTCACCAG
  51 CTGCTCCTCC GTCTTCTCAG GAGACCAGCT GGTCCAACAT ACCCTTGGAA
 101 CAGAAGATCT TATTGTGGAA GTGACTTCCA ATGATGCTGT GAGATTTTAT
 151 CCCTGGACCA TTGATAATAA ATACTATTCA GCAGACATCA ATCTATGTGT
 201 GGTGCCAAAC AAATTTCTTG TTACTGCAGA GATTGCAGAA TCTGTCCAAG
 251 CATTTGTGGT TTACTTTGAC AGCACACGAA AATCGGGCCT TGATAGTGTC
 301 TCCTCATGGC TTCCACTGGC AAAAGCATGG TTACCTGAGG TGATGATCTT
 351 GGTCTGCGAT AGAGTGTCTG AAGATGGTAT AAACCGACAA AAAGCTCAAG
 401 AATGGAGCCT CAAACATGGC TTTGAATTGG TAGAACTTAG TCCAGAGGAG
 451 TTGCCTGAGG AGGATGATGA CTTCCCAGAA TCTACAGGAG TAAAGCGAAT
 501 TGTCCAAGCC CTGAATGCCA ATGTGTGGTC CAATGTAGTG ATGAAGAATG
 551 ATAGGAACCA AGGCTTTAGC CTTCTCAACT CATTGACTGG AACAAACCAT
 601 AGCATTGGGT CAGCAGATCC CTGTCACCCA GAGCAACCCC ATTTGCCAGC
 651 AGCAGATAGT ACTGAATCCC TCTCTGATCA TCGGGGTGGT GCATCTAACA
 701 CAACAGATGC CCAGGTTGAT AGCATTGTGG ATCCCATGTT AGATCTGGAT
 751 ATTCAAGAAT TAGCCAGTCT TACCACTGGA GGAGGAGATG TGGAGAATTT
 801 TGAAAGACCC TTTTCAAAGT TAAAGGAAAT GAAAGACAAG GCTGCGACGC
 851 TTCCTCATGA GCAAAGAAAA GTGCATGCAG AAAAGGTGGC CAAAGCATTC
 901 TGGATGGCAA TCGGGGGAGA CAGAGATGAA ATTGAAGGCC TTTCATCTGA
 951 TGGAGAGCAC TGAATTATTC ATACTAGGGT TTGACCAACA AAGATGCTAG
1001 CTGTCTCTGA GATACCTCTC TACTCAGCCC AGTCATATTT TGCCAAAATT
1051 GCCCTTATCA TGTTGGCTGC CTGACTTGTT TATAGGGTCC CCTTAATTTT
1101 AGTTTTTAGT AGGAGGTTAA GGAGAAATCT TTTTTTTCCT CAGTATATTG
1151 TAAGAGAGTG AGGAATACAG TGATAGTAAT GAGTGAGGAT TTCTTAAATA
1201 TACTTTTTTT TTGTTCTAGG AATGAGGGTA GGATAAATCT CAGAGGTCTG
1251 TGTGATTTAC TCAAGTTGAA GACAACCTCC AGGCCATTCC TGGTCAACCT
1301 TTTAAGTAGC ATTTCCAGCA TTCACACTTG ATACTGCACA TCAGGAGTTG
1351 TGTCACCTTT CCTGGGTGAT TTGGGTTTTC TCCATTCAAG GAGCTTGTAG
1401 CTCTGAGCTA TGATGCTTTT ATTGGGAGGA AAGGAGGCAG CTGCAGAATT
1451 GATGTGAGCT ATGTGGGGCC GAAGTCTCAG CCCGCAGCTA AGTCTCTACC
1501 TAAGAAAATG CCTCTGGGCA TTCTTTTGAA GTATAGTGTC TGAGCTCATG
1551 CTAGAAAGAA TCAAAAAGCC AGTGTGGATT TTTAGGCTGT AATAAATGAG
1601 GCAAAGGATT TCTATTCCAG TGGGAAGGAA ACCTCTCTAC TGAGTTGTGG
1651 GGGATATGTT GTATGTTAGA GAGAACCTTA AGGAGTCCTT GTATGGGCCA
1701 TGGAGACAGT ATGTGATAAC ATACCGTGAT TTTCATGAAG AAATTCTTCT
1751 GTCCTAGAGT TCTCCCCTGC TGCTTGAGAT GCCAGAGCTG TGTTGTTGCA
1801 CACCTGCAAA ACAAGGCACA TTTCCCCCTT TCTCTTTAAA GCCAAAGAGA
1851 GATCACTGCC AAAGTGGGAG CACTAAGGGG TGGGTGGGGA AGTGAAATGT
1901 TAGGCGATGA ATTCCTGAGC ACCTTGTTTT TCTTCCAAGG TTCGTAGCTC
1951 CTCTCTGCCC TTCCAAGCCT GTAACCTCGG AGGACTATCT TTTGTTCTCT
2001 ATCCTTTGTC TTGTTAGAGT GGGTCAGCCC CAGAGGAACT GATAAGCAAA
2051 TGGCAAGTTT TTAAAGGAAG AGTGGAAAGT ACTGCAAATA AAAATCCTTA
2101 TTTGTTTTTG TAGACTTTGT AATGCATATC ATTAGCCCTC ACTGTGATCA
2151 TTACTGCTGT GGCTCTGAAC TGGCACATAG TACAGTGGAT GGAAGGTGCC
2201 CGCACACCAG CTGAGAACTG GTTCTGGCCT AGGTGGGCTC TAGAACCATT
2251 TACACAGCAT GAAAGAAACA GGTTGGGTTA GGAGCAGAAA GAAATAAGGC
2301 TCACACCCCT CCAGACACTA CCTTATAAGC ACTGCAGAAC CTGAAACAGA
2351 TGGCAGAAGG AATGGAATGC TACAGGGGCC AGCAGGAGTG ACCACAGGGA
2401 GGGGACAGCT CAGTGACTGG AGCATTCAGG AAGAGGCTTT CCAGGGAACA
2451 CTGGACATTG CTTAGTGACC TTTTGTTCCT TTTTTTTTTT TTTTCTTTTA
2501 CTGTTCTGAA AGACTTTGAG TCTGTGGTTC ACCACCAGCC CATCAGTGTT
2551 TCTTTGAGGT GATTGCATTA GGGAAGTTGG CTCTGGGATT GCAAAAAAAA
2601 AAAAAAGGTG GAACATGTTT TCCTTAAAAG ATGGAAGGTT TTAGAAAATA
2651 TACTAGGCCA TCTGGTTAGA AAAAACAGAC CAGACTAGAA AAAGCTGTGA
```

```
2701 ATTTGATTTT GTAGATTAAA CAAAGCCAGA TGATTAAAAT GTGATTTATT
2751 TATAAAAAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry HS463358 from database EMBL:
human STS WI-14364.
Length = 472
Minus Strand HSPs:
Score = 1605 (240.8 bits), Expect = 5.0e-68, P = 5.0e-68
Identities = 347/361 (96%)

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 16 bp to 960 bp; peptide length: 315
Category: putative protein
Classification: unset

```
  1 MAAGVPCALV TSCSSVFSGD QLVQHTLGTE DLIVEVTSND AVRFYPWTID
 51 NKYYSADINL CVVPNKFLVT AEIAESVQAF VVYFDSTRKS GLDSVSSWLP
101 LAKAWLPEVM ILVCDRVSED GINRQKAQEW SLKHGFELVE LSPEELPEED
151 DDFPESTGVK RIVQALNANV WSNVVMKNDR NQGFSLLNSL TGTNHSIGSA
201 DPCHPEQPHL PAADSTESLS DHRGGASNTT DAQVDSIVDP MLDLDIQELA
251 SLTTGGGDVE NFERPFSKLK EMKDKAATLP HEQRKVHAEK VAKAFWMAIG
301 GDRDEIEGLS SDGEH
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46a6, frame 1

PIR:T04362 probable GTP-binding protein yptm3 - maize, N = 1, Score = 87, P = 0.21

PIR:S71585 GTP-binding protein GB2 - Arabidopsis thaliana, N = 1, Score = 86, P = 0.27

```
>PIR:T04362 probable GTP-binding protein yptm3 - maize
          Length = 210

  HSPs:

 Score = 87 (13.1 bits), Expect = 2.4e-01, P = 2.1e-01
 Identities = 34/160 (21%), Positives = 67/160 (41%)

Query:    48 TIDNKYYSADINLCVVPNKFL-VTAEIAESVQAFVVYFDSTRKSGLDSVSSWLPLAKAWL 106
             TIDNK      I         F  +T             ++ +D TR+    + ++SWL  A+
Sbjct:    49 TIDNKPIKLQIWDTAGQESFRSITRSYYRGAAGALLVYDITRRETFNHLASWLEDARQHA 108

Query:   107 PE---VMIL--VCDRVSEDGINRQKAQEWSLKHGFELVELSPEELPEEDDDFPESTGVKR 161
                  VM++   CD       ++ ++ ++++ +HG   +E S +      ++ F ++ G
Sbjct:   109 NANMTVMLIGNKCDLSHRRAVSYEEGEQFAKEHGLVFMEASAKTAQNVEEAFIKTAGT-- 166

Query:   162 IVQALNANVWSNVVMKNDRNQGFSLLNSLTGTNHSIGSADPC 203
             I + +   ++       N    G+++ NS  G    S  A  C
Sbjct:   167 IYKKIQDGIFDVSNESNGIKVGYAVPNSSGGGAGSSSQAGGC 208
```

Pedant information for DKFZphfkd2_46a6, frame 1

Report for DKFZphfkd2_46a6.1

[LENGTH] 315

```
[MW]        34505.54
[pI]        4.55
[KW]        Alpha_Beta
[KW]        LOW_COMPLEXITY      6.67 %

SEQ    MAAGVPCALVTSCSSVFSGDQLVQHTLGTEDLIVEVTSNDAVRFYPWTIDNKYYSADINL
SEG    ............................................................
PRD    cccccceeeeecccccccccceeeecccccceeeeeeccccceeeeecccccccccccee

SEQ    CVVPNKFLVTAEIAESVQAFVVYFDSTRKSGLDSVSSWLPLAKAWLPEVMILVCDRVSED
SEG    ............................................................
PRD    eeecccchhhhhhhhheeeeeeeccccccccccccccccccccccceeeeccccccccc

SEQ    GINRQKAQEWSLKHGFELVELSPEELPEEDDDFPESTGVKRIVQALNANVWSNVVMKNDR
SEG    ...............xxxxxxxxxxxxxxxxxxxxx........................
PRD    cchhhhhhhhhhhhcccceeeecccccccccccccccccchhhhhhhcccceeeeeeeccc

SEQ    NQGFSLLNSLTGTNHSIGSADPCHPEQPHLPAADSTESLSDHRGGASNTTDAQVDSIVDP
SEG    ............................................................
PRD    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccccch

SEQ    MLDLDIQELASLTTGGGDVENFERPFSKLKEMKDKAATLPHEQRKVHAEKVAKAFWMAIG
SEG    ............................................................
PRD    hhhhhhhhhhhccccccccccchhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhhhhhc

SEQ    GDRDEIEGLSSDGEH
SEG    ...............
PRD    ccccccccccccccc
```

(No Prosite data available for DKFZphfkd2_46a6.1)

(No Pfam data available for DKFZphfkd2_46a6.1)

DKFZphfkd2_46b10
----

group: kidney derived

DKFZphfkd2_46b10.1 encodes a novel 315 amino acid protein with similarity to C.elegans cosmide F25B5.3

The novel protein contains a HTH-LYSR-family PROSITE pattern. Proteins of the lysR family are bacterial transcriptional regulatory proteins which bind DNA using a helix-turn-helix motif. Most of these proteins are transcription activators and usually negatively regulate their own expression. They all possess a potential 'helix-turn-helix' DNA-binding motif in their N-terminal section. The 'helix-turn-helix' motif is missing in DKFZphfkd2_46a6.1.
No informative BLAST results, no predictive PFAM or SCOP motive.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to C.elegans F25B5.3

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: unknown

Insert length: 1285 bp
Poly A stretch at pos. 1266, no polyadenylation signal found

```
   1 CAGTCTACGC GAGCTGCCTG TTTTTTTCCT GCTTGGACGC GCATGAGGGC
  51 CCCGTCCATG GACCGCGCGG CCGTGGCGAG GGTGGGCGCG GTAGCGAGCG
 101 CCAGCGTGTG CGCCCTGGTG GCGGGGGTGG TGCTGGCTCA GTACATATTC
 151 ACCTTGAAGA GGAAGACGGG GCGGAAGACC AAGATCATCG AGATGATGCC
 201 AGAATTCCAG AAAAGTTCAG TTCGAATCAA GAACCCTACA AGAGTAGAAG
 251 AAATTATCTG TGGTCTTATC AAAGGAGGAG CTGCCAAACT TCAGATAATA
 301 ACGGACTTTG ATATGACACT CAGTAGATTT TCATATAAAG GGAAAAGATG
 351 CCCAACATGT CATAATATCA TTGACAACTG TAAGCTGGTT ACGGATGAAT
 401 GTAGAAAAAA GTTATTGCAA CTAAAGGAAA AATATTACGC TATTGAAGTT
 451 GATCCTGTTC TTACTGTAGA AGAGAAGTAC CCTTATATGG TGGAATGGTA
 501 TACTAAATCA CATGGTTTGC TTGTTCAGCA AGCTTTACCA AAAGCTAAAC
 551 TTAAAGAAAT TGTGGCAGAA TCTGACGTTA TGCTCAAAGA AGGATATGAG
 601 AATTTCTTTG ATAAGCTCCA ACAACATAGC ATCCCCGTGT TCATATTTTC
 651 GGCTGGAATC GGCGATGTAC TAGAGGAAGT TATTCGTCAA GCTGGTGTTT
 701 ATCATCCCAA TGTCAAAGTT GTGTCCAATT TTATGGATTT TGATGAAACT
 751 GGGGTGCTCA AAGGATTTAA AGGAGAACTA ATTCATGTAT TTAACAAACA
 801 TGATGGTGCC TTGAGGAATA CAGAATATTT CAATCAACTA AAAGACAATA
 851 GTAACATAAT TCTTCTGGGA GACTCCCAAG GAGACTTAAG AATGGCAGAT
 901 GGAGTGGCCA ATGTTGAGCA CATTCTGAAA ATTGGATATC TAAATGATAG
 951 AGTGGATGAG CTTTTAGAAA AGTACATGGA CTCTTATGAT ATTGTTTTAG
1001 TACAAGATGA ATCATTAGAA GTAGCCAACT CTATTTTACA GAAGATTCTA
1051 TAAACAAGCA TTCTCCAAGA AGACCTCTCT CCTGTGGGTG CAATTGAACT
1101 GTTCATCCGT TCATCTTGCT GAGAGACTTA TTTATAATAT ATCCTTACTC
1151 TCGAAGTGTT CCCTTTGTAT AACTGAAGTA TTTTCAGATA TGGTGAATGC
1201 ATTGACTGGA AGCTCCTTTT CTCCACCTCT CTCAACACAC TCCTCACCGT
1251 ATCTTTTAAC CCATTTAAAA AAAAAAAAAA AAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 43 bp to 1050 bp; peptide length: 336
Category: similarity to unknown protein
Classification: unset
Prosite motifs: HTH_LYSR_FAMILY (16-47)

```
  1 MRAPSMDRAA VARVGAVASA SVCALVAGVV LAQYIFTLKR KTGRKTKIIE
 51 MMPEFQKSSV RIKNPTRVEE IICGLIKGGA AKLQIITDFD MTLSRFSYKG
101 KRCPTCHNII DNCKLVTDEC RKKLLQLKEK YYAIEVDPVL TVEEKYPYMV
151 EWYTKSHGLL VQQALPKAKL KEIVAESDVM LKEGYENFFD KLQQHSIPVF
201 IFSAGIGDVL EEVIRQAGVY HPNVKVVSNF MDFDETGVLK GFKGELIHVF
251 NKHDGALRNT EYFNQLKDNS NIILLGDSQG DLRMADGVAN VEHILKIGYL
301 NDRVDELLEK YMDSYDIVLV QDESLEVANS ILQKIL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46b10, frame 1

SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III., N = 1, Score = 524, P = 2.2e-50

TREMBL:AC005499_12 gene: "T6A23.12"; Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence., N = 2, Score = 194, P = 1.4e-26

```
>SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME
     III.
          Length = 376

  HSPs:

 Score = 524 (78.6 bits), Expect = 2.2e-50, P = 2.2e-50
 Identities = 112/300 (37%), Positives = 174/300 (58%)

Query:    44 RKTKIIEMMPEFQ--KSSVRIKNPTRVEEIICGLIKGGAAKLQIITDFDMTLSRFSYK-G 100
             +KT ++ ++  +    + + +PT V   +  ++ GGA K  +I+DFD TLSRF+ + G
Sbjct:    73 KKTDVVPLLMNYLLGEEQILVADPTAVAAKLRKMVVGGAGKTVVISDFDYTLSRFANEQG 132

Query:   101 KRCPTCHNIID-NCKLVTDECRKKLLQLKEKYYAIEVDPVLTVEEKYPYMVEWYTKSHGL 159
             +R  T H + D N    +  E  +K + LK KYY IE  P LT+EEK P+M +W+  SH L
Sbjct:   133 ERLSTTHGVFDDNVMRLKPELGQKFVDLKNKYYPIEFSPNLTMEEKIPHMEKWWGTSHSL 192

Query:   160 LVQQALPKAKLKEIVAESDVMLKEGYENFFDKLQQHSIPVFIFSAGIGDVLEEVIRQA-G 218
             +V +    K  +++ V +S ++ K+G E+F + L  H+IP+ IFSAGIG+++E  ++Q  G
Sbjct:   193 IVNEKFSKNTIEDFVRQSRIVFKDGAEDFIEALDAHNIPLVIFSAGIGNIIEYFLQQKLG 252

Query:   219 VYHPNVKVVSNFMDFDETGVLKGFKGELIHVFNKHDGAL-RNTEYFNQLKDNSNIILLGD 277
                 N   +SN + FDE         F   LIH F K+   + + T +F+ +    N+ILLGD
Sbjct:   253 AIPRNTHFISNMILFDEDDNACAFSEPLIHTFCKNSSVIQKETSFFHDIAGRVNVILLGD 312

Query:   278 SQGDLRMADGVANVEHILKIGYLNDRVDEL--LEKYMDSYDIVLVQDESLEVANSILQKI 335
             S GD+ M  GV       LK+GY N  +D+   L+ Y + YDIVL+ D +L VA  I+  I
Sbjct:   313 SMGDIHMDVGVERDGPTLKVGYYNGSLDDTAALQHYEEVYDIVLIHDPTLNVAQKIVDII 372
```

Pedant information for DKFZphfkd2_46b10, frame 1

Report for DKFZphfkd2_46b10.1

```
[LENGTH]        336
[MW]            37948.37
[pI]            6.67
[HOMOL]         SWISSPROT:YQT3_CAEEL HYPOTHETICAL 42.0 KD PROTEIN F25B5.3 IN CHROMOSOME III.
3e-51
[PROSITE]       HTH_LYSR_FAMILY         1
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY      7.44 %

SEQ      MRAPSMDRAAVARVGAVASASVCALVAGVVLAQYIFTLKRKTGRKTKIIEMMPEFQKSSV
SEG      .......xxxxxxxxxxxxxxxxxxxxxxx............................
PRD      ccchhhhhcchhhhhhheeehhhhhhhhhhhhhhhhhhhhhccceeeehhhhhhhhee
MEM      .............MMMMMMMMMMMMMMMMMMMMMMMMMMMM.................

SEQ      RIKNPTRVEEIICGLIKGGAAKLQIITDFDMTLSRFSYKGKRCPTCHNIIDNCKLVTDEC
SEG      ............................................................
PRD      eccccchhhhhhhhhhccccceeeeecccccceeeecccccccccccccccccchhhhhh
MEM      ............................................................
```

```
SEQ      RKKLLQLKEKYYAIEVDPVLTVEEKYPYMVEWYTKSHGLLVQQALPKAKLKEIVAESDVM
SEG      ............................................................
PRD      hhhhhhhhhhhheeecccccccccccchhhhhhccccchhhhhhcchhhhhhhhhhhhcc
MEM      ............................................................

SEQ      LKEGYENFFDKLQQHSIPVFIFSAGIGDVLEEVIRQAGVYHPNVKVVSNFMDFDETGVLK
SEG      ............................................................
PRD      ccccchhhhhhhhhcccceeeeecccchhhhhhhhhhcccccceeeeeeecccccccccee
MEM      .............MMMMMMMMMMMMMMMMMMM............................

SEQ      GFKGELIHVFNKHDGALRNTEYFNQLKDNSNIILLGDSQGDLRMADGVANVEHILKIGYL
SEG      ............................................................
PRD      eccceeeeeeeccccccccccchhhhhhhceeeeeeccccccccccccccccccceeeeeec
MEM      ............................................................

SEQ      NDRVDELLEKYMDSYDIVLVQDESLEVANSILQKIL
SEG      ....................................
PRD      cchhhhhhhhhhhheeeeeecchhhhhhhhhhhccc
MEM      ....................................
```

Prosite for DKFZphfkd2_46b10.1

```
PS00044      16->47   HTH_LYSR_FAMILY      PDOC00043
```

(No Pfam data available for DKFZphfkd2_46b10.1)

DKFZphfkd2_46d13
----

group: kidney derived

DKFZphfkd2_46d13 encodes a novel 506 amino acid protein with weak similarity to KE03 protein

The novel protein contains a RGD site.
No informative BLAST results; No predictive prosite, pfam or SCOP motive

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to KE03 protein

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="227.6 cR from top of Chr1 linkage group"

Insert length: 3346 bp
Poly A stretch at pos. 3328, polyadenylation signal at pos. 3308

```
   1 CTCTCGCGAG AGGAGCAAGA GGAAGATGGC CGTGCCCTGT TTTTCGGTGT
  51 AAGGCAGCAG ACGGCGGCTG CGACGGCGAG ACTGAGATCC TGGTGTCGTG
 101 GGCACCTGAG TTCTAGCTTC CCCCAGCGAG CGCGCGTCCC TTCGTGCCTA
 151 GGCGAGAGCC GGCTCTTCCC CGGGAGATGC GTTTGTCCCA GGCTCGGGGG
 201 CTCAGTGGGA GTTCATGCTG CGCTGGAGGC TCTTGGCCAC CGCTCTAATC
 251 GCCTTGTGCC GCCGCAGCGC CAGCTCCGTC GCCAGCGGTG AGCCTCCCGA
 301 TTCCCCCCCT TGCCCCTGGC GGCGGCGATG ACCGGGGAGA AGATCCGCTC
 351 ACTGCGGAGG GACCACAAGC CCAGCAAAGA AGAAGGGGAC CTGCTGGAGC
 401 CCGGGGATGA AGAAGCGGCG GCTGCCCTCG GCGGTACCTT TACCAGAAGC
 451 AGGATTGGCA AGGGCGGCAA AGCTTGTCAT AAGATCTTCA GTAACCATCA
 501 CCACCGGCTA CAGCTGAAGG CAGCTCCGGC CTCCTCCAAT CCCCCCGGCG
 551 CCCCGGCTCT GCCGCTGCAC AATTCCTCCG TGACTGCCAA CTCCCAGTCC
 601 CCGGCCCTTC TGGCCGGCAC CAACCCCGTT GCTGTCGTCG CGGATGGAGG
 651 CAGTTGCCCC GCACACTACC CGGTGCACGA GTGCGTCTTC AAGGGGGATG
 701 TGAGGAGACT CTCCTCTCTC ATCCGCACGC ACAATATCGG GCAGAAAGAT
 751 AATCACGGAA ATACTCCTTT ACACCTTGCT GTGATGTTAG GAAATAAAGT
 801 TACAGCTCTT TTGAGGAAGC TTAAGCAGCA ATCCAGGGAA AGTGTTGAAG
 851 AAAAACGACC TCGATTATTA AAAGCCCTGA AAGAGCTAGG TGACTTTTAT
 901 CTAGAACTTC ACTGGGATTT TCAAAGCTGG GTGCCTTTAC TTTCCCGAAT
 951 TCTGCCTTCC GATGCATGTA AAATATACAA ACAAGGTATC AATATCAGGC
1001 TTGACACAAC TCTCATAGAC TTTACTGACA TGAAGTGCCA ACGAGGGGAT
1051 CTAAGCTTCA TTTTCAATGG GGATGCGGCG CCCTCTGAAT CTTTTGTAGT
1101 ATTAGACAAT GAACAAAAAG TTTATCAGCG AATACATCAT GAGGAATCAG
1151 AGATGGAAAC AGAAGAAGAG GTGGATATTT TAATGAGCAG TGATATTTAC
1201 TCTGCAACTT TATCAACAAA ATCAATTTCT TTCACGCGTG CCCAGACAGG
1251 ATGGCTTTTT CGGGAAGATA AAACAGAAAG AGTAGGAAAC TTTTTGGCAG
1301 ACTTTTACCT GGTGAATGGA CTTGTTATAG AATCAAGGAA AAGAAGAGAA
1351 CATCTCAGTG AAGAGGATAT TCTTCGAAAT AAGGCCATCA TGGAGAGTTT
1401 GAGTAAAGGT GGAAACATAA TGGAACAGAA TTTTGAGCCG ATTCGAAGAC
1451 AGTCTCTTAC ACCGCCTCCT CAGAACACTA TTACATGGGA AGAATATATA
1501 TCTGCTGAAA ATGGAAAAGC TCCTCATCTG GGTAGAGAAT TGGTGTGCAA
1551 AGAGAGTAAG AAAACGTTTA AAGCTACGAT AGCCATGAGC CAGGAATTTC
1601 CCTTAGGGAT AGAGTTATTA TTGAATGTTT TAGAAGTAGT AGCTCCCTTC
1651 AAGCACTTTA ACAAGCTTAG AGAATTTGTT CAGATGAAGC TTCCTCCAGG
1701 CTTTCCTGTA AAATTAGATA TACCTGTGTT TCCCACAATC ACAGCCACTG
1751 TGACTTTTCA GGAGTTTCGA TACGATGAAT TTGATGGCTC CATCTTTACT
1801 ATACCTGATG ACTACAAGGA AGACCCAAGC CGTTTTCCTG ATCTTTAACT
1851 GACGTGGAAA AGGATGCCGT CTAACCAAGG AAAGAAAATA CAGAGACCCT
1901 AGAAGTGGAT CCAAATAGAA GGGACAAATG CTTTCAGTGA AGAAAAGGGA
1951 ATTACACATT GAATCGACAC ATCAGTAATA CGATACAGTG AAATGGGCCT
2001 CTAATAAGAA TTTCAGCGAG TTTTCTGATG TGCCATTTTT TGTCTTTTTA
2051 AAAATATACA TATTATAAAT GTAATAGTTT GACACATTAA TGACCCTAAG
2101 ACCTGCGTAT GTGAAGCAGC TATGAGTGCT GTGATTTGTT TTTAAAAATT
2151 TTTACACTTC TTGTTGAAAT ATATATGCAT ATAAATATAT CTATATCTAT
2201 ATCTATATCT AAAACACTCC TGGACCATTA ACGTAAATTA AATGTCTTAA
2251 GAGATATGGA GCCCTTTTAA ACTTGTCATC TTTATGCAAG GTGACATTTA
2301 TAAATATTCC TTCGAGCTTT GTTTTCATAA AATGTAAACT ATGTAACATT
2351 ATGTATAGTT CAGTAATTTG AATGTTTGTT CAATATAATG AACTAGAAGG
2401 AATGCAATTT TCTGTAGATG AATGAACCAA ATGGTAACCA TTAAACAATT
2451 GCATTTATAT GTTGCAATAC ATTTCAGAAG GAGCGTTCAC TCTGCAGGGA
2501 ATAAGGTACC TCCTTTAGCA CCTTAGTGCA ATTCATTGTG GTGCTATTTG
2551 TTTTTACCTG AATGTTTGTT ACTAATCTTC CTTTCATAGA ACCTCTATTT
2601 TTTTTTTTTC TAAACTTGAG TTTGAGTCCT TGTTATGGTC ATCATAAGGT
```

```
2651 AATGGTTAGC ATGTTTAAAG ATATTCCTCT TCCAAATCTC AGCACTTTAA
2701 AAAAAAATCC AAATTTTTAA ACTTGCTTCC TAATAAGTAC ACATCGGTCT
2751 GATTATTTTG TTTGTTTTTA GTAGAATATG GATGCATTGG TGTCAGTTTT
2801 AAAAAACAAT ACACATATTT TGGACAACCC TACATATTTA ATCCTTTCAA
2851 AATAAGATAA AAACATTTTA TATGCTAACA GAATATATTT GTTACAAGTT
2901 AAAGTCCAGA AGTATACACA AGATTGATTA CTCCTATTAT TTTTTTTAAA
2951 TCACAGGAAA ATATTGATTT CATTGTCTCC AAAGTGATAA AATCTTGTAT
3001 TACTCATTTT TGCACTTAAA ATTTTTCTTA TTTATTCCAA GGTGGTTTGA
3051 AGGTCCAAGT ATGAAAATAA ATTAGGGGGA TTAATGTATA ACAGTTATAA
3101 AGTATCATGT TGTATTAAAG AGCTTACTTA GATTGATGTT TTTAAAATGT
3151 ATCCTGATGA ATGTCTCAAG AATGCATCTG TCAAGTTTTT TAGACTGACC
3201 AGTAGCTTAA ACTTTTTTCA GGATTTTAGG TAATTTGAAA GGAGTTTAGA
3251 GACCCTTATT GAAAATATGA TTTAAAAATC CAAAGCATAA ACCGTAAGAA
3301 AAATTTTAAA TAAACATCTT TAAAGCTGAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HS121353 from database EMBL:
human STS WI-14729.
Score = 1697, P = 1.9e-69, identities = 363/379

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 328 bp to 1845 bp; peptide length: 506
Category: similarity to unknown protein

```
  1 MTGEKIRSLR RDHKPSKEEG DLLEPGDEEA AAALGGTFTR SRIGKGGKAC
 51 HKIFSNHHHR LQLKAAPASS NPPGAPALPL HNSSVTANSQ SPALLAGTNP
101 VAVVADGGSC PAHYPVHECV FKGDVRRLSS LIRTHNIGQK DNHGNTPLHL
151 AVMLGNKVTA LLRKLKQQSR ESVEEKRPRL LKALKELGDF YLELHWDFQS
201 WVPLLSRILP SDACKIYKQG INIRLDTTLI DFTDMKCQRG DLSFIFNGDA
251 APSESFVVLD NEQKVYQRIH HEESEMETEE EVDILMSSDI YSATLSTKSI
301 SFTRAQTGWL FREDKTERVG NFLADFYLVN GLVIESRKRR EHLSEEDILR
351 NKAIMESLSK GGNIMEQNFE PIRRQSLTPP PQNTITWEEY ISAENGKAPH
401 LGRELVCKES KKTFKATIAM SQEFPLGIEL LLNVLEVVAP FKHFNKLREF
451 VQMKLPPGFP VKLDIPVFPT ITATVTFQEF RYDEFDGSIF TIPDDYKEDP
501 SRFPDL
```

BLASTP hits

Entry CEC01F1_3 from database TREMBL:
gene: "C01F1.6"; Caenorhabditis elegans cosmid C01F1.
Score = 371, P = 4.5e-61, identities = 69/138, positives = 96/138

Entry CEC18F10_9 from database TREMBL:
gene: "C18F10.7"; Caenorhabditis elegans cosmid C18F10.
Score = 383, P = 3.4e-39, identities = 103/349, positives = 182/349

Entry AF064604_1 from database TREMBL:
product: "KE03 protein"; Homo sapiens KE03 protein mRNA, partial cds.
Score = 348, P = 8.3e-32, identities = 95/295, positives = 148/295

Alert BLASTP hits for DKFZphfkd2_46d13, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_46d13, frame 1

Report for DKFZphfkd2_46d13.1

[LENGTH]	506
[MW]	57003.12
[pI]	6.40

```
[HOMOL]        TREMBL:CEC18F10_9 gene: "C18F10.7"; Caenorhabditis elegans cosmid C18F10. 2e-35

[BLOCKS]       BL01288E
[PROSITE]      RGD       1
[PROSITE]      MYRISTYL        7
[PROSITE]      CAMP_PHOSPHO_SITE     2
[PROSITE]      CK2_PHOSPHO_SITE      9
[PROSITE]      PKC_PHOSPHO_SITE      6
[PROSITE]      ASN_GLYCOSYLATION     1
[KW]           Alpha_Beta
[KW]           LOW_COMPLEXITY     7.51 %

SEQ   MTGEKIRSLRRDHKPSKEEGDLLEPGDEEAAAALGGTFTRSRIGKGGKACHKIFSNHHHR
SEG   ................xxxxxxxxxxxx................................
PRD   ccceeeeeccccccccccccccccccchhhhhhccccccccccccceeeeeeecchhhh

SEQ   LQLKAAPASSNPPGAPALPLHNSSVTANSQSPALLAGTNPVAVVADGGSCPAHYPVHECV
SEG   ....xxxxxxxxxxxxxxx.........................................
PRD   hhhhhhcccccccccceeeccccccccccccccceeecccccceeeecccccccccccceee

SEQ   FKGDVRRLSSLIRTHNIGQKDNHGNTPLHLAVMLGNKVTALLRKLKQQSRESVEEKRPRL
SEG   ............................................................
PRD   ecchhhhhhhhhhcccccccccccccceeeeccchhhhhhhhhhhcchhhhhhhhhh

SEQ   LKALKELGDFYLELHWDFQSWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRG
SEG   ............................................................
PRD   hhhhhhcccccceeehhhhhcccceeeeccccccceeeeecccceeeeeeeeccccccccc

SEQ   DLSFIFNGDAAPSESFVVLDNEQKVYQRIHHEESEMETEEEVDILMSSDIYSATLSTKSI
SEG   ..............................xxxxxxxxxx....................
PRD   ceeeeecccceeeeeeeeeccccceeehhhhhhhhhhhhhhhhhhccceeeecccccc

SEQ   SFTRAQTGWLFREDKTERVGNFLADFYLVNGLVIESRKRREHLSEEDILRNKAIMESLSK
SEG   ............................................................
PRD   eeeeccccceeeecccchhhhhhheeeeeeeeeeeeehhhhhhhhhhhhhhhhhhhhhhc

SEQ   GGNIMEQNFEPIRRQSLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIAM
SEG   ............................................................
PRD   cceeeccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhh

SEQ   SQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKLDIPVFPTITATVTFQEF
SEG   ............................................................
PRD   hhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhcccccceeeeeeeeeeeehhhhhhhcc

SEQ   RYDEFDGSIFTIPDDYKEDPSRFPDL
SEG   ..........................
PRD   cccccccceeecccccccccccccc
```

Prosite for DKFZphfkd2_46d13.1

PS00001	82->86	ASN_GLYCOSYLATION	PDOC00001
PS00004	126->130	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	373->377	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	8->11	PKC_PHOSPHO_SITE	PDOC00005
PS00005	296->299	PKC_PHOSPHO_SITE	PDOC00005
PS00005	316->319	PKC_PHOSPHO_SITE	PDOC00005
PS00005	336->339	PKC_PHOSPHO_SITE	PDOC00005
PS00005	410->413	PKC_PHOSPHO_SITE	PDOC00005
PS00005	413->416	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	172->176	CK2_PHOSPHO_SITE	PDOC00006
PS00006	228->232	CK2_PHOSPHO_SITE	PDOC00006
PS00006	274->278	CK2_PHOSPHO_SITE	PDOC00006
PS00006	278->282	CK2_PHOSPHO_SITE	PDOC00006
PS00006	344->348	CK2_PHOSPHO_SITE	PDOC00006
PS00006	386->390	CK2_PHOSPHO_SITE	PDOC00006
PS00006	476->480	CK2_PHOSPHO_SITE	PDOC00006
PS00006	491->495	CK2_PHOSPHO_SITE	PDOC00006
PS00008	35->41	MYRISTYL	PDOC00008
PS00008	46->52	MYRISTYL	PDOC00008
PS00008	108->114	MYRISTYL	PDOC00008
PS00008	138->144	MYRISTYL	PDOC00008
PS00008	155->161	MYRISTYL	PDOC00008
PS00008	320->326	MYRISTYL	PDOC00008
PS00008	487->493	MYRISTYL	PDOC00008
PS00016	239->242	RGD	PDOC00016

(No Pfam data available for DKFZphfkd2_46d13.1)

DKFZphfkd2_46j20

group: metabolism

DKFZphfkd2_346j20 encodes a novel 224 amino acid protein similar to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.

The new protein seems to be the human ortholog of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase.

The new protein can find application in modulating the homoprotocatechuate degradative pathway and as a enzyme for biotechnologic production processes.

strong similarity to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase

complete cDNA, complete cds, EST hits,
potential start at Bp 16 matches kozak consensus ANCatgG
strong similarity to proteins of worm plant archea and bacteria
2-hydroxyhepta-2,4-diene-1,7-dioate isomerase is part of
the tyrosine metabolism (degradation of tyrosine late step) EC 5.3.1.-
complete cds according to similar C.elegans and A.thaliana protein

Sequenced by MediGenomix

Locus: unknown

Insert length: 1706 bp
Poly A stretch at pos. 1686, polyadenylation signal at pos. 1667

```
   1 CACTTGATGG GAATCATGGC AGCATCCAGG CCATTGTCCC GCTTCTGGGA
  51 GTGGGGAAAG AACATCGTCT GCGTGGGGAG GAACTACGCG GACCACGTCA
 101 GGGAGATGCG CAGCGCGGTG TTGAGCGAGC CCGTGCTGTT CCTGAAGCCG
 151 TCCACGGCCT ACGCGCCCGA GGGCTCGCCC ATCCTCATGC CCGCGTACAC
 201 TCGCAACCTG CACCACGAGC TGGAGCTGGG CGTGGTGATG GGCAAGCGCT
 251 GCCGCGCAGT CCCCGAGGCT GCGGCCATGG ACTACGTGGG CGGCTATGCC
 301 CTGTGCCTGG ATATGACCGC CCGGGACGTG CAGGACGAGT GCAAGAAGAA
 351 GGGGCTGCCC TGGACTCTGG CGAAGAGCTT CACGGCGTCC TGCCCGGTCA
 401 GCGCGTTCGT GCCCAAGGAG AAGATCCCTG ACCCTCACAA GCTGAAGCTC
 451 TGGCTCAAGG TCAACGGCGA ACTCAGACAG GAGGGTGAGA CATCCTCCAT
 501 GATTTTTTCC ATCCCCTACA TCATCAGCTA TGTTTCTAAG ATCATAACCT
 551 TGGAAGAAGG AGATATTATC TTGACTGGGA CGCCAAAGGG AGTTGGACCG
 601 GTTAAAGAAA ACGATGAGAT CGAGGCTGGC ATACACGGGC TGGTCAGTAT
 651 GACATTTAAA GTGGAAAAGC CAGAATATTG AGTTATTTCT TAACAAGTTT
 701 CGAGAGAGAA GGGAGCAAGA CAAGAGCAAG CAACGGCTAT TAAATGTCAC
 751 AATCCTTTAA TTAGAAACCA TTTATTGGCC GGACGCGGTG GCTCACGCCT
 801 GTAATCGCAG CACTTTGGGA GGCCGAGGCG GGCGGCTCAC GACGTCAGGA
 851 GATCCAGACC ATCTTGGCTA ACAGGGTGAA ACCCCGTCTC TACTAAAAAT
 901 ACAAAAAATT AGCCGGGCGT GGTGGCGGGC GCCTGTAGTC CCAGCTACTC
 951 TGGAGGCTGA GGCAGGAGAA TCAATTGAAC CCGGGAGGCG GAGCTTACAG
1001 TGAGCTGAGA TTGCGCCACT GTACTCCTGG GCAACAGCGA GACTCCGTCT
1051 CAAAAAAAAA AAAAAAAAAA AGAAACCATT TATTTTAAAA ATGATTAGAT
1101 TGCTATGCCT CAACTCATAG AAGATGAACC CTTCAAGAAA ACGTGAAGTA
1151 GAACGGGTGG GCCAGAAATG AAAACAGGCA AGTAAAGTAT TTCTTCGGAA
1201 AACATTTTAT CAAACCAAAT GTTAAAAAGA CTTTCCTTTT GTAAAACTGG
1251 ATTAGAGAAG ACTTTTCAGT GGGTTATCTC TAGGATGATC AGTAGTTCAG
1301 CACTTAAAAA CTGCAGAGAA AACTGAAAGT TATGTTCCAG ATAACTTTCC
1351 GTTGTTTACC AAATTTTCTT AGATTTGGTC ATCATCAGGA AGCATTTGTA
1401 AAAATAAAAA TCTCCACAAA TTACTGGCCC ATCTCGGACT TGCTGAATCA
1451 ATTTGATAGG ATTAATCTCC AGTGAAGCTG TGTTTACAGG GCATTCCAAG
1501 TGATTCTTAT CAGGAAATGT GAAAAACACT CCTGTACATA ATCGGTTAAT
1551 TTAAAATTTT ACTTAATAAG TGAACAAGTA ATGAAGATTT CACCTGTTTA
1601 CTTAGGGTAT CTACCCAGAC CCATCGATTC TGAGTTCGGG AGATGATTTT
1651 GAAATTACTG TTTTCCAAAT AAAGGTGCTC CCTTCCAAAA AAAAAAAAAA
1701 AAAAAA
```

BLAST Results

No BLAST result

Medline entries

94039092: Purification, nucleotide sequence and some properties of a bifunctional isomerase/decarboxylase from the homoprotocatechuate degradative pathway of Escherichia coli C.

Peptide information for frame 1

ORF from 7 bp to 678 bp; peptide length: 224
Category: strong similarity to known protein

```
    1 MGIMAASRPL SRFWEWGKNI VCVGRNYADH VREMRSAVLS EPVLFLKPST
   51 AYAPEGSPIL MPAYTRNLHH ELELGVVMGK RCRAVPEAAA MDYVGGYALC
  101 LDMTARDVQD ECKKKGLPWT LAKSFTASCP VSAFVPKEKI PDPHKLKLWL
  151 KVNGELRQEG ETSSMIFSIP YIISYVSKII TLEEGDIILT GTPKGVGPVK
  201 ENDEIEAGIH GLVSMTFKVE KPEY
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46j20, frame 1

PIR:S44919 ZK688.3 protein - Caenorhabditis elegans, N = 1, Score = 537, P = 8.7e-52

PIR:D71109 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase - Pyrococcus horikoshii, N = 1, Score = 529, P = 6.1e-51

PIR:C71425 hypothetical protein - Arabidopsis thaliana, N = 1, Score = 519, P = 7e-50

PIR:A64864 probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180 - Escherichia coli, N = 1, Score = 474, P = 4.1e-45

```
>PIR:S44919 ZK688.3 protein - Caenorhabditis elegans
            Length = 214

  HSPs:

 Score = 537 (80.6 bits), Expect = 8.7e-52, P = 8.7e-52
 Identities = 99/211 (46%), Positives = 138/211 (65%)

Query:    10 LSRFWEWGKNIVCVGRNYADHVREMRSAVLSEPVLFLKPSTAYAPEGSPILMPAYTRNLH 69
             L+ F       IVCVGRNY DH  E+ +A+  +P+LF+K    ++  EG PI+ P   +NLH
Sbjct:     4 LAGFRNLATKIVCVGRNYKDHALELGNAIPKKPMLFVKTVNSFIVEGEPIVAPPGCQNLH 63

Query:    70 HELELGVVMGKRCRAVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWTLAKSFTASC 129
              E+ELGVV+ K+   + ++ AMDY+GGY + LDMTARD QDE KK G PW LAKSF  SC
Sbjct:    64 QEVELGVVISKKASRISKSDAMDYIGGYTVALDMTARDFQDEAKKAGAPWFLAKSFDGSC 123

Query:   130 PVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPYIISYVSKIITLEEGDIIL 189
             P+  F+P   IP+PH ++L+ K+NG+ +Q   T  MIF IP ++ Y ++  TLE GD++L
Sbjct:   124 PIGGFLPVSDIPNPHDVELFCKINGKDQQRCRTDVMIFDIPTLLEYTTQFFTLEVGDVVL 183

Query:   190 TGTPKGVGPVKENDEIEAGIHGLVSMTFKVE 220
             TGTP GV  +    D IE G+    ++  F V+
Sbjct:   184 TGTPAGVTKINSGDVIEFGLTDKLNSKFNVQ 214
```

Pedant information for DKFZphfkd2_46j20, frame 1

Report for DKFZphfkd2_46j20.1

```
[LENGTH]     224
[MW]         24843.07
[pI]         6.96
[HOMOL]      PIR:S44919 ZK688.3 protein - Caenorhabditis elegans 8e-55
[FUNCAT]     r general function prediction        [M. jannaschii, MJ1656] 9e-40
[FUNCAT]     99 unclassified proteins      [S. cerevisiae, YNL168c] 4e-38
[EC]         5.3.3.10 5-Carboxymethyl-2-hydroxymuconate delta-isomerase 1e-35
[PIRKW]      isomerase 1e-35
[PIRKW]      intramolecular oxidoreductase 1e-35
[SUPFAM]     2-hydroxyhepta-2,4-diene-1,7-dioate isomerase 1e-46
[PROSITE]    MYRISTYL      4
[PROSITE]    AMIDATION     1
```

[PROSITE]	CK2_PHOSPHO_SITE	2
[PROSITE]	PKC_PHOSPHO_SITE	3
[KW]	Alpha_Beta	

```
SEQ  MGIMAASRPLSRFWEWGKNIVCVGRNYADHVREMRSAVLSEPVLFLKPSTAYAPEGSPIL
PRD  cccccccccchhhhhhcceeeeeecchhhhhhhhhcccccccceeeecccccccccccccc

SEQ  MPAYTRNLHHELELGVVMGKRCRAVPEAAAMDYVGGYALCLDMTARDVQDECKKKGLPWT
PRD  ccccchhhhhhheeecccccccccchhhhhhhheeeeeecccchhhhhhhhhhhhhcccccc

SEQ  LAKSFTASCPVSAFVPKEKIPDPHKLKLWLKVNGELRQEGETSSMIFSIPYIISYVSKII
PRD  cccccccccccceeeeccccccccccceeeeecccccccccccccccceeechhhhhhhhhh

SEQ  TLEEGDIILTGTPKGVGPVKENDEIEAGIHGLVSMTFKVEKPEY
PRD  hcccccceeeeccccccccccccccceeeeeecccccccccccccccc
```

Prosite for DKFZphfkd2_46j20.1

PS00005	104->107	PKC_PHOSPHO_SITE	PDOC00005
PS00005	192->195	PKC_PHOSPHO_SITE	PDOC00005
PS00005	216->219	PKC_PHOSPHO_SITE	PDOC00005
PS00006	104->108	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00008	2->8	MYRISTYL	PDOC00008
PS00008	75->81	MYRISTYL	PDOC00008
PS00008	116->122	MYRISTYL	PDOC00008
PS00008	191->197	MYRISTYL	PDOC00008
PS00009	78->82	AMIDATION	PDOC00009

(No Pfam data available for DKFZphfkd2_46j20.1)

DKFZphfkd2_46k19
----

group: transcription factors

DKFZphfkd2_46k19.3 encodes a novel 130 amino acid protein similar to rat Dcoh, a bifunctional protein-binding transcriptional co-activator.

Dcoh is a bifunctional protein, complexed with biopterin. It serves as dimerization cofactor of hepatocyte nuclear factor-1 and catalyzes the dehydration of the biopterin cofactor of phenylalanine hydroxylase.

The new protein can find application in modulating/blocking the expression of genes controlled by the hepatocyte nuclear factor-1.

strong similarity to pterin-4-alpha-carbinolamine dehydratase

potential start at Bp 102 according to similar proteins,
both genomic sequences are from chromosome 5,

Sequenced by MediGenomix

Locus: map="5"

Insert length: 5641 bp
Poly A stretch at pos. 5617, polyadenylation signal at pos. 5598

```
   1 CAGCCCTCGG CAGACGGCCA ATGGCGGCGG TGCTCGGGGC GCTCGGGGCG
  51 ACGCGGCGCT TGTTGGCGGC GCTGCGAGGC CAGAGCCTAG GGCTAGCGGC
 101 CATGTCATCA GGTACTCACA GGTTGATTGC AGAGGAGAGG AACCAAGCTA
 151 TACTTGACCT TAAAGCAGCA GGATGGTCGG AATTAAGTGA GAGAGATGCC
 201 ATCTACAAAG AATTCTCCTT CCACAATTTT AATCAGGCAT TTGGCTTTAT
 251 GTCCCGAGTT GCCCTACAAG CAGAGAAGAT GAATCATCAC CCAGAATGGT
 301 TCAATGTATA CAACAAGGTC CAGATAACTC TCACCTCACA TGACTGTGGT
 351 GAACTGACCA AAAAAGATGT GAAGCTGGCC AAGTTTATTG AAAAAGCAGC
 401 TGCTTCTGTG TGATTTCTTC CAAAATACAT AAGTCTGAGA GGCTAAACTT
 451 GATGGCTGTG TTAACATATG TCACGTGTAG CACAGTGGAG AAAGCAGGAT
 501 ATGGCTCATA ATGACAGTGG TGAAGACCTG CGAATGAAGT TGCTAGTTAA
 551 CACCTACATT AGGGTTTGAC ATAGGTCTAT GTTATGGGTC GCTGCATCTG
 601 CTGGAACTCA CAGACTTTAC TATAGAGAAT CAAAGATCCC GTATCCGAAG
 651 TCTATGGAAA TGCTCATGGT GGTAAATTCC AACAGAATGA AACACCAAAC
 701 TTGCTTAAAG TAACTCACGT TTCAATTTGA AAGAGATATT GTCAAAATTG
 751 GAGGCCCCCA GGTTCCTGTC TGTTCCAAAT CTTTGCATGA TGACAGTGGT
 801 TTCTCTGATG TGGTAAGCTT TGGCTTTCTT CTGTTTTCTT TCTAAAAGAT
 851 CACTGGAGTA GAGAGGAGTT AAACAGACAT GACCTTTGAC CTCTTGCATG
 901 ACCTCCACAG ATAGCAAACC GGGCCGACAC ATGGTTGACG ATGTCCTTTT
 951 CTACAATGAA GTTAATGAAA GTTCTGAAAA TAGTGATTAC TTTCTGACAT
1001 TGATAGGATT TAGGAAACCT CTGGATAAAT AGCTTAAGCA TGGCTGTTTA
1051 TGTTTTTGCT ATAGACAAAA AGCAGCAGCA TGTACATTGT ATTTGGACAC
1101 AAGCCTGCCT CGGTTAATAT ATTGAACTAT TGGACCACTA GGGTTAGTAG
1151 GGAGCGGTCT GTACACTTTC TGATTCAGCA TTCAGAAACA TTCTAGGTGG
1201 ACTCTGTAGC TTTCAGTTTT GTAAAGTTAT CGGAAAAACA TCGGGAGGGT
1251 TTGGCCATCA TATGTGAGCT TTGTGTTTCA ATGCCAGTTA CTCAGGATTA
1301 GTAAATTAAT GACTGTCCAG AGGACTTCAG GGTCACCAAG CTGCTGCACC
1351 TGCCATTGGC TGACTCTCCC CGGCTATCTG TGGCTGAGAT GGTGCTGCTT
1401 AGGTCACGCA GAGCATGAGC TGCTGCTGAA AGGGCACAGG AGATGGCCCT
1451 TGGGCTTCTC ATCCCAGGAT GCCTGCCCTG CCCACCAATC CATGAGAAGA
1501 TATGTATGAT TTCAGTAGGC CCTGGATCAG CTTGTCACCT CTGGTTTCCT
1551 GTTTGCTTTC CACTCACTCA GCTGGAGTTT CATTTCCAGA CTAAAGTCTT
1601 CATCATTGGC TTCAGAAACA GCATTCATCT GTGGCTGTGC TGATGTAGTA
1651 CACCAAGAAC AACTGGGCTC TTCTCTGTCA CTTTCAGTGG GCTACCTTCC
1701 CTCACCTCTC CAAGCAGCAT GAAAGAATTC TTTACATTTT TAATCTCTTT
1751 TTTGTTTTTC CCTGAAAGTA TGCTTTGGTG CTTAAAGAGA GAAGTCACAA
1801 AAGTATACTA CTGAGTTTCC TGGAGATGAA ATCCTGTTGT CCCTAGCTAT
1851 GTGAATGAGC ACAGGGATCC CTGATGCCAT TATTTTGTAT ATTCATACGG
1901 CACACACTTA CTGAGGGCCT TCTGTGTGCC CTAGGGGATT GAGCACAGTG
1951 ACATATCAGG GCAGGTAGAA ACAGATGGAG AGCTGATGCG GGCTGTCTTA
2001 GAGCAGCTGC CCCAGGAGGC CCCTGTGGAT GGATGTTGGG CAGGAGCCCT
2051 GAGACGTTAG GGGCATATAA CTAAAGGACA TAGCAGGAGT TATAGGAGGA
2101 GCTGATCCCT GAGGGAAACA ATGAAGACGG AGAAGATGGG GCTAAAGTTT
2151 GAATTGTGGG GACATTAATC ACGGTGATTC TTAAAACTTT GCTGTTGATG
2201 ATTTTAAATG GAGAAAATGA GTACGTAAGA TGTTATTTCC CAGTTCAGTA
2251 TATAGGTTGC CCACAAAGTA TTTTCCTACC ATGAATGGTC ATATATACTT
2301 GTTGTAGAAT ACCAGGGACA GCAGAGATGG TGGGGTAGTT ACTTCCTTTT
2351 CTTACAGCCC AAGAACTTTG GTGTCCAGGA GATTGACCAA TTTAGCCACT
2401 GAGCATTTAA TACAACACAG GGCTACCCAG ATCCCACTGT CCTGATTTGC
2451 CCTGAAAGCC AAAGGAGTCA GGAGAAGGTG AGTGGGGTGA ATATATTAAT
2501 CCTGAGAGTT GAACAGAGCA AAAATCCCTA TTACTTTTGT ACTTAAAACA
```

```
2551 TCTCTGCCAC ATGTGCTCAC TCTTTATATT CTGTTTAGGT GGTTTATATG
2601 TGCACATCCC ATCCTATGCC TGCAGTTAGC CAACTCAGGG TTTATATTGC
2651 CTCCTTTCTT TTTTTCTTTT TTTTTTTTTT TTTTAAGAGA TGGGGTCTCG
2701 TTCTGTCATG CAGACTGGAG TGCAGTGGTG TGATCACAGC TCATTGTAAC
2751 CTCCAACGCC TGGACTGAAG TGATCCTCCT GCCTTGGCCT CTCTGGTAGC
2801 TGGGACTACA GGTGCATGCC ACCACACCCA CCTAATTTTT TTTATTTTTA
2851 TTTTTTGTAG AGACAGTCTC ACTATCTTGC TCGGGCTGGT CCTGAACTCC
2901 TGGGCTCAAG TTATCTTGCT GCCTCAGCCT CCCATGGGTA ATCTTTATTT
2951 CCTTTTTTTT TTTTTTTTGG AGATGGAGTT TCGCTCTTGT CGCCCAGGCT
3001 GGAGTGCAAT GGCACGATCT TGGCTCACTG CAGTCTCCAC CTCCTGGGTT
3051 CAGGTGATTC TCCATCCTCG GCCTACTGAG TAGCTGAGAT TACAGGCAAC
3101 TGCCACCATG CGCGGCTAAT TTGTGTATTT TTTTTTAGTA AGAGATGGGG
3151 TTTCGCCATG TTGGCCGGAC TGGTCTTAGA CTCCTGACCT CAAGCGACCT
3201 GCCTGCCTTG GCCTCCCAAA GTGCTGGGAT TACAGGCATG AGCCGCTATG
3251 CCTCGTCGCT GATTTTTATT TCTTATTTTT TTTTTAGAGA TGGGGGTCTC
3301 ACTATGCTGC TCAGGCTGAT CTCAAACTCC TGGCCTCAAG TGATCCTCCC
3351 ACCTTAGCCT CCCAAGTTGC TGGGATTATA AGTGTGAGCC ACTATCCCTA
3401 CCTCACTATT ACCTTCTTTG CTTCTCTTGT TTTCTTTTGT TCTAAGTCAA
3451 ACCCATCACA ATCTTTTCTT GTCCTTCCAG GTGTTTTCCA GTGCTGTGCC
3501 CTGGATGTGC TCTCTTTCTC TTAGAGCCCA GAGAACTTGC TTTTCCCCCT
3551 TATATATGAC CCTTAACTTT TTCTAACACA TTATTAAGGG CCTGTGTCTA
3601 TCAGCTGGGG GCACTTCTTG AAGGGAGGGC CTTTGTGTGG TCTGTTTCTA
3651 GTGACTTCCA GCTTTAACCC AGAGCCTCAT GATTGCTGGG TGCCCATAGC
3701 CTTTTTGCTG AATGGAGGCA CTCAGTCTCC TTGGGAAGAG AGAATCCATG
3751 ATAGACCCAC TTGGGAGCTC CCCACTTCAG GGGCCTACAC ACTGGTAATG
3801 CAACAGAATG CCCAAGAGTG ACCTCATAAA GCAAGGATTC CCTTCGTGGC
3851 CCCTTCTCTG CTGCCTCTCA GAATCCAGAC GCTAAGGAAA ATCCCTAAGC
3901 AGAGATTTTC TGTTGGATGC TAAAAGCAAG GAATAAAAGT TGAAAATTTG
3951 GAAAATGTCT CAACACCGTC ACCAGCGCCA CTCGAGAGTC ATTTCTAGTT
4001 CACCAGTTGA CACTACATCG GTGGGATTTT GCCCAACATT CAAGAAATTT
4051 AAGTAAATAT TATCTATCTC CATTGCCTGT TAAGAAATGT GCTAGTAGAA
4101 GTGTGAGGGC AGGGTGTCAG TGTTCTCTCA GCCTCTTCCC TCAGATACTC
4151 GTCTGCTTAC CAAAATAAGT TGCATGTCCT TGACAATCTG GTTTCTATGA
4201 TTGGTGAGGC TGGCATGCTA TTACCTTTAT GTGCCCTGTA GACTTGAATG
4251 ACCAGTTTGA CCAGTTTGAC TGTTAGATAA TCAGAAGGCT TTTCTCTTTT
4301 TTTATAATAG ACCCCATCTC AAATCAGATA ATGAAAATTA CATATCTTGA
4351 TATATTAGAA AAGTATATAC ATTCTGGCTG GGCACGGTGG CTCACGCCTG
4401 TAATCCCTGC ACTTTGAGAG GCTGGGGCGG ATCACTTGAG GTCAGGAGTT
4451 TGAGACCGGC CTGGCCAGCG TGGCGAAACC CCATCTCTAC TAAAAATACA
4501 CAGATTAGCC CGGAGTGATG GTGTGCACCT GTTGTCCCAG CTACTCAGGA
4551 TGCTGAGGCA GGAGAATCCC TTTAACCTGG GGGGCGAAGG TTGCAGTGAG
4601 CCAGGATTGC ACCACTGCAC TCCAGCCTGG GTGACGGAAC GGGACTCTGT
4651 CTCAGAAAAA AAAAAAAAGA AGAGGAAAAA GAAAAATATA TATTCTATAT
4701 TTTTTTAACT TATGAGAATG TGTTCATTTC ATTTGTAACA TATAATGGGA
4751 AACAGTAATA CGTACTCTGA GAAAAATTGC AAAGCACAGA TAAATGGAAA
4801 TAAACAGGAA AAAGAATCAC CTATAACCTC ACCATCCATA GACAGACACT
4851 GTTAAAATTT TGGCATATTT CCTGCTGATT TTTTCTACTG CTGATTTTTG
4901 CACAGGTGAG ATAATTTTGA ACAGAGAATT TTGTATCTTT GGTTTTTGTG
4951 TTTCGCTGCA CACAAAAACA AAAGATATAA AAATGGATCA TAAACATTTT
5001 TCTAAATCCT GAAAAGTGCA TAGACATATT TTAGTGCCTG TATTTCACAA
5051 GATGGACATA CCATAATTTA CTTACACAGT CCTTTTTGTT AGATGTTTAA
5101 GTTGTTTTCA AGCTTCTCAG TGCTGGAAAA AATACTGAGA TAGACATGTT
5151 TAGTTGAAGT TATTTCATTT CAGGTTATAT TATCTTGGGT CAGAGAATGA
5201 ATGGTTCTCA GGCTTTTCAA AAGAGCTGGT CAGTTTTTAT GCCTCTGGCA
5251 GTTTTTGAGA GTGCTCAATC ATACTACACT GTTGCCAGCA TTAGATCTTA
5301 TCACATTTAA GTCATTGCTA ATTTTATAAA CAAAAACAAT GGTTTTACTT
5351 TGCATCTCCC TGATTGGTGT TGCTGTAGAA CATATTTGGA GAAGTTTGTT
5401 TGTCTTTGGT GTTTATTCCA TGAATAGATT GTGTGCCCAT TTTCTCTTGG
5451 GGTATTCAGT TTTTTATTAC TGATGTGAGC ATGTGTATGG GTGATTATTT
5501 GATGATTATC AGTTTTGCTT AGTAGACTGG CAATATTTAG TCTTGCTGTC
5551 ACTGTGTTCC CAGTGCCAAC TAGATTGCTT GATATGTAGT TGCCACTCAA
5601 TAAAGATTTG TTGAGTCAAT GAAAAAAAAA AAAAAAAAAA A
```

BLAST Results

Entry AC004764 from database EMBL:
Homo sapiens chromosome 5, P1 clone 255g5 (LBNL H61), complete sequence.
Score = 11057, P = 0.0e+00, identities = 2217/2224
Bp 428-5625 of cDNA == Bp 2912-8107 of AC004764

Entry HSAC1555 from database EMBL:
Homo sapiens (subclone 1_d8 from BAC H75) DNA sequence, complete sequence.
Score = 575, P = 5.1e-30, identities = 115/115
Bp ~240- 430 of cDNA == HSAC1555 splice pattern

Medline entries

93186787:
Phenylalanine hydroxylase-stimulating protein/pterin-4 alpha-carbinolamine dehydratase from rat and human liver. Purification, characterization, and complete amino acid sequence.

93101632:
Identity of 4a-carbinolamine dehydratase, a component of the phenylalanine hydroxylation system, and DCoH, a transregulator of homeodomain proteins.

95242099:
Crystal structure of DCoH, a bifunctional, protein-binding transcriptional coactivator

Peptide information for frame 3

ORF from 21 bp to 410 bp; peptide length: 130
Category: strong similarity to known protein

```
    1 MAAVLGALGA TRRLLAALRG QSLGLAAMSS GTHRLIAEER NQAILDLKAA
   51 GWSELSERDA IYKEFSFHNF NQAFGFMSRV ALQAEKMNHH PEWFNVYNKV
  101 QITLTSHDCG ELTKKDVKLA KFIEKAAASV
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_46k19, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_46k19, frame 3

Report for DKFZphfkd2_46k19.3

```
[LENGTH]        130
[MW]            14377.56
[pI]            9.17
[HOMOL]         PIR:A47189 pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) - rat 4e-34
[FUNCAT]        01.07.99 other vitamin, cofactor, and prosthetic group activities   [S.
cerevisiae, YHL018w] 5e-04
[SCOP]          d1dchg_ 4.38.1.1.1 Pterin-4a-carbinolamine dehydratas 4e-50
[EC]            4.2.1.96 Tetrahydrobiopterin dehydratase 6e-34
[PIRKW]         nucleus 6e-34
[PIRKW]         carbon-oxygen lyase 6e-34
[PIRKW]         homotetramer 6e-34
[PIRKW]         hydro-lyase 6e-34
[PIRKW]         cytosol 6e-34
[PIRKW]         acetylated amino end 6e-34
[PIRKW]         homodimer 6e-34
[SUPFAM]        pterin-4-alpha-carbinolamine dehydratase 6e-34
[PROSITE]       MYRISTYL        2
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        4
[KW]            Alpha_Beta
[KW]            3D
[KW]            LOW_COMPLEXITY    14.62 %
```

```
SEQ    MAAVLGALGATRRLLAALRGQSLGLAAMSSGTHRLIAEERNQAILDLKAAGWSELSERDA
SEG    .xxxxxxxxxxxxxxxxxxx........................................
1dchB  ...............................CCCCHHHHHHHHHHHHHHCCEEECCCCE

SEQ    IYKEFSFHNFNQAFGFMSRVALQAEKMNHHPEWFNVYNKVQITLTSHDCGELTKKDVKLA
SEG    ............................................................
1dchB  EEEEEECCCHHHHHHHHHHHHHHHHHHCCCCEEEETTTEEEEEECBTTTTBTCCHHHHHH

SEQ    KFIEKAAASV
```

```
SEG       ..........
1dchB     HHHHHHHHHH
```

Prosite for DKFZphfkd2_46k19.3

PS00005	11->14	PKC_PHOSPHO_SITE	PDOC00005
PS00005	32->35	PKC_PHOSPHO_SITE	PDOC00005
PS00005	56->59	PKC_PHOSPHO_SITE	PDOC00005
PS00005	113->116	PKC_PHOSPHO_SITE	PDOC00005
PS00006	56->60	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	113->117	CK2_PHOSPHO_SITE	PDOC00006
PS00008	6->12	MYRISTYL	PDOC00008
PS00008	20->26	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphfkd2_46k19.3)

DKFZphfkd2_46m4
----

group: signal transduction

DKFZphfkd2_46m4.3 encodes a novel 198 amino acid putative GTP-binding protein related to the SAR-1 family of Ras superfamily members.

SAR1 proteins are involved in vesicular transport between the endoplasmic reticulum and the Golgi apparatus.

The new protein can find clinical application in modulating the transport of vesicles to the Golgi Apparatus, thus enabling post-translational modifications of the vesicles contents. Blocking of the molecule is expected to result modulation/blocking of secretory pathways.

nearly identical to mouse GTP-binding protein

complete cDNA, complete cds, EST hits

Sequenced by MediGenomix

Locus: /map="438.9 cR from top of Chr10 linkage group"

Insert length: 2996 bp
Poly A stretch at pos. 2969, polyadenylation signal at pos. 2958

```
   1 ACATCCGGCG AGTAGCTGGC GGTCCCGGGT GCTGCTGGTT AGTGTGCTCT
  51 GAGGGAGGGT CCGAGCCAGC CGCTGTTTTG CCGGAGGAGC CCCTCAGGCC
 101 GTAGTAAGCA TTAATAATGT CTTTCATCTT TGAGTGGATC TACAATGGCT
 151 TCAGCAGTGT GCTCCAGTTC CTAGGACTGT ACAAGAAATC TGGAAAACTT
 201 GTATTCTTAG GTTTGGATAA TGCAGGCAAA ACCACTCTTC TTCACATGCT
 251 CAAAGATGAC AGATTGGGCC AACATGTTCC AACACTACAT CCGACATCAG
 301 AAGAGCTAAC AATTGCTGGA ATGACCTTTA CAACTTTTGA TCTTGGTGGG
 351 CACGAGCAAG CACGTCGCGT TTGGAAAAAT TATCTCCCAG CAATTAATGG
 401 GATTGTCTTT CTGGTGGACT GTGCAGATCA TTCTCGCCTC GTGGAATCCA
 451 AAGTTGAGCT TAATGCTTTA ATGACTGATG AAACAATATC CAATGTGCCA
 501 ATCCTTATCT TGGGTAACAA AATTGACAGA ACAGATGCAA TCAGTGAAGA
 551 AAAACTCCGT GAGATATTTG GGCTTTATGG ACAGACCACA GGAAAGGGGA
 601 ATGTGACCCT GAAGGAGCTG AATGCTCGCC CCATGGAAGT GTTCATGTGC
 651 AGTGTGCTCA AGAGGCAAGG TTACGGCGAG GGTTTCCGCT GGCTCTCCCA
 701 GTATATTGAC TGATGTTTGG ACGGTGAAAA TAAAAGAGTT TTACTTCTCT
 751 GGACTGATCC TATTCACAGC TTCCTCATGA ACTTTTCTAA TAGAACAAGG
 801 ATAGCTCTCC AACCATGTCT GGCGTTGAGA AGCCAAGAGT CTCTGTCAAC
 851 TCTCTCATTG CCCAGTGGTG ACATGTGCTC TTCTCCACAC TGTTGGGAGG
 901 TAATGCTGCC CCACGTGCTG GTGCAGGTCA GTATCCTGGG ACTTGGAAGC
 951 TGGCAGGATT TGCCGGGTAA AGCTGTATGC CATCATGGGG CACCTGAAAA
1001 GAAAAACACG TCTCACCACT GTGGTTGATT CAAAAGAAAG TGATTCTATT
1051 TTTTAAAGAA AGCGTTGTTA ATGTAATTGG TATCCCTCCT AACTTTTTGA
1101 GTTCACAATT TACTTGGTCC AGAGTTTTCT ATTCTTTTTT TTTTTTTAAA
1151 CTAATGAATG ACATTTAGAT ACTTCATAAA ATTATGAACA GATATGGAGG
1201 CCAGAGCTCA TTTGGGTAAA CTTACTCCTG CTGAGTTAGC AGGTTGGTGA
1251 GAGAAGCTCC CCTGAGCTCA CCTGTCTCTC TGACTGCCTT GGAGTAGGTG
1301 GCATAACCTT GTGCACAGAG AACTAGAAAA GGGGCAGAAC CCCGGCCTTG
1351 CAGTTGTGGC AGGTTTCCAC TGTGGTAAGC TAGGTTCATT CCTCATCAAG
1401 GAATGTGTAG CAGATTGTTC ACTGTGGAGG AGGTAATTAT AGAATGGGTT
1451 ATTGTTGTTA TTCTTACTCA TGAAGTTACA GATTTTAGCC AGTCTTTGCT
1501 TTTATACTTT TGTGAAATTT AATTTCTCTC TATAGCACCT TCCTTTTTCG
1551 TTTTCAGTTA TCAAAAGTGA CTTTGACCTC ATAAGAGAGT TGAGAACATC
1601 TCTCGTGTCA CATACTGCAG GTGCATCAGT TACTTTTGCA CAGATTCTAG
1651 GGGGACATTT TTCTGAATAG GAAGACAGGA CAAAGTTAAC AGCTTAAGGG
1701 CTCTTAATTC TGTGAGTTGA GGACTTAAAA GTATTGTAGC ATTTGTTTGG
1751 ATCCATGAAA AATGTATTCA GTGGGCTTTA AAATTTCCAT TTGCAGAATT
1801 TGGTCTCTCA GGCTGTTTGG GAGCTCTTTT TTTTACATTT TTTCTCCTTT
1851 GACACCTATT TTATTGGTGT TTAAAGTAAA GGTTAACATC TGTAGCTTTT
1901 CCAGGTTTTT TTTTTTTTTT TTGATATGAA ATTGTCTTTC TCCATTGCAG
1951 AAATAAGCTA GGGAAACACT AACCCAAAAA CTTTCTGTAG AGCTGTTCCT
2001 TTGGAGGCAG CATCACTTAT TGGCAGTAAA GACTCAGTAT AAAAGCACCA
2051 GCATCCCTAC TTGGGTGATG GGGATTAATT TTATAGCATT CCATTTTCCT
2101 AGTGCCACAT GTGAAATTGG ATTTTGATGA TCTTAATCTA TATTCTACCC
2151 TTATAATAAA AGATCAAAAG ATATATCTCC TATGAACAGA TTGGAGATAG
2201 GAGATGAAAA GTTGGGAGGA TGCCTTTATT CTAATGTGAG GGTAGGGAAA
2251 ATGTGGATAA CATTACTGGG GTGAAGGAGG CATTGTTCTT TAGTTGGAGT
2301 TCTCATTTTT ATTCTCCAGT ACTGACTTGT GGGGAAAGCA TACTTTTTCA
2351 CTGCCAGGTA CTGAATGCAG AGGCTCAGTG AAGTATATAT GTGGGAAGTG
2401 CATGCATTTC GTTTATTAGC AAACATAGCT GGATTAAGAC GAAGTTGTTG
2451 GTTTGGAAAG GGGTTAAAGC CTTAAGTGAA CAAATCTAGC TAACAGTGAA
2501 TGAACTAGGT AATATAACTT GCATATTTTT AATTTCCTTT GGTTAAAGGT
2551 CCCCCATACT TCTCTGTTCG GAGACATGAG AAGTATGATT ACTTCAGTGT
```

```
2601 TAGTTTTCTT AATTTTTTTT TTCCCCTATT TGTCCCTTGT CACTTTGTTG
2651 CAAGCTAGAA ATCTGTGGGT TATACATAGG GCAGCTCTTT GCGAAAGTGG
2701 TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT
2751 TCTTGCCCCA CGGAACACTA TTCCTATAAG ATAGCTGAAA GAAGCTGCTG
2801 TGAGGAGCTC AGCTCCAACA CAGGATCAGC ACCTTGTATA GGAATTCCCA
2851 TGAATTATGA CTTCTCATTC TGTTTTATCA GAGTGCATAT ATGTCCTACT
2901 TCAGGAAAAG TAAAACAGTC ATTTACGAAA GAAAGTCAAT CTGTATCCTA
2951 AGCATTTTAA TAAAAAGTTA AAACAAAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HS679348 from database EMBL:
human STS WI-16722.
Length = 265
Minus Strand HSPs:
Score = 1242 (186.4 bits), Expect = 2.8e-50, P = 2.8e-50
Identities = 260/265 (98%)

Medline entries

94085558:
Molecular analysis of SAR1-related cDNAs from a mouse pituitary cell line.

Peptide information for frame 3

ORF from 117 bp to 710 bp; peptide length: 198
Category: strong similarity to known protein

```
  1 MSFIFEWIYN GFSSVLQFLG LYKKSGKLVF LGLDNAGKTT LLHMLKDDRL
 51 GQHVPTLHPT SEELTIAGMT FTTFDLGGHE QARRVWKNYL PAINGIVFLV
101 DCADHSRLVE SKVELNALMT DETISNVPIL ILGNKIDRTD AISEEKLREI
151 FGLYGQTTGK GNVTLKELNA RPMEVFMCSV LKRQGYGEGF RWLSQYID
```

BLASTP hits

Entry S39543 from database PIR:
GTP-binding protein - mouse
Length = 198
Score = 1029 (362.2 bits), Expect = 5.1e-104, P = 5.1e-104
Identities = 197/198 (99%), Positives = 198/198 (100%)

Entry SARA_MOUSE from database SWISSPROT:
GTP-BINDING PROTEIN SARA.
Length = 198
Score = 1012 (356.2 bits), Expect = 3.2e-102, P = 3.2e-102
Identities = 195/198 (98%), Positives = 196/198 (98%)

Entry CEZK180_4 from database TREMBL:
gene: "ZK180.4"; Caenorhabditis elegans cosmid ZK180.
Length = 193
Score = 679 (239.0 bits), Expect = 6.3e-67, P = 6.3e-67
Identities = 125/197 (63%), Positives = 161/197 (81%)

Alert BLASTP hits for DKFZphfkd2_46m4, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_46m4, frame 3

Report for DKFZphfkd2_46m4.3

[LENGTH]	198
[MW]	22367.00
[pI]	6.21
[HOMOL]	PIR:S39543 GTP-binding protein - mouse 1e-112

[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YPL218w] 1e-58
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YPL218w] 1e-58
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YOR094w] 2e-23
[FUNCAT] 06.07 protein modification (glycolsylation, acylation, myristylation, palmitylation, farnesylation and processing) [S. cerevisiae, YPL051w] 4e-22
[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YDL192w] 3e-20
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YBR164c] 3e-19
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YMR138w] 2e-09
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YMR138w] 2e-09
[FUNCAT] 98 classification not yet clear-cut [S. cerevisiae, YHR168w] 7e-05
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YHR005c] 1e-04
[FUNCAT] 30.07 organization of endoplasmatic reticulum [S. cerevisiae, YKL154w] 1e-04
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YHR005c] 1e-04
[FUNCAT] 10.05.07 g-proteins [S. cerevisiae, YHR005c] 1e-04
[FUNCAT] 06.04 protein targeting, sorting and translocation [S. cerevisiae, YKL154w] 1e-04
[FUNCAT] 08.19 cellular import [S. cerevisiae, YML001w] 3e-04
[BLOCKS] BL00395A Alanine racemase pyridoxal-phosphate attachment site proteins
[BLOCKS] BL01019B ADP-ribosylation factors family proteins
[BLOCKS] BL01019A ADP-ribosylation factors family proteins
[BLOCKS] BL01020D SAR1 family proteins
[BLOCKS] BL01020C SAR1 family proteins
[BLOCKS] BL01020B SAR1 family proteins
[BLOCKS] BL01020A SAR1 family proteins
[SCOP] d1plj__ 3.25.1.3.1 cH-p21 Ras protein [human (Homo sapiens) 7e-36
[SCOP] d1guaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens) 8e-40
[SCOP] d1rrf__ 3.25.1.3.5 ADP-ribosylation factor 1 (ARF1) [rat (Rattu 2e-55
[SCOP] d1hurb_ 3.25.1.3.4 ADP-ribosylation factor 1 (ARF1) [human (Hom 1e-58
[SCOP] d1gota2 3.25.1.3.3 (1-54,171-326) Transducin (alpha subunit) [ra 2e-33
[SCOP] d1tadb2 3.25.1.3.2 (1-30,152-316) Transducin (alpha subunit 6e-36
[PIRKW] glycoprotein 4e-19
[PIRKW] monomer 1e-16
[PIRKW] P-loop 3e-64
[PIRKW] lipoprotein 4e-19
[PIRKW] GTP binding 3e-64
[SUPFAM] ADP-ribosylation factor 5e-22
[PROSITE] ATP_GTP_A 1
[PROSITE] MYRISTYL 3
[PROSITE] SAR1 1
[PROSITE] CK2_PHOSPHO_SITE 4
[PROSITE] PKC_PHOSPHO_SITE 3
[PROSITE] ASN_GLYCOSYLATION 1
[PFAM] ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)
[KW] Alpha_Beta
[KW] 3D

```
SEQ    MSFIFEWIYNGFSSVLQFLGLYKKSGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPT
1hurA  .................TTTTTCCCCEEEEEETTTTCHHHHHHHHCCCCEEEEEEETTEE

SEQ    SEELTIAGMTFTTFDLGGHEQARRVWKNYLPAINGIVFLVDCADHSRLVESKVELNALMT
1hurA  EEEEEETTEEEEEEETTTTTTTCCCHHHHHHCEEEEEEEEETTTTTHHHHHHHHHHHHHH

SEQ    DETISNVPILILGNKIDRTDAISEEKLREIFGLYGQTTGKGNVTLKELNARPMEVFMCSV
1hurA  TTTTTTTEEEEEEETTTTTTTCCHHHHHHHHCGG..........................

SEQ    LKRQGYGEGFRWLSQYID
1hurA  ..................
```

Prosite for DKFZphfkd2_46m4.3

PS00001	162->166	ASN_GLYCOSYLATION	PDOC00001
PS00005	25->28	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00006	60->64	CK2_PHOSPHO_SITE	PDOC00006
PS00006	72->76	CK2_PHOSPHO_SITE	PDOC00006
PS00006	111->115	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	68->74	MYRISTYL	PDOC00008
PS00008	155->161	MYRISTYL	PDOC00008
PS00017	32->40	ATP_GTP_A	PDOC00017
PS01020	171->197	SAR1	PDOC00782

Pfam for DKFZphfkd2_46m4.3

```
HMM_NAME        ADP-ribosylation factors (Arf family) (contains ATP/GTP binding P-loop)

HMM                 *GMgWfsIFrkMWGlWNKEMRILMLGLDNAGKTTILYMLKlgEIVTTIPT
                      ++ FS++++++GL++K++++++LGLDNAGKTT+L+MLK++++ +++PT
Query           9   -YNGFSSVLQFLGLYKKSGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPT    56

HMM                 IGFNVETVeYKNIKFNVWDVGGQdsIRPYWRHYYpNTDGIIWVVDSaDRD
                    +++++E++++ +++F+++D+GG++++R++W++Y P+++GI+++VD+AD++
Query          57   LHPTSEELTIAGMTFTTFDLGGHEQARRVWKNYLPAINGIVFLVDCADHS   106

HMM                 RMeEaKqELHaMLNEEELrDAPlLIFANKQDLPgAMSesEIREaLGLHeI
                    R+ E+K+EL+A++++E ++++P+LI++NK+D+ +A+SE+++RE+ GL+ +
Query         107   RLVESKVELNALMTDETISNVPILILGNKIDRTDAISEEKLREIFGLYGQ   156

HMM                 RCn...........RPWYIQMCCAVtGEGLYEGMDWLSNYInkRkK*
                    +++           RP++++MC++++++G++EG++WLS+YI
Query         157   TTGKGNVTLKELNARPMEVFMCSVLKRQGYGEGFRWLSQYI-----    197
```

DKFZphfkd2_47a4
----

group: transcription factor

DKFZphfkd2_47a4.1 encodes a novel 280 amino acid protein with similarity to zinc finger proteins.

The new protein is a putative transcription factor with one C2H2 zinc fingers.

The new protein can find application in modulating/blocking the expression of genes controlled by this transcription factor.

similarity to C.elegans F46B6.7

potential frame shift at 1092, will be checked see BLASTX

Sequenced by MediGenomix

Locus: map="7q31"

Insert length: 1756 bp
Poly A stretch at pos. 1737, no polyadenylation signal found

```
   1 CCCTTTTCTT TTCTGCCGGG TAATGGCTGC TTCCAAGACC CAGGGGGCTG
  51 TCGCCCGAAT GCAGGAAGAC CGTGATGGGA GCTGCAGCAC AGTCGGGGGT
 101 GTAGGTTATG GGGTAAGGAT TGTATCCTGG AGCCGCTTTC CCTGCCAGAA
 151 AGTCCAGGTG GCACCACCAC TTTAGAAGGT TCTCCATCTG TGCCTTGTAT
 201 TTTCTGTGAA GAACATTTTC CTGTGGCTGA ACAAGACAAA CTTCTGAAGC
 251 ACATGATTAT TGAGCATAAG ATTGTCATAG CTGATGTCAA GTTGGTTGCT
 301 GATTTCCAAA GGTACATTTT ATATTGGAGG AAAAGGTTCA CTGAACAGCC
 351 CATCACAGAT TTTTGTAGTG TAATAAGAAT TAATTCCACT GCTCCATTTG
 401 AAGAACAAGA GAATTATTTT TTGTTATGTG ACGTTTTACC AGAAGATAGA
 451 ATTCTTAGAG AAGAGCTTCA GAAACAGAGA CTGAGAGAAA TTCTGGAACA
 501 ACAGCAGCAA GAACGAAATG ATAACAATTT TCATGGCGTT TGTATGTTTT
 551 GCAATGAAGA ATTCCTTGGA AACAGATCTG TTATTTTGAA CCACATGGCC
 601 AGAGAACATG CTTTCAACAT TGGATTGCCA GACAACATTG TAAACTGCAA
 651 TGAATTTTTG TGTACATTAC AGAAAAAGCT TGACAATTTG CAGTGCTTGT
 701 ACTGTGAGAA GACCTTCAGG GGCAAAAATA CACTTAAAGA TCACATGAGG
 751 AAAAAACAGC ATCGTAAGAT TAATCCTAAG AACAGAGAAT ATGACAGATT
 801 TTATGTCATC AATTATTTGG AACTTGGAAA ATCGTGGGAG GAAGTTCAGT
 851 TGGAAGATGA TCGGGAGTTG CTGGACCATC AGGAAGATGA CTGGTCTGAT
 901 TGGGAAGAAC ACCCTGCCTC TGCAGTCTGC TTATTTTGTG AAAAGCAAGC
 951 AGAAACAATT GAGAAGTTGT ATGTCCACAT GGAGGATGCA CACGAATTTG
1001 ATCTTCTCAA AATAAAGTCA GAACTTGGAT TAAATTTCTA TCAGCAAGTG
1051 AAACTGGTCA ATTTTATTCG GAGGCAAGTT CACCAATGCA GATGATGGCT
1101 GCCATGTGAA GTTCAAATCC AAAGCAGACT TAAGAACTCA CATGGAAGAA
1151 ACTAAACACA CTTCGCTGCT CCCCGATAGA AAGACGTGGG ATCAACTGGA
1201 GTATTATTTT CCAACCTATG AAAATGACAC TCTCCTGTGT ACACTATCTG
1251 ACAGTGAAAG TGACCTGACA GCTCAGGAAC AAAATGAAAA TGTTCCCATC
1301 ATCAGTGAAG ATACATCTAA ACTGTATGCT TTGAAACAAA GCAGTATTTT
1351 GAACCAGTTG CTACTATAAG AGTACTTGAA AACCTAGAAG AAACTACCAC
1401 AGAAGCAATT TTTCATGTTT TTCTCCTATG AGACAGATAT GAAAGAACAA
1451 TTTAAATTTG AACATCAACA AAAGATTGGT CCTTGGTGAA ATAAACTTTT
1501 CAAAAATGAA TGTTCTTTTC AAAAAATAAA GTAGAAAAAT GCACTTACTA
1551 AGAACATGAA AAAAAAATGA AGTAGGAAAA TAAGATGAAG ACTTTGTATT
1601 TTGGCTGTAA AGTTTTATTG TGTGATCATC TTAAATTATC TCACTTCATT
1651 AAACTCATAA TTATATATAG AAGTATATGT CAATTACAAA GAAATGAAAT
1701 GTTCAAATTA TTTATAAACC TGATTTTTCA ATCAGCGAAA AAAAAAAAAA
1751 AAAAAA
```

BLAST Results

Entry AC004112 from database EMBL:
Homo sapiens BAC clone RG313E03 from 7q31, complete sequence.
Score = 2660, P = 3.0e-241, identities = 534/535
> 10 exons

Entry AC004111 from database EMBL:
Homo sapiens BAC clone RG103H13 from 7q31, complete sequence.
Score = 598, P = 5.8e-17, identities = 128/137
1 exon

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 253 bp to 1092 bp; peptide length: 280
Category: similarity to unknown protein

```
  1 MIIEHKIVIA DVKLVADFQR YILYWRKRFT EQPITDFCSV IRINSTAPFE
 51 EQENYFLLCD VLPEDRILRE ELQKQRLREI LEQQQQERND NNFHGVCMFC
101 NEEFLGNRSV ILNHMAREHA FNIGLPDNIV NCNEFLCTLQ KKLDNLQCLY
151 CEKTFRGKNT LKDHMRKKQH RKINPKNREY DRFYVINYLE LGKSWEEVQL
201 EDDRELLDHQ EDDWSDWEEH PASAVCLFCE KQAETIEKLY VHMEDAHEFD
251 LLKIKSELGL NFYQQVKLVN FIRRQVHQCR
```

BLASTP hits

Entry CEF46B6_6 from database TREMBLNEW:
product: "F46B6.7"; Caenorhabditis elegans cosmid F46B6
>TREMBL:CEF46B6_6 product: "F46B6.7"; Caenorhabditis elegans cosmid F46B6
Score = 630, P = 1.1e-61, identities = 123/289, positives = 183/289

Entry AF059531_1 from database TREMBLNEW:
gene: "PRMT3"; product: "protein arginine N-methyltransferase 3"; Homo sapiens protein arginine N-methyltransferase 3 (PRMT3) mRNA, partial cds. >TREMBL:AF059531_1 gene: "PRMT3"; product: "protein arginine N-methyltransferase 3"; Homo sapiens protein arginine N-methyltransferase 3 (PRMT3) mRNA, partial cds.
Score = 120, P = 1.5e-04, identities = 23/78, positives = 42/78

Entry YB9M_YEAST from database SWISSPROT:
34.7 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.
Score = 112, P = 4.6e-04, identities = 43/165, positives = 71/165

Alert BLASTP hits for DKFZphfkd2_47a4, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphfkd2_47a4, frame 1

Report for DKFZphfkd2_47a4.1

```
[LENGTH]     280
[MW]         33921.94
[pI]         5.63
[HOMOL]      TREMBL:CEF46B6_5 gene: "F46B6.7"; Caenorhabditis elegans cosmid F46B6 1e-56

[BLOCKS]     BL01032B Protein phosphatase 2C proteins
[BLOCKS]     BL00028 Zinc finger, C2H2 type, domain proteins
[PROSITE]    MYRISTYL          1
[PROSITE]    ZINC_FINGER_C2H2       1
[PROSITE]    CAMP_PHOSPHO_SITE      1
[PROSITE]    CK2_PHOSPHO_SITE       3
[PROSITE]    TYR_PHOSPHO_SITE       2
[PROSITE]    PKC_PHOSPHO_SITE       2
[PROSITE]    ASN_GLYCOSYLATION      2
[PFAM]       Zinc finger, C2H2 type
[KW]         Alpha_Beta
[KW]         LOW_COMPLEXITY    8.21 %

SEQ   MIIEHKIVIADVKLVADFQRYILYWRKRFTEQPITDFCSVIRINSTAPFEEQENYFLLCD
SEG   ............................................................
PRD   cccccceeehhhhhhhhhhhhhhhhhhhhhhhhhcccceeeeeecccccchhhhheeeecc

SEQ   VLPEDRILREELQKQRLREILEQQQQERNDNNFHGVCMFCNEEFLGNRSVILNHMAREHA
SEG   .....xxxxxxxxxxxxxxxxxxxxxxx................................
PRD   cccccchhhhhhhhhhhhhhhhhhhhhhhhhccccceeeeeeccccccccceeeehhhhhhhh

SEQ   FNIGLPDNIVNCNEFLCTLQKKLDNLQCLYCEKTFRGKNTLKDHMRKKQHRKINPKNREY
```

```
SEG     ............................................................
PRD     hcccccccccchhhhhhhhhhhhhhhhheeecccccccchhhhhhhhhhhccccccccccc

SEQ     DRFYVINYLELGKSWEEVQLEDDRELLDHQEDDWSDWEEHPASAVCLFCEKQAETIEKLY
SEG     ............................................................
PRD     ceeeeeeeecccccchhhhhhhcchhhhhhhccccccccccccccchhhhhhhhhhhhhhh

SEQ     VHMEDAHEFDLLKIKSELGLNFYQQVKLVNFIRRQVHQCR
SEG     ........................................
PRD     hhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhhcccc
```

Prosite for DKFZphfkd2_47a4.1

PS00001	44->48	ASN_GLYCOSYLATION	PDOC00001
PS00001	107->111	ASN_GLYCOSYLATION	PDOC00001
PS00004	27->31	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	154->157	PKC_PHOSPHO_SITE	PDOC00005
PS00005	160->163	PKC_PHOSPHO_SITE	PDOC00005
PS00006	160->164	CK2_PHOSPHO_SITE	PDOC00006
PS00006	194->198	CK2_PHOSPHO_SITE	PDOC00006
PS00006	215->219	CK2_PHOSPHO_SITE	PDOC00006
PS00007	178->185	TYR_PHOSPHO_SITE	PDOC00007
PS00007	13->22	TYR_PHOSPHO_SITE	PDOC00007
PS00008	124->130	MYRISTYL	PDOC00008
PS00028	148->171	ZINC_FINGER_C2H2	PDOC00028

Pfam for DKFZphfkd2_47a4.1

```
HMM_NAME       Zinc finger, C2H2 type

HMM                *CpwPDCgKtFrrwsNLrRHMR..T.H*
                    C +  C+KTFR + +L+ HMR    H
Query         148   CLY--CEKTFRGKNTLKDHMRKK-QH     170
```

DKFZphfkd2_4b6
----

group: kidney derived

DKFZphfkd2_4b6 encodes a novel 133 amino acid protein with similarity to Homo sapiens clone 25003 partial CDS.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to Homo sapiens clone 25003

complete cDNA, complete cds, few EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1936 bp
Poly A stretch at pos. 1916, polyadenylation signal at pos. 1890

```
   1 GGGAGACTTG CAATGAAGTT AGAATGAACA GGAGGAGTCT GCAGCTTTTC
  51 AGTGCCTGGG ATAACTATAG TTTAAAGATC ATTGTGTAAA ATAGGATTTT
 101 TAGTCAGCAT GCATTGTTTT AAACCGACTA ACTGATAGCC TAAAACTTTA
 151 TTTTTGCATT TTGCCAATCC TTGGAGTTTT GTTTTGCAGA ATTAAGAAAA
 201 AAATGAATGT ATGATCATCT GAAAAGGGCT TTCTCTCAAT CCCACTTCAT
 251 GGCATGACCT CTGCTGGATC ATTAGTTCTA GCCAGAGAAG TAGCAAAGGA
 301 ACATGACGTC TGAGACCTCC CTTCCCTCAT CAGTGGGGCT GACTGAGCTG
 351 GGGGCTTGAA GCCGGAGGTA ACCTTTCCTG TCGAATGTTT CTTTAGAGAA
 401 TGGCAATGGT CTCTGCGATG TCCTGGGTCC TGTATTTGTG GATAAGTGCT
 451 TGTGCAATGC TACTCTGCCA TGGATCCCTT CAGCACACTT TCCAGCAGCA
 501 TCACCTGCAC AGACCAGAAG GAGGGACGTG TGAAGTGATA GCAGCACACC
 551 GATGTTGCAA CAAGAATCGC ATTGAGGAGC GGTCACAAAC AGTAAAGTGT
 601 TCCTGTCTAC CTGGAAAAGT GGCTGGAACA ACAAGAAACC GGCCTTCTTG
 651 CGTCGATGCC TCCATAGTGA TTTGGAAATG GTGGTGTGAG ATGGAGCCTT
 701 GCCTAGAAGG AGAAGAATGT AAGACACTCC CTGACAATTC TGGATGGATG
 751 TGCGCAACAG GCAACAAAAT TAAGACCACG AGAATTCACC CAAGAACCTA
 801 ACAGAAGCAT TTGTGGTAGT AAAGGAAAAC CAACCCTCTG GAAAATACAT
 851 TTTGAGAATC TCAAACATCT CACATATATA CAAGCCAAAT GGATTTCTTA
 901 CTTGCACTTT GACTGGCTAC CAGATAATCA CAGTGCGTTT AGTGTGTGTA
 951 ACGAAATATC CTACAGTGAG AAGACACAGC GTTTTGGCAT CACCATGGAA
1001 AGTGGGCTTA AAAAAGGGTC TTCTCAGTGA AATTTTTGGG CATCATGAAG
1051 AACGATCAAC TATCTTCTAA TTTGAATCTA TAGTTACTTT GTACCATTTG
1101 AAATATATGT ATATATATAT ATATAATATT TTGAAATATT ATCTATTCTC
1151 TTCAAGAAAT GAACAGTACC ACAGTTTGAG ACGGCTGGTG TACCCCTTTG
1201 AGTTTTGGAT GTTTTGTCTG TTTTGCTTTG TTTTGTTAGT CATTTCTTTT
1251 TCTAACGGCA AGGAAGATAT GTGCCCTTTT GAGAATTCAA GATGGCACTG
1301 ACACGGGAAG GCCAGCTACA GGTGGACTCC TGGAATTTGA GGCATCATAA
1351 TGATACTGAA TCAAGAACTT CCTTCTGCTT CTACCAGATG GCCCAAGGAA
1401 GCACATCGTC CTGTTTTATT GCTTTCTACC CTGTGCAATA TTAGCATGCA
1451 AGCTTGGCTT ACATAGTCAT ACTTTATATT CAATTGATAT ATAATAACCG
1501 TTCTAACCTC TTCCAGGAAA ATATTTTTAG AACTACTAGC TTTTCCACTT
1551 AGAAGAAAAT GAGGATTCTT AAGGGAGCCA CTCCACCATG CTATTAAGAC
1601 TCTGGCAGAG TTATGGGTAG GATATGGATC CCTACATGAA TAAGTCCTGT
1651 AAATACAATG TCTTAAGGCT TTGTATAGCT GTCCTAGACT GCAGAAATGT
1701 CCTCTGATTA AATCCAAAGT CTGGCATCGT TAACTACATA GTGCTGTAGC
1751 AACAAGTCTT ATCATGGCAT CTCTTTCTAT GTTTGGTTTG CTTTTTCCAA
1801 GAGTATTCAG GTCTCCTCTT GTGAGATAGG AAGGCCATGA AAACAATTAG
1851 ATTTCAAGAT GATCTATGTG ACCAAATGTT GGACAGCCCT ATTAAAGTGG
1901 TAAACAACTT CTTTCTAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

```
ORF from 400 bp to 798 bp; peptide length: 133
Category: similarity to unknown protein
Classification: no clue

    1 MAMVSAMSWV LYLWISACAM LLCHGSLQHT FQQHHLHRPE GGTCEVIAAH
   51 RCCNKNRIEE RSQTVKCSCL PGKVAGTTRN RPSCVDASIV IWKWWCEMEP
  101 CLEGEECKTL PDNSGWMCAT GNKIKTTRIH PRT
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4b6, frame 1

```
TREMBLNEW:AF131851_1 product: "Unknown"; Homo sapiens clone 25003 mRNA
sequence, partial cds., N = 1, Score = 242, P = 1.7e-20

>TREMBLNEW:AF131851_1 product: "Unknown"; Homo sapiens clone 25003 mRNA
     sequence, partial cds.
            Length = 165

  HSPs:

 Score = 242 (36.3 bits), Expect = 1.7e-20, P = 1.7e-20
 Identities = 44/89 (49%), Positives = 58/89 (65%)

Query:    42 GTCEVIAAHRCCNKNRIEERSQTVKCSCLPGKVAGTTRNRPSCVDASIVIWKWWCEMEPC 101
             GTCE++   R  ++ R      QT +C+C  G++AGTTR RP+CVDA I+  K WC+M PC
Sbjct:    76 GTCEIVTLDRDSSQPRRTIARQTARCACRKGQIAGTTRARPACVDARIIKTKQWCDMLPC 135

Query:   102 LEGEECKTLPDNSGWMCAT-GNKIKTTRI 129
             LEGE C  L + SGW C   G +IKTT +
Sbjct:   136 LEGEGCDLLINRSGWTCTQPGGRIKTTTV 164
```

Pedant information for DKFZphfkd2_4b6, frame 1

Report for DKFZphfkd2_4b6.1

```
[LENGTH]        133
[MW]            15030.64
[pI]            8.49
[HOMOL]         TREMBLNEW:AF131851_1 product: "Unknown"; Homo sapiens clone 25003 mRNA
sequence, partial cds. 4e-20
[KW]            Alpha_Beta
[KW]            SIGNAL_PEPTIDE 26

SEQ     MAMVSAMSWVLYLWISACAMLLCHGSLQHTFQQHHLHRPEGGTCEVIAAHRCCNKNRIEE
PRD     cchhhhhhhhhhhhhhhhhhhhcccccchhhhhhcccccccceeeeeeeccccchhhh

SEQ     RSQTVKCSCLPGKVAGTTRNRPSCVDASIVIWKWWCEMEPCLEGEECKTLPDNSGWMCAT
PRD     hhhhhhccccccccccccccccceeeeeehhhhhhcccccccccceeeecccccceeec

SEQ     GNKIKTTRIHPRT
PRD     ccccccccccccc
```

(No Prosite data available for DKFZphfkd2_4b6.1)

(No Pfam data available for DKFZphfkd2_4b6.1)

DKFZphfkd2_4c8
----

group: kidney derived

DKFZphfkd2_4c8 encodes a novel 153 amino acid protein with partial similarity to huntington's associated protein HAP1.

The novel protein contains a leucine zipper involved in protein-protein interaction.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes.

similarity to KIAA0549 and HAP1

potential frame shift at Bp ~1350-1500 will be checked

Sequenced by GBF

Locus: unknown

Insert length: 3182 bp
Poly A stretch at pos. 3162, polyadenylation signal at pos. 3135

```
   1 GGGCTTCCCC CATAGAATTT TTCTTTTCAT TGCCCACTTT ACTGTTTTGG
  51 CTCCAGACTG TCGTTAAGAA TGTACAGCCT AATTCTGGTG TGTTTCGGGA
 101 TATTCTTCTG TCCAGTATTC TGGAAGGGCG GGGAGGCATG GCAGCGTTTT
 151 ACTTGACGTT GATGGTGCTG TGAAGTCCAT TCTTTCCTCT GCAAGACTAC
 201 TGACTATGCA GAAATTTATC GAAGCGGATT ATTATGAACT AGACTGGTAT
 251 TATGAAGAAT GCTCGGATGT TTTATGTGCT GAAAGAGTTG GCCAGATGAC
 301 TAAGACATAT AATGACATAG ATGCTGTCAC TCGGCTTCTT GAGGAGAAAG
 351 AGCGGGATTT AGAATTGGCC GCTCGCATCG GCCAGTCGTT GTTGAAGAAG
 401 AACAAGACCC TAACCGAGAG GAACGAGCTG CTGGAGGAGC AGGTGGAACA
 451 CATCAGGGAG GAGGTGTCTC AGCTCCGGCA TGAGCTGTCC ATGAAGGATG
 501 AGCTGCTTCA GTTCTACACC AGCGCAGCGG AGGAGAGTGA GCCCGAGTCC
 551 GTTTGCTCAA CCCCGTTGAA GAGGAATGAG TCGTCCTCCT CAGTCCAGAA
 601 TTACTTTCAT TTGGATTCTC TTCAAAAGAA GCTGAAAGAC CTTGAAGAGG
 651 AGAATGTTGT ACTTCGATCC GAGGCCAGCC AGCTGAAGAC AGAGACCATC
 701 ACCTATGAGG AGAAGGAGCA GCAGCTGGTC AATGACTGCG TGAAGGAGCT
 751 GAGGGATGCC AATGTCCAGA TTGCTAGTAT CTCAGAGGAA CTGGCCAAGA
 801 AGACGGAAGA TGCTGCCCGC CAGCAAGAGG AGATCACACA CCTGCTATCG
 851 CAAATAGTTG ATTTGCAGAA AAAGGCAAAA GCTTGCGCAG TGGAAAATGA
 901 AGAACTTGTC CAGCATCTGG GGGCTGCTAA GGATGCCCAG CGGCAGCTCA
 951 CAGCCGAGCT GCGTGAGCTG GAGGACAAGT ACGCAGAGTG CATGGAGATG
1001 CTGCATGAGG CGCAGGAGGA GCTGAAGAAC CTCCGGAACA AAACCATGCC
1051 CAATACCACG TCTCGGCGCT ACCACTCACT GGGCCTGTTT CCCATGGATT
1101 CCTTGGCAGC AGAGATTGAG GGAACGATGC GCAAGGAGCT GCAGTTGGAA
1151 GAGGCCGAGT CTCCAGACAT CACTCACCAG AAGCGTGTCT TTGAGACAGT
1201 AAGAAACATC AACCAGGTTG TCAAGCAGAG ATCTCTGACC CCTTCTCCCA
1251 TGAACATCCC CGGCTCCAAC CAGTCCTCGG CCATGAACTC CCTCCTGTCC
1301 AGCTGCGTCA GCACCCCCCG GTCCAGCTTC TACGGCAGCG ACATAGGCAA
1351 CGTCGTCCTC GACAACAAGA CCAACAGCAT CATTCTGGAA ACAGAGGCAG
1401 CCGACCTGGG AAACGATGAG CGGAGTAAGA AGCCGGGGAC GCCGGGCACC
1451 CCCAGGCTCC CACGACCTGG AGACGGCGCT GAGGCGGCTG TCCCTGCGCC
1501 GGGAGAACTA CCTCTCGGAG AGGAGGTTCT TTGAGGAGGA GCAAGAGAGG
1551 AAGCTCCAGG AGCTGGCGGA GAAGGGCGAG CTGCGCAGCG GCTCCCTCAC
1601 ACCCACTGAG AGCATCATGT CCCTGGGCAC GCACTCCCGC TTCTCCGAGT
1651 TCACCGGCTT CTCTGGCATG TCCTTCAGCA GCCGCTCCTA CCTGCCTGAG
1701 AAGCTCCAGA TCGTGAAGCC GCTGGAAGGT GATCACGCGG GGCCTCGGCC
1751 CCTCTCTGTC CTCCTGGGGG ACTCCCTTTG GTCCCTGATC CACCTGCGGA
1801 AGGCGGGGCA CCTCTGTCAC GCCTACTCCT TTTTCTTCCG CGACAGCCAC
1851 CCGCGCTGCT GGTTTGAGTT CCTCTGAGGG TGGTGCTCAG CCTAGGCCTC
1901 CGTCCCTCCC CTCTGGCTGG CAGGTGTGAC AATGCACACA TAGGCCATGA
1951 AACTCGCCGA GGAAAGACAA GCATGTGCAC TGTGGTCTTC TAGTTCTTTC
2001 CTTTGCCTTT AGAACCTTAG AAATAAAAAC TTTTGTGGCG GTAGAGGCAC
2051 TGCTAACTGA TTCAAAAATT AATTAGGTTT TGCCTGTGGG TGTGAGGAAT
2101 GCAGAAAATT AATGCTTTAG CTTTTCTGCA GTTTTGGTGT CGGGGAGAGG
2151 TTCCAAGCAA ACTCTATTAA ATGGGGATTT TTTTTTCCCC ATAACCACCT
2201 GAATGTGATT TGTGGGCTTA TGTGTTCTGA TTTGAACTTC ATATAGCAAG
2251 GTTGTGGCTT TTGGCAGATG CAGTATGTTC TGAGCGCGGC TCCTAGAGTC
2301 TACAATTTGG AGTCCAGGAA GGGGTGGCTG TGGAGACAAG TGAGTTTTGT
2351 ACCTCCGTAA GCCACCCTTT TTCAGGGTCA GTTCATGTGT TAGTATCAGG
2401 GGCATCTCAG ATGATTAAAC TCATGGGAAA AACTTCCTCC TTCCCTCTCT
2451 CCCTCTTGCC CTCCTGCCTC TTTTTTTTTT TTTTTTTTTT AATTTGGGCA
2501 CTTATAAAAT GTTTTCCCTC TACCTGCTGC TACTCTGCCA AGAGCCACCA
2551 AGTGCTTATA TTTTTCATTT TTTACTCCTT TAGTTTGGAA AGCCATATAC
2601 GTTTGAGAAG GTGTTTTAAA ACTCTGTGTT ACACTTACGA TGCAAAGCCA
2651 AATCAGAACT TCTGTAAGGC AGAACTTTCC CAACTTTAAA AAAATTATTG
```

```
2701 TCCCCTCTAG GAGCCTTCTT AGACGTTTTT TCCTAATCAC CCCCCAAAGA
2751 CATTTTAATA CCACATATAT ATTGTTTATG TACTATATGT ATATACATAA
2801 ACAATACATA AGCAATACAT CTGTGGTATT AAAATTAAAA AGAATCCAAT
2851 TATGTTTACC TCAAAAGAAC CTGTTTTTGC TTCTTGGGAG CAATATTGCC
2901 CCTGTGAGAC TGCATGCTAT AAGGTAAGGT TGTGCTTGTT AAAGACCCAA
2951 GACATGACTG GGTTCCACAG TCTCCAAAGG AAGAGGGTGG GCTAGTTTGT
3001 TTTTATTATT ATTTTAAAAT TGTATAATTG GGGTCTTTCT TAGAGTTCAG
3051 AAAAGGTATA GCTTACTCTT TTTTAATTGT TTATTTAGTT GTAAGCTTAG
3101 TGATTGTTTT CTGATCCACA TTGTGTGTGT TCTTCAATAA AATCTTTCAT
3151 TTCTGCAATT TTAAAAAAAA AAAAAAAAAA AA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 206 bp to 1531 bp; peptide length: 442
Category: similarity to known protein
Classification: unset
Prosite motifs: LEUCINE_ZIPPER (139-161)

```
  1 MQKFIEADYY ELDWYYEECS DVLCAERVGQ MTKTYNDIDA VTRLLEEKER
 51 DLELAARIGQ SLLKKNKTLT ERNELLEEQV EHIREEVSQL RHELSMKDEL
101 LQFYTSAAEE SEPESVCSTP LKRNESSSSV QNYFHLDSLQ KKLKDLEEEN
151 VVLRSEASQL KTETITYEEK EQQLVNDCVK ELRDANVQIA SISEELAKKT
201 EDAARQQEEI THLLSQIVDL QKKAKACAVE NEELVQHLGA AKDAQRQLTA
251 ELRELEDKYA ECMEMLHEAQ EELKNLRNKT MPNTTSRRYH SLGLFPMDSL
301 AAEIEGTMRK ELQLEEAESP DITHQKRVFE TVRNINQVVK QRSLTPSPMN
351 IPGSNQSSAM NSLLSSCVST PRSSFYGSDI GNVVLDNKTN SIILETEAAD
401 LGNDERSKKP GTPGTPRLPR PGDGAEAAVP APGELPLGEE VL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4c8, frame 2

PIR:S72555 huntingtin-associated protein HAP1 - human (fragment), N = 1, Score = 234, P = 8.6e-19

TREMBL:CEUT27A3_7 gene: "T27A3.1"; Caenorhabditis elegans cosmid T27A3., N = 1, Score = 226, P = 9.9e-16

PIR:S67495 huntingtin-associated protein HAP1-A - rat, N = 1, Score = 215, P = 1.6e-14

>PIR:S72555 huntingtin-associated protein HAP1 - human (fragment)
Length = 320

HSPs:

Score = 234 (35.1 bits), Expect = 8.6e-19, P = 8.6e-19
Identities = 66/189 (34%), Positives = 110/189 (58%)

```
Query:   109 EESEPESVCSTPLKRNE--SSSSVQNYFH---LDSLQKKLKDLEEENVVLRSEASQLKTE 163
             EE+E +  C+ P     +  S  ++ +  H    L++LQ+KL+ LEEEN  LR EASQL T
Sbjct:     28 EEAEEDLQCAHPCDAPKLISQEALLHQHHCPQLEALQEKLRLLEEENHQLREEASQLDT- 86

Query:   164 TITYEEKEQQLVNDCVKELRDANVQIASISEELAKKTEDAARQQEEITHLLSQIVDLQKK 223
                 E++EQ L+ +CV++  +A+ Q+A +SE L  + E+  RQQ+E+  L +Q++ LQ++
Sbjct:     87 ---LEDEEQMLILECVEQFSEASQQMAELSEVLVLRLENYERQQQEVARLQAQVLKLQQR 143

Query:   224 AKACAVENEELVQHLGAAKDAQRQLTAE--LRELEDKYAECME--MLHEAQEELKNL-RN 278
             +     E E+L + L + K+ Q QL  E  L   ++  AE +   +     + + + RN
```

```
Sbjct:    144 CRMYGAETEKLQKQLASEKEIQMQLQEEETLPGFQETLAEELRTSLRRMISDPVYFMERN 203

Query:    279 KTMP--NTTSRRY 289
                MP  +T+S RY
Sbjct:    204 YEMPRGDTSSLRY 216
```

Peptide information for frame 3

ORF from 1416 bp to 1874 bp; peptide length: 153
Category: similarity to known protein
Classification: unset

```
  1 MSGVRSRGRR APPGSHDLET ALRRLSLRRE NYLSERRFFE EEQERKLQEL
 51 AEKGELRSGS LTPTESIMSL GTHSRFSEFT GFSGMSFSSR SYLPEKLQIV
101 KPLEGDHAGP RPLSVLLGDS LWSLIHLRKA GHLCHAYSFF FRDSHPRCWF
151 EFL
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4c8, frame 3

TREMBL:AB011121_1 gene: "KIAA0549"; product: "KIAA0549 protein"; Homo sapiens mRNA for KIAA0549 protein, partial cds., N = 1, Score = 252, P = 5.5e-21

>TREMBL:AB011121_1 gene: "KIAA0549"; product: "KIAA0549 protein"; Homo sapiens mRNA for KIAA0549 protein, partial cds.
Length = 469

HSPs:

Score = 252 (37.8 bits), Expect = 5.5e-21, P = 5.5e-21
Identities = 57/98 (58%), Positives = 69/98 (70%)

```
Query:      8 GRRAPPGSHDLETALRRLSLRRENYLSERRFFEEEQERKLQELAEKGELRSGSLTPTESI 67
              G+   P G  DL TAL RLSLRR+NYLSE++FF EE +RK+Q LA++ E  SG +TPTES+
Sbjct:     27 GQPGPSGDSDLATALHRLSLRRQNYLSEKQFFAEEWQRKIQVLADQKEGVSGCVTPTESL 86

Query:     68 MSLGTHSRFSEFTGFSGMSFSSRSYLPEKLQIVKPLEG 105
                SL T     SE T  S  S    R ++PEKLQIVKPLEG
Sbjct:     87 ASLCTTQ--SEITDLSSAS-CLRGFMPEKLQIVKPLEG 121
```

Pedant information for DKFZphfkd2_4c8, frame 2

Report for DKFZphfkd2_4c8.2

[LENGTH] 442
[MW] 50020.14
[pI] 4.77
[HOMOL] TREMBL:AF040723_1 product: "neuroanl"; Homo sapiens neuroanl mRNA, complete cds. 5e-29
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 5e-08
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YIL149c] 5e-08
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 5e-08
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YIL138c] 6e-08
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YGR130c] 2e-07
[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 1e-06
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR356w] 1e-06
[FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1643] 1e-06
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-06
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 3e-06
[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 4e-06
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YKR095w] 4e-06
[FUNCAT] 03.13 meiosis [S. cerevisiae, YNL250w] 2e-05
[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 2e-05

[FUNCAT] 08.99 other intracellular-transport activities [S. cerevisiae, YNL079c] 5e-05
[FUNCAT] 03.01 cell growth [S. cerevisiae, YNL079c] 5e-05
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YNL079c] 5e-05
[FUNCAT] 10.05.99 other pheromone response activities [S. cerevisiae, YHR158c] 1e-04
[FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 1e-04
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YNL272c] 3e-04
[FUNCAT] 08.16 extracellular transport [S. cerevisiae, YNL272c] 3e-04
[BLOCKS] BL01289B
[BLOCKS] BL00415M Synapsins proteins
[EC] 3.6.1.32 Myosin ATPase 2e-07
[PIRKW] tandem repeat 2e-07
[PIRKW] heterodimer 1e-06
[PIRKW] endocytosis 9e-07
[PIRKW] heart 1e-06
[PIRKW] transmembrane protein 4e-07
[PIRKW] zinc finger 9e-07
[PIRKW] metal binding 9e-07
[PIRKW] DNA binding 3e-06
[PIRKW] muscle contraction 2e-07
[PIRKW] acetylated amino end 3e-06
[PIRKW] actin binding 2e-07
[PIRKW] mitosis 1e-06
[PIRKW] microtubule binding 1e-06
[PIRKW] ATP 2e-07
[PIRKW] chromosomal protein 1e-06
[PIRKW] receptor 3e-08
[PIRKW] thick filament 2e-07
[PIRKW] phosphoprotein 8e-06
[PIRKW] glycoprotein 3e-08
[PIRKW] skeletal muscle 3e-06
[PIRKW] DNA condensation 1e-06
[PIRKW] alternative splicing 2e-06
[PIRKW] coiled coil 2e-07
[PIRKW] P-loop 2e-07
[PIRKW] heptad repeat 4e-07
[PIRKW] methylated amino acid 2e-07
[PIRKW] peripheral membrane protein 9e-07
[PIRKW] cardiac muscle 6e-06
[PIRKW] hydrolase 2e-07
[PIRKW] muscle 2e-06
[PIRKW] cytoskeleton 2e-06
[PIRKW] Golgi apparatus 4e-07
[PIRKW] calmodulin binding 9e-07
[SUPFAM] myosin motor domain homology 2e-07
[SUPFAM] tropomyosin TPM1 2e-06
[SUPFAM] giantin 4e-07
[SUPFAM] protein kinase C zinc-binding repeat homology 2e-06
[SUPFAM] human early endosome antigen 1 9e-07
[SUPFAM] unassigned kinesin-related proteins 4e-07
[SUPFAM] M5 protein 8e-08
[SUPFAM] cytoskeletal keratin 3e-06
[SUPFAM] myosin heavy chain 2e-07
[SUPFAM] conserved hypothetical P115 protein 1e-06
[SUPFAM] centromere protein E 1e-06
[SUPFAM] pleckstrin repeat homology 2e-06
[SUPFAM] kinesin motor domain homology 4e-07
[PROSITE] LEUCINE_ZIPPER 1
[KW] All_Alpha
[KW] LOW_COMPLEXITY 6.79 %
[KW] COILED_COIL 27.15 %

```
SEQ    MQKFIEADYYELDWYYEECSDVLCAERVGQMTKTYNDIDAVTRLLEEKERDLELAARIGQ
SEG    ..........................................xxxxxxxxxxxxxxx...
PRD    ccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ...........................................................C

SEQ    SLLKKNKTLTERNELLEEQVEHIREEVSQLRHELSMKDELLQFYTSAAEESEPESVCSTP
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC........................

SEQ    LKRNESSSSVQNYFHLDSLQKKLKDLEEENVVLRSEASQLKTETITYEEKEQQLVNDCVK
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ............CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC...............
```

```
SEQ     ELRDANVQIASISEELAKKTEDAARQQEEITHLLSQIVDLQKKAKACAVENEELVQHLGA
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   .................................................CCCCCCCCCCC

SEQ     AKDAQRQLTAELRELEDKYAECMEMLHEAQEELKNLRNKTMPNTTSRRYHSLGLFPMDSL
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS   CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC.....................

SEQ     AAEIEGTMRKELQLEEAESPDITHQKRVFETVRNINQVVKQRSLTPSPMNIPGSNQSSAM
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccchhhh
COILS   ............................................................

SEQ     NSLLSSCVSTPRSSFYGSDIGNVVLDNKTNSIILETEAADLGNDERSKKPGTPGTPRLPR
SEG     .................................................xxxxxxxxxxx
PRD     hhhhhcccccccccccccccceeeeeccccceeeccccccccccccccccccccccccc
COILS   ............................................................

SEQ     PGDGAEAAVPAPGELPLGEEVL
SEG     xxxx..................
PRD     cccccccccccccccccccccc
COILS   ......................
```

Prosite for DKFZphfkd2_4c8.2

```
PS00029     139->161    LEUCINE_ZIPPER        PDOC00029
```

(No Pfam data available for DKFZphfkd2_4c8.2)

Pedant information for DKFZphfkd2_4c8, frame 3

Report for DKFZphfkd2_4c8.3

```
[LENGTH]        153
[MW]            17642.03
[pI]            9.38
[HOMOL]         TREMBL:AB011121_1 gene: "KIAA0549"; product: "KIAA0549 protein"; Homo sapiens
mRNA for KIAA0549 protein, partial cds. 2e-12
[KW]            Alpha_Beta
[KW]            LOW_COMPLEXITY    12.42 %
```

```
SEQ     MSGVRSRGRRAPPGSHDLETALRRLSLRRENYLSERRFFEEEQERKLQELAEKGELRSGS
SEG     ..................................xxxxxxxxxxxxxxxxxxx.......
PRD     cccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccc

SEQ     LTPTESIMSLGTHSRFSEFTGFSGMSFSSRSYLPEKLQIVKPLEGDHAGPRPLSVLLGDS
SEG     ............................................................
PRD     cccccceeeccccceeecccccccccccccccccchhhhhhhcccccccccceeeeeccc

SEQ     LWSLIHLRKAGHLCHAYSFFFRDSHPRCWFEFL
SEG     .................................
PRD     chhhhhhhhhcccccceeeeecccccccccccc
```

(No Prosite data available for DKFZphfkd2_4c8.3)

(No Pfam data available for DKFZphfkd2_4c8.3)

DKFZphfkd2_4k14
----

group: intracellular transport and trafficking

DKFZphfkd2_4k14.3 encodes a novel 254 amino acid putative GTP-binding protein nearly identical to Rab6.

Rab proteins are members of the Ras superfamily of GTPases. Rab proteins are localised to the cytoplasmic side of organelles and vesicles involved in the secretory (biosynthetic) and endocytotic pathways in eukaryotic cells. Rab proteins direct the targeting and fusion of transport vesicles to their acceptor membranes.
rab6 is a ubiquitous ras-like GTPase involved in intra-Golgi transport.

The new protein can find application in modulating the transport of vesicles inside the Golgi apparatus.

strong similarity to Rab6

complete cDNA, complete cds, EST hits

Sequenced by GBF

Locus: unknown

Insert length: 3084 bp
Poly A stretch at pos. 3061, polyadenylation signal at pos. 3043

```
   1 GGGGCACTCA GCAGGTTGGG CTGCGGCGGC GGCGGCTGGG GAAGCCGAAG
  51 CGCCGCGCGT GAGAGATCCC GGATACATCT GCGGTTTGGG CTCCGCCACC
 101 CTCCGTCTCT CTCCCGCAGG TCTCTGAGCC GGGTGCGGAA GGAGGGAACG
 151 GCCCTAGCCT TGGGAAGCCA AAGCACACCC CTGGCTCCCG CCGACACCGC
 201 CCTCCTTCCC TTCCCAGCCG CGGGCCTCGC TCCGTGCTCG GCTACTCTGC
 251 CGGGAGGCGG CGGCGGCTGC CAGTCTGTGG CGAGCCCTGC TGCCCTCCAG
 301 CCGGGCTTCT CCAGCCGGGC TCCTCCACCG GCCCTTGCAG GGGCACAGAG
 351 AGCTCGGCGC CCGCCCTTCC GCTCGCCTTT TTCGTCAGCC GGCTGGAGGA
 401 GCATCGGTCC GGGAGGTCTC TGGGCTGAGG CGGCGACAGC TCCTCTAGTT
 451 CCACCATGTC CGCGGGCGGA GACTTCGGGA ATCCGCTGAG GAAATTCAAG
 501 CTGGTGTTCC TGGGGGAGCA AAGCGTTGCA AAGACATCTT TGATCACCAG
 551 ATTCAGGTAT GACAGTTTTG ACAACACCTA TCAGGCAATA ATTGGCATTG
 601 ACTTTTTATC AAAAACTATG TACTTGGAGG ATGGAACAAT CGGGCTTCGG
 651 CTGTGGGATA CGGCGGGTCA GGAACGTCTC CGTAGCCTCA TTCCCAGGTA
 701 CATCCGTGAT TCTGCTGCAG CTGTAGTAGT TTACGATATC ACAAATGTTA
 751 ACTCATTCCA GCAAACTACA AAGTGGATTG ATGATGTCAG AACAGAAAGA
 801 GGAAGTGATG TTATCATCAC GCTAGTAGGA AATAGAACAG ATCTTGCTGA
 851 CAAGAGGCAA GTGTCAGTTG AGGAGGGAGA GAGGAAAGCC AAAGGGCTGA
 901 ATGTTACGTT TATTGAAACT AGGGCAAAAA CTGGATACAA TGTAAAGCAG
 951 CTCTTTCGAC GTGTAGCAGC AGCTTTGCCG GGAATGGAAA GCACACAGGA
1001 CGGAAGCAGA GAAGACATGA GTGACATAAA ACTGGAAAAG CCTCAGGAGC
1051 AAACAGTCAG CGAAGGGGGT TGTTCCTGCT ACTCTCCCAT GTCATCTTCA
1101 ACCCTTCCTC AGAAGCCCCC TTACTCTTTC ATTGACTGCA GTGTGAATAT
1151 TGGCTTGAAC CTTTTCCCTT CATTAATAAC GTTTTGCAAT TCATCATTGC
1201 TGCCTGTCTC GTGGAGGTGA TCTATTAGCT TCACAAGCAC AAAAAAAGTC
1251 AGCGTCTTCA TTATTTATAT TTTACAAAAA GCCAAATTAT TTCAGCATAT
1301 TCCGGTGATA ACTTTAAAAA TTAGATACAT TTTCTTAACA TTTTTTTCTT
1351 TTTTAATGTT ATGATAATGT ACTTCAAAAT GATGGAAATC TCAACAGTAT
1401 GAGTATGGCT TGGTTAACGA GCAGTATGTT CACAGCCTGC TTTATCTCTC
1451 CTTGCTCTTC TCACCTCTCC CTTACCCCGT TCCCTATTTC CGTGTTCTTA
1501 CCTAGCCTCC CCCCACTTCC TCAAAACAAA CAAGAGATGG CAAAGCAGCA
1551 GTCCGACCAA GCCCACTGGA ATTATCCTTT AATTTTACAG ATACCACTTG
1601 CTGTAGGCTG TGGACCAAGA TGTCCAGAAT TATTCTTGAG CACTGATGTA
1651 AATTACTTAG ATCTTCTTTG AGGTCAGAAT TCAGCGATCA CGGTAGGCAG
1701 TGCTTGAATG AGAAAAGCCT CCTGGTGCAT CTTCAAAATG AGTCCTAAAG
1751 AACATACTGA GTACTTATAA GTAGCAGAAC ATAAAATGTA TTTCTGACTA
1801 ACACAAATGG TCCTTTCACA TGTGCTTTAT TAGACTCTGG GAGAGAAAAG
1851 TAACCAAGTG CTTCAGAACA GGTTTTTAGT ATTTACTTCT TCATGGTAAG
1901 ATAATGAAGT TCTAATGAAC TATTTCTCCC AAGGTTTTAA AATTGTCAAG
1951 AGTTATTCTG TTTGTTTAAA AAGTAAGAAA CCTCTGTAAG CAATAGATTT
2001 TGCTTGGGTT TTCTTTCTTA AAAAAATAAT ACTATGCAGG CAAGACACCA
2051 TAAAAGTTTA ATTCCTTACA GAAGAACCAG TGGAAGAATT TAAATTTGGC
2101 ACTACGATCA AAACTACTGA ATTAGCAGAA ATAACGATAT CTAAAGCTTA
2151 CCAGCAAAAG AACCCTCAGC AGAATAGCAA AAACTTTGCT CAGGACATTT
2201 GAGGTCAAAT TGAAGACGGA AGACGGAAAC CGGAAACCGT TTTCTTGTAA
2251 GCCCCTAGAG GCAGATCAGG TAAGCATACA TAGTAGAGGG AAAGGAGAGA
2301 ATGGAAATAA AACTGAATAT TATGCAGATT TATGCCTTAT TTTTTAGCAT
2351 TTTTTAAGGT TGGGTCTTTC AGGCTGGTTT TGGTTTGTAT TAGATCTGTA
2401 TAGTTTAGTG ATTTAGTTTT ATATTTAAGC TACGATTAAT ATTTTTTCTT
2451 TGGCGATATT TCTTTGCTTT TTTTTTTTAA CAACTTTCCA TTTTTAGATG
```

```
2501 TTTCGTTGAA TCTATTTAGA GCTTCACCAT GGCAATATGT ATTTCCCTTA
2551 AAACACTGCA AACAAATATA CTAGGAGTGT GCCCTTTTAA TCTTTACTAG
2601 TTATTGTGAG ACTGCTGTGT AAGCTAATAA ACACATTTGT AAAAACATTG
2651 TTTGCAGGAA GAAAACTTCG AGTTACAGGT CAGGAAAAGC CTGCTGAATT
2701 TATGTTGTAA ACGTTACTTA ACACAGTATA AAGATGAAAA GACAACAAAA
2751 GTATCTTCAT ACTTCCTCAT CCCCTCATTG CAACAAAACC TTAAACTGGG
2801 AGAACCTTAG TCCCCTCTCT TTCCTCTTCC TCCTCCACTT CCCACTTATT
2851 GCCACTTTGT AATATTCAGA GAGCACTTGG ATTATGGATC TGAATAGAGA
2901 AATGCTTACA GATAATCATT AGCCCACATA CCAGTAACTT ATACTTAAAG
2951 ATGGGATGGA GTTATAAAGT GCTTTTATAA TCCAATATAA TTGCTAAAGG
3001 CAAGGGTTGA CTCTTTGTTT TATTTTGACA TGGCATGTCC TGAAATAAAT
3051 ATTGGTTCAC TATGAAAAAA AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

98382468:
Rab proteins.

97203146:
GTP-bound forms of rab6 induce the redistribution of Golgi proteins into the endoplasmic reticulum.

Peptide information for frame 3

ORF from 456 bp to 1217 bp; peptide length: 254
Category: strong similarity to known protein
Classification: unset
Prosite motifs: BACTERIAL_OPSIN_RET (45-57)

```
  1 MSAGGDFGNP LRKFKLVFLG EQSVAKTSLI TRFRYDSFDN TYQAIIGIDF
 51 LSKTMYLEDG TIGLRLWDTA GQERLRSLIP RYIRDSAAAV VVYDITNVNS
101 FQQTTKWIDD VRTERGSDVI ITLVGNRTDL ADKRQVSVEE GERKAKGLNV
151 TFIETRAKTG YNVKQLFRRV AAALPGMEST QDGSREDMSD IKLEKPQEQT
201 VSEGGCSCYS PMSSSTLPQK PPYSFIDCSV NIGLNLFPSL ITFCNSSLLP
251 VSWR
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphfkd2_4k14, frame 3

PIR:G34323 GTP-binding protein Rab6 - human, N = 1, Score = 944, P = 6.5e-95

TREMBL:CET25G12_2 gene: "T25G12.4"; Caenorhabditis elegans cosmid T25G12., N = 1, Score = 756, P = 5.4e-75

TREMBL:NTNTRAF_1 gene: "Nt-rab6"; Nicotiana tabacum SR1 Nt-rab6 mRNA, complete cds., N = 1, Score = 698, P = 7.6e-69

TREMBL:D84314_1 product: "rab6"; Drosophila melanogaster mRNA for rab6, complete cds., N = 1, Score = 836, P = 1.9e-83

PIR:T01588 small GTP-binding protein F16B22.10 - Arabidopsis thaliana, N = 1, Score = 704, P = 1.8e-69

>PIR:G34323 GTP-binding protein Rab6 - human
Length = 208

HSPs:

Score = 944 (141.6 bits), Expect = 6.5e-95, P = 6.5e-95
Identities = 186/208 (89%), Positives = 190/208 (91%)

```
Query:     1 MSAGGDFGNPLRKFKLVFLGEQSVAKTSLITRFRYDSFDNTYQAIIGIDFLSKTMYLEDG 60
             MS GGDFGNPLRKFKLVFLGEQSV KTSLITRF YDSFDNTYQA IGIDFLSKTMYLED
Sbjct:     1 MSTGGDFGNPLRKFKLVFLGEQSVGKTSLITRFMYDSFDNTYQATIGIDFLSKTMYLEDR 60

Query:    61 TIGLRLWDTAGQERLRSLIPRYIRDSAAAVVVYDITNVNSFQQTTKWIDDVRTERGSDVI 120
             T+ L+LWDTAGQER RSLIP YIRDS  AVVVYDITNVNSFQQTTKWIDDVRTERGSDVI
Sbjct:    61 TVRLQLWDTAGQERFRSLIPSYIRDSTVAVVVYDITNVNSFQQTTKWIDDVRTERGSDVI 120

Query:   121 ITLVGNRTDLADKRQVSVEEGERKAKGLNVTFIETRAKTGYNVKQLFRRVAAALPGMEST 180
             I LVGN+TDLADKRQVS+EEGERKAK LNV FIET AK GYNVKQLFRRVAAALPGMEST
Sbjct:   121 IMLVGNKTDLADKRQVSIEEGERKAKELNVMFIETSAKAGYNVKQLFRRVAAALPGMEST 180

Query:   181 QDGSREDMSDIKLEKPQEQTVSEGGCSC 208
             QD SREDM DIKLEKPQEQ VSEGGCSC
Sbjct:   181 QDRSREDMIDIKLEKPQEQPVSEGGCSC 208
```

Pedant information for DKFZphfkd2_4k14, frame 3

Report for DKFZphfkd2_4k14.3

```
[LENGTH]    254
[MW]        28385.29
[pI]        7.58
[HOMOL]     PIR:G34323 GTP-binding protein Rab6 - human 1e-102
[FUNCAT]    08.07 vesicular transport (golgi network, etc.)  [S. cerevisiae, YLR262c] 7e-60
[FUNCAT]    30.08 organization of golgi  [S. cerevisiae, YLR262c] 7e-60
[FUNCAT]    30.09 organization of intracellular transport vesicles  [S. cerevisiae, YOR089c] 2e-33
[FUNCAT]    08.19 cellular import [S. cerevisiae, YOR089c] 2e-33
[FUNCAT]    08.13 vacuolar transport  [S. cerevisiae, YOR089c] 2e-33
[FUNCAT]    06.04 protein targeting, sorting and translocation  [S. cerevisiae, YOR089c] 2e-33
[FUNCAT]    09.09 biogenesis of intracellular transport vesicles  [S. cerevisiae, YGL210w] 3e-28
[FUNCAT]    30.02 organization of plasma membrane  [S. cerevisiae, YFL005w] 8e-27
[FUNCAT]    03.04 budding, cell polarity and filament formation [S. cerevisiae, YFL005w] 8e-27
[FUNCAT]    01.05.04 regulation of carbohydrate utilization  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    11.10 cell death  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    01.03.13 regulation of nucleotide metabolism  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    30.03 organization of cytoplasm  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    03.99 other cell growth, cell division and dna synthesis activities  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    10.04.07 g-proteins  [S. cerevisiae, YOR101w] 2e-21
[FUNCAT]    03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 6e-19
[FUNCAT]    11.01 stress response [S. cerevisiae, YNL098c] 6e-19
[FUNCAT]    03.10 sporulation and germination  [S. cerevisiae, YNL098c] 6e-19
[FUNCAT]    04.07 rna transport  [S. cerevisiae, YOR185c] 6e-16
[FUNCAT]    30.10 nuclear organization  [S. cerevisiae, YOR185c] 6e-16
[FUNCAT]    08.01 nuclear transport  [S. cerevisiae, YOR185c] 6e-16
[FUNCAT]    30.04 organization of cytoskeleton  [S. cerevisiae, YPR165w] 4e-13
[FUNCAT]    10.02.07 g-proteins  [S. cerevisiae, YPR165w] 4e-13
[FUNCAT]    10.99 other signal-transduction activities  [S. cerevisiae, YCR027c] 2e-09
[FUNCAT]    10.05.07 g-proteins  [S. cerevisiae, YLR229c] 8e-08
[FUNCAT]    03.07 pheromone response, mating-type determination, sex-specific proteins  [S. cerevisiae, YLR229c] 8e-08
[FUNCAT]    03.01 cell growth  [S. cerevisiae, YNL180c] 1e-05
[FUNCAT]    06.10 assembly of protein complexes  [S. cerevisiae, YOR094w] 5e-05
[BLOCKS]    BL01115A GTP-binding nuclear protein ran proteins
[SCOP]      d1as3_2 3.29.1.4.12 Transducin (alpha subunit), insertion domai 1e-32
[SCOP]      d1mh1__ 3.29.1.4.2 Rac1 (Human (Homo sapiens)  2e-51
[SCOP]      d5p21__ 3.29.1.4.1 cH-p21 Ras protein (human (Homo sapiens)  7e-53
[SCOP]      d1hura_ 3.29.1.4.8 ADP-ribosylation factor 1 (ARF1)  [human (Hom 1e-46
[SCOP]      d1a2kc_ 3.29.1.4.5 Ran Nuclear transport factor-2 (NTF2)  (Do 6e-60
[PIRKW]     nucleus 2e-14
[PIRKW]     cell cycle control 5e-15
[PIRKW]     membrane trafficking 3e-71
[PIRKW]     endoplasmic reticulum 1e-29
[PIRKW]     phosphoprotein 1e-29
[PIRKW]     prenylated cysteine 2e-36
[PIRKW]     signal transduction 5e-15
[PIRKW]     transforming protein 5e-30
[PIRKW]     purine nucleotide binding 1e-28
[PIRKW]     alternative splicing 1e-18
[PIRKW]     P-loop 3e-71
```

```
[PIRKW]        lipoprotein 2e-36
[PIRKW]        proto-oncogene 1e-20
[PIRKW]        methylated carboxyl end 1e-20
[PIRKW]        membrane protein 1e-29
[PIRKW]        GTP binding 3e-71
[PIRKW]        thiolester bond 1e-29
[PIRKW]        Golgi apparatus 1e-29
[SUPFAM]       ras transforming protein 1e-76
[PROSITE]      BACTERIAL_OPSIN_RET    1
[PFAM]         Ras family (contains ATP/GTP binding P-loop)
[KW]           Alpha_Beta
[KW]           3D
```

```
SEQ    MSAGGDFGNPLRKFKLVFLGEQSVAKTSLITRFRYDSFDNTYQAIIGIDFLSKTMYLEDG
1kao-  ..........CCEEEEEEEECTTTTCHHHHHHHHHHCCCCCCCTTTTC-EEEEEEEEETTE

SEQ    TIGLRLWDTAGQERLRSLIPRYIRDSAAAVVVYDITNVNSFQQTTKWIDDVRTERGSDVI
1kao-  EEEEEEEECCTTTTCHHHHHHHHHHCCEEEEEEETTTHHHHHHHHHHHHHHHHHTTTCCC

SEQ    ITLVGNRTDLADKRQVSVEEGERKAKGLNVTFIETRAKTGYNVKQLFRRVAAALPGMEST
1kao-  EEEEEETTTTGGGCCCCHHHHHHHHHHHCCCEEECTTTTHHHHHHHHHHH..........

SEQ    QDGSREDMSDIKLEKPQEQTVSEGGCSCYSPMSSSTLPQKPPYSFIDCSVNIGLNLFPSL
1kao-  ............................................................

SEQ    ITFCNSSLLPVSWR
1kao-  ..............
```

Prosite for DKFZphfkd2_4k14.3

```
PS00327       45->57    BACTERIAL_OPSIN_RET     PDOC00291
```

Pfam for DKFZphfkd2_4k14.3

```
HMM_NAME       Ras family (contains ATP/GTP binding P-loop)

HMM                *KLVLIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIEIDGKtIK
                    KLV++G+ +V K++L  RF +++F++ Y + IG+DF++KT+++++ TI
Query          15   KLVFLGEQSVAKTSLITRFRYDSFDNTYQAIIGIDFLSKTMYLEDGTIG     63

HMM                LQIWDTAGQERYRsMRPMYYRGAMGFMLVYDITNRqSFENIrNWweEIrR
                   L +WDTAGQER RS+ P Y+R++ ++++VYDITN  SF+   ++W++++R+
Query          64  LRLWDTAGQERLRSLIPRYIRDSAAAVVVYDITNVNSFQQTTKWIDDVRT    113

HMM                HCDrDENVPIMLVGNKCDLEDQRQVStEEGQeFAREWGAIPFMETSAKTN
                    +   ++V+I LVGN +DL+D+RQVS EEG+  A+ ++ + F+ET AKT+
Query         114  ERG--SDVIITLVGNRTDLADKRQVSVEEGERKAKGLN-VTFIETRAKTG    160

HMM                iNVEEAFMEIvReIlqrMqe.q.NqteNinidQpsrnrk....rCCCIM*
                   +NV++ F +++ +++ +++  + +++++++I+ ++++ +        +C+ +
Query         161  YNVKQLFRRVAAALPGMESTQDGSREDMSDIKLEKPQEQTVSEGGCS-C    208
```

DKFZphfkd2_4m11
----

group: transmembrane protein

DKFZphfbr2-4m11 encodes a novel 159 amino acid protein with weak similarity to the putative membrane protein YMR034c of S. cerevisiae.

The novel protein contains 4 transmembrane regions.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of kidney-specific genes and as a new marker of neuronal cells.

weak similarity to YMR034c

complete cDNA, complete cds, no EST hits

Sequenced by GBF

Locus: unknown

Insert length: 1749 bp
Poly A stretch at pos. 1727, polyadenylation signal at pos. 1713

```
   1 GGGGTCCTCA AAGCCGCCGG AGCAACCCCC AGGTCTTTAC TTTACAATCG
  51 GCAATTTGAC TTGCTCTGCT GCATGTCTGG AGGGACCAAG GAAAGTGTGG
 101 AGACGCTCCA AGGATTAGGT GATCGGAGCT TGAAAAGAAA AAAAGCCAAA
 151 CAAATAAACA AAACCCACCC ACCCTAACGA ATATGAGGCT GCTGGAGAGA
 201 ATGAGGAAAG ACTGGTTCAT GGTCGGAATA GTGCTGGCGA TCGCTGGAGC
 251 TAAACTGGAG CCGTCCATAG GGGTGAATGG GGGACCACTG AAGCCAGAAA
 301 TAACTGTATC CTACATTGCT GTTGCAACAA TATTCTTTAA CAGTGGACTA
 351 TCATTGAAAA CAGAGGAGCT GACCAGTGCT TTGGTGCATC TAAAACTGCA
 401 TCTTTTTATT CAGATCTTTA CTCTTGCATT CTTCCCAGCA ACAATATGGC
 451 TTTTTCTTCA GCTTTTATCA ATCACACCCA TCAACGAATG GCTTTTAAAA
 501 GGTTTGCAGA CAGTAGGTTG CATGCCTCCG CCTGTGTCTT CTGCAGTGAT
 551 TTTAACCAAG GCAGTTGGTG GAAATGAGGC AGCTGCAATA TTTAATTCAG
 601 CCTTTGGAAG TTTTTTGGTA AGTAAACATA GTTTAACTTG TCTATTACAA
 651 CTTTTGCTGT GATATTGTGT ATATGAAAGA TTTAGTGAAA GCTGGATTTG
 701 TTTTACTCTT TGGTTAAGTA TAAAAATTGT TGAATCTTTT CATGTGCCAG
 751 TATCCATACC CTGAAGAAAA GTAGTTAATG AATAAAGCAA ATGTTCTCTT
 801 ACAATATATT TTGGAGGTTT GGATTTTAAA ATTCCATTTA ATGAATTCAA
 851 GGAATCAATT AAAACACTAT GTGTCTCCTT ATAGAGGTTA TGTCAATATA
 901 TTGATCATTT AATGAGGTCT TTTAGATTAT TATTATTTTG TATCATGGGA
 951 CTGAGGATTT TGAAAAGGAA ACATGACCCA GCTGGTCAGA AAGGGAATGC
1001 TAATTTACTT GTTGACATGC CATTTATTTT GTACATTTCA CTGTCAAAGA
1051 AGCTACTGGC TTGGATGCTT CTGAGAAATC TATGTGAGAA AAAATTTGAA
1101 AGGAAGATAT GACTAATGAG TAATTTGCAA GTAAATGTTG TATCTATATA
1151 TATATATATA TAAAGATTCA AAAGTAGTTC AGCTTTCATA AGTAGAACCA
1201 ATATAAGGAC GTTGTTTTAG CATTTTTAAT CATTATTTTT AAATAAATGA
1251 TGTAACAGAG GCTTGATTTG TGTTATGAAA GATTGAGAAA CTAAATTTTC
1301 TGTTGATTTA ATTTTTTTGT GCCTTAAAAC TTTGTTAAAT TCCTGAAGTT
1351 AATTATCATA TTGTACTTTT TGGGGCATAA CTCATTAGCA GATATGTAGT
1401 GCAGTGATTT ACAAATAATT GAGAGTAAAA TCAGTGATGT ATAAACTAGT
1451 TCATGAGTCT AGGTAAAATA TCAATTACCT CTGTTTAAAA TGCTCTGTTA
1501 ATTATTATTG TATGTATTTA AATGTAGTTA AAGCTTTTAA ACATGTTGTT
1551 ACATAGTGTT AATTCTACAC AGTGCTACAC AGCTTTTAGT GTCACATAGC
1601 CTTACAGAGT TTATAATGAT GTAGCATCTG CAAAATATAT GCATAGCTTA
1651 TATCCTATTT TTATAGAGCC AGTAATGGTT TTTGTGATGC TGTATTACTT
1701 CTGGGTTTTA GACAATAAAG TCTGTTTAAC AAAAAAAAAA AAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

```
ORF from 183 bp to 659 bp; peptide length: 159
Category: similarity to unknown protein


    1 MRLLERMRKD WFMVGIVLAI AGAKLEPSIG VNGGPLKPEI TVSYIAVATI
   51 FFNSGLSLKT EELTSALVHL KLHLFIQIFT LAFFPATIWL FLQLLSITPI
  101 NEWLLKGLQT VGCMPPPVSS AVILTKAVGG NEAAAIFNSA FGSFLVSKHS
  151 LTCLLQLLL

                              BLASTP hits

No BLASTP hits available

             Alert BLASTP hits for DKFZphfkd2_4m11, frame 3

PIR:S53951 probable membrane protein YMR034c - yeast (Saccharomyces
cerevisiae), N = 1, Score = 171, P = 3.2e-12

PIR:A65015 yfeH protein - Escherichia coli (strain K-12), N = 1, Score
= 131, P = 4.2e-08


>PIR:S53951 probable membrane protein YMR034c - yeast (Saccharomyces
     cerevisiae)
            Length = 434

  HSPs:

 Score = 171 (25.7 bits), Expect = 3.2e-12, P = 3.2e-12
 Identities = 38/144 (26%), Positives = 72/144 (50%)

Query:      5 ERMRKDWFMVGIVLAIAGAKLEPSIGVNGGPLKPEITVSYIAVATIFFNSGLSLKTEELT 64
              E ++  WF + + + I  A+  P+    +GG +K + ++ Y  VA IF  SGL +K+  L
Sbjct:     18 EFLKSQWFFICLAILIVIARFAPNFARDGGLIKGQYSIGYGCVAWIFLQSGLGMKSRSLM 77

Query:     65 SALVHLKLHLFIQIFTLAFFPATIWLF---LQLLSITPINEWLLKGLQTVGCMPPPVSSA 121
              + +++ + H  I + +     + ++ F    ++  +   I++W+L GL       P  V+S
Sbjct:     78 ANMLNWRAHATILVLSFLITSSIVYGFCCAVKAANDPKIDDWVLIGLILTATCPTTVASN 137

Query:    122 VILTKAVGGNEAAAIFNSAFGSFL 145
              VI+T   GGN    +      G+ L
Sbjct:    138 VIMTTNAGGNSLLCVCEVFIGNLL 161


            Pedant information for DKFZphfkd2_4m11, frame 3
            -----------------------------------------------

                      Report for DKFZphfkd2_4m11.3

[LENGTH]        159
[MW]            17282.92
[pI]            9.06
[HOMOL]         PIR:S53951 probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae)
5e-12
[FUNCAT]        99 unclassified proteins        [S. cerevisiae, YMR034c] 2e-13
[PROSITE]       MYRISTYL        2
[PROSITE]       PKC_PHOSPHO_SITE        1
[KW]            TRANSMEMBRANE  4


SEQ    MRLLERMRKDWFMVGIVLAIAGAKLEPSIGVNGGPLKPEITVSYIAVATIFFNSGLSLKT
PRD    ccchhhhhhhhhhhhhhhhhhhhhccccccccccccccceeeeeeeccccccccccchhhh
MEM    .....MMMMMMMMMMMMMMMMMMMMMMM.....MMMMMMMMMMMMMMMMMMMMM..

SEQ    EELTSALVHLKLHLFIQIFTLAFFPATIWLFLQLLSITPINEWLLKGLQTVGCMPPPVSS
PRD    hhhhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhccccchhhhhhhheeeecccccccc
MEM    ........MMMMMMMMMMMMMMMMMMMMMMMMMMM.......................

SEQ    AVILTKAVGGNEAAAIFNSAFGSFLVSKHSLTCLLQLLL
PRD    ceeeeccccchhhhhhhcccccceeecceeeeeeeccc
MEM    ...........MMMMMMMMMMMMMMMMMMMMMMMMMMM


                      Prosite for DKFZphfkd2_4m11.3

PS00005       57->60   PKC_PHOSPHO_SITE        PDOC00005
PS00008       15->21   MYRISTYL                PDOC00008
PS00008      129->135  MYRISTYL                PDOC00008

(No Pfam data available for DKFZphfkd2_4m11.3)
```

PAGE INTENTIONALLY LEFT BLANK

DKFZphutel_17k7
----

group: uterus derived

DKFZphutel_17k7 encodes a novel 520 amino acid protein with weak similarity to S. Cerevisiae Fipl.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to S.cerevisiae Fipl

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: unknown

Insert length: 1914 bp
Poly A stretch at pos. 1897, polyadenylation signal at pos. 1867

```
   1 CGGACGCGTG GGCGGACGCG TGGGGCCTTC CTGGGATTGG AGTCTCGAGC
  51 TTTCTTCGTT CGTTCGCCGG CGGGTTCGCG CCCTTCTCGC GCCTCGGGGC
 101 TGCGAGGCTG GGGAAGGGGT TGGAGGGGGC TGTTGATCGC CGCGTTTAAG
 151 TTGCGCTCGG GGCGGCCATG TCGGCCGGCG AGGTCGAGCG CCTAGTGTCG
 201 GAGCTGAGCG GCGGGACCGG AGGGGATGAG GAGGAAGAGT GGCTCTATGG
 251 CGATGAAAAT GAAGTTGAAA GGCCAGAAGA AGAAAATGCC AGTGCTAATC
 301 CTCCATCTGG AATTGAAGAT GAAACTGCTG AAAATGGTGT ACCAAAACCG
 351 AAAGTGACTG AGACCGAAGA TGATAGTGAT AGTGACAGCG ATGATGATGA
 401 AGATGATGTT CATGTCACTA TAGGAGACAT TAAAACGGGA GCACCACAGT
 451 ATGGGAGTTA TGGTACAGCA CCTGTAAATC TTAACATCAA GACAGGGGGA
 501 AGAGTTTATG GAACTACAGG GACAAAAGTC AAAGGAGTAG ACCTTGATGC
 551 ACCTGGAAGC ATTAATGGAG TTCCACTCTT AGAGGTAGAT TTGGATTCTT
 601 TTGAAGATAA ACCATGGCGT AAACCTGGTG CTGATCTTTC TGATTATTTT
 651 AATTATGGGT TTAATGAAGA TACCTGGAAA GCTTACTGTG AAAAACAAAA
 701 GAGGATACGA ATGGGACTTG AAGTTATACC AGTAACCTCT ACTACAAATA
 751 AAATTACGGT ACAGCAGGGA AGAACTGGAA ACTCAGAGAA AGAAACTGCC
 801 CTTCCATCTA CAAAAGCTGA GTTTACTTCT CCTCCTTCTT TGTTCAAGAC
 851 TGGGCTTCCA CCGAGCAGGA GATTACCTGG GGCAATTGAT GTTATCGGTC
 901 AGACTATAAC TATCAGCCGA GTAGAAGGCA GGCGACGGGC AAATGAGAAC
 951 AGCAACATAC AGGTCCTTTC TGAAAGATCT GCTACTGAAG TAGACAACAA
1001 TTTTAGCAAA CCACCTCCGT TTTTCCCTCC AGGAGCTCCT CCCACTCACC
1051 TTCCACCTCC TCCATTTCTT CCACCTCCTC CGACTGTCAG CACTGCTCCA
1101 CCTCTGATTC CACCACCGGG TTTTCCTCCT CCACCAGGCG CTCCACCTCC
1151 ATCTCTTATA CCAACAATAG AAAGTGGACA TTCCTCTGGT TATGATAGTC
1201 GTTCTGCACG TGCATTTCCA TATGGCAATG TTGCCTTTCC CCATCTTCCT
1251 GGTTCTGCTC CTTCGTGGCC TAGTCTTGTG GACACCAGCA AGCAGTGGGA
1301 CTATTATGCC AGAAGAGAGA AAGACCGAGA TAGAGAGAGA GACAGAGACA
1351 GAGAGCGAGA CCGTGATCGG GACAGAGAAA GAGAACGCAC CAGAGAGAGA
1401 GAGAGGGAGC GTGATCACAG TCCTACACCA AGTGTTTTCA ACAGCGATGA
1451 AGAACGATAC AGATACAGGG AATATGCAGA AAGAGGTTAT GAGCGTCACA
1501 GAGCAAGTCG AGAAAAAGAA GAACGACATA GAGAAAGACG ACACAGGGAG
1551 AAAGAGGAAA CCAGACATAA GTCTTCTCGA AGTAATAGTA GACGTCGCCA
1601 TGAAAGTGAA GAAGGAGATA GTCACAGGAG ACACAAACAC AAAAAATCTA
1651 AAAGAAGCAA AGAAGGAAAA GAAGCGGGCA GTGAGCCTGC CCCTGAACAG
1701 GAGAGCACCG AAGCTACACC TGCAGAATAG GCATGGTTTT GGCCTTTTGT
1751 GTATATTAGT ACCAGAAGTA GATACTATAA ATCTTGTTAT TTTTCTGGAT
1801 AATGTTTAAG AAATTTACCT TAAATCTTGT TCTGTTTGTT AGTATGAAAA
1851 GTTAACTTTT TTTCCAAAAT AAAAGAGTGA ATTTTTCATG TTAAGTTAAA
1901 AAAAAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 168 bp to 1727 bp; peptide length: 520
Category: similarity to known protein

```
  1 MSAGEVERLV SELSGGTGGD EEEEWLYGDE NEVERPEEEN ASANPPSGIE
 51 DETAENGVPK PKVTETEDDS DSDSDDDEDD VHVTIGDIKT GAPQYGSYGT
101 APVNLNIKTG GRVYGTTGTK VKGVDLDAPG SINGVPLLEV DLDSFEDKPW
151 RKPGADLSDY FNYGFNEDTW KAYCEKQKRI RMGLEVIPVT STTNKITVQQ
201 GRTGNSEKET ALPSTKAEFT SPPSLFKTGL PPSRRLPGAI DVIGQTITIS
251 RVEGRRRANE NSNIQVLSER SATEVDNNFS KPPPFFPPGA PPTHLPPPPF
301 LPPPPTVSTA PPLIPPPGFP PPPGAPPPSL IPTIESGHSS GYDSRSARAF
351 PYGNVAFPHL PGSAPSWPSL VDTSKQWDYY ARREKDRDRE RDRDRERDRD
401 RDRERERTRE RERERDHSPT PSVFNSDEER YRYREYAERG YERHRASREK
451 EERHRERRHR EKEETRHKSS RSNSRRRHES EEGDSHRRHK HKKSKRSKEG
501 KEAGSEPAPE QESTEATPAE
```

BLASTP hits

Entry AF016427_4 from database TREMBL:
gene: "F32D1.9"; Caenorhabditis elegans cosmid F32D1.
Score = 392, P = 1.8e-36, identities = 156/519, positives = 212/519

Entry S62454 from database PIR:
hypothetical protein SPAC22G7.10 - fission yeast (Schizosaccharomyces pombe)
Score = 246, P = 2.0e-22, identities = 62/163, positives = 91/163

Entry A56545 from database PIR:
FIP1 protein - yeast (Saccharomyces cerevisiae)
Score = 186, P = 2.9e-16, identities = 56/206, positives = 92/206

Alert BLASTP hits for DKFZphute1_17k7, frame 3

TREMBLNEW:AF109907_1 product: "S164"; Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds., N = 2, Score = 236, P = 1.5e-16

```
>TREMBLNEW:AF109907_1 product: "S164"; Homo sapiens S164 gene, partial cds;
     PS1 and hypothetical protein genes, complete cds; and S171 gene, partial
     cds.
          Length = 735

  HSPs:

 Score = 236 (35.4 bits), Expect = 1.5e-16, Sum P(2) = 1.5e-16
 Identities = 51/120 (42%), Positives = 76/120 (63%)

Query:    383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEERYRYREYA---ER 439
              REK+++RER+R+R+RDRDR +ER+R R+RER+RD     S  + +++R R RE +    ER
Sbjct:    227 REKEKERERERERDRDRDRTKERDRDRDRERDRDRDRERSS-DRNKDRSRSREKSRDRER 285

Query:    440 GYERHRASREKEERHRER-RHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSKRSK 498
                 ER R    + ER RER R RE+E  R +     + +R  E +E D++ R K ++  R K
Sbjct:    286 ERERERERERERERERERERERERERERERERERERERERERERKDKKRDREEDEEDAYERRKLERKLREK 345

Query:    499 E 499
              E
Sbjct:    346 E 346

 Score = 214 (32.1 bits), Expect = 4.4e-14, Sum P(2) = 4.4e-14
 Identities = 50/133 (37%), Positives = 75/133 (56%)

Query:    383 REKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPSVFNS-DEERYRYREYAERG 440
              RE++R+R ER+R+RER+R+R++E+ER RERER+RD    T          D ER R R+  ER
Sbjct:    208 RERERERERERERERERERKEKERERERERDRDRDRTKERDRDRDRERDRDRD-RERS 266

Query:    441 YERHRASREKEERHRERRHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSKRSKEG 500
              +R++       E+ R+R  RE+E  R +  R   R R    E +  R  + ++ K  K
Sbjct:    267 SDRNKDRSRSREKSRDRE-RERERERE-RERERERERERERERERERERERKDKKRD 324

Query:    501 KEAGSEPAPEQESTE 515
              +E   E A E+   E
Sbjct:    325 REEDEEDAYERRKLE 339
```

```
 Score = 214 (32.1 bits), Expect = 4.4e-14, Sum P(2) = 4.4e-14
 Identities = 55/141 (39%), Positives = 80/141 (56%)

Query:   383 REKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPSVFNS-DEERYRYREYAERG 440
             RE++R+R ER+R+RER+R+R++E+ER RERER+RD    T        D ER R R+   ER
Sbjct:   208 RERERERERERERERERERERERERERERERERERERERERERERERERERERERERERERE 266

Query:   441 YERHR-ASREKEE-RHRER-RHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSKRS 497
              +R++  SR +E+ R RER R RE+E  R +         R  E E       R K KK  R
Sbjct:   267 SDRNKDRSRSREKSRDRERERERERERERERERERERERERERERERERERERERERERERE 326

Query:   498 KEGKEAGSEPAPEQESTEATPA 519
             ++ ++A        E++  E   A
Sbjct:   327 EDEEDAYERRKLERKLREKEAA 348

 Score = 210 (31.5 bits), Expect = 1.2e-13, Sum P(2) = 1.2e-13
 Identities = 59/142 (41%), Positives = 78/142 (54%)

Query:   383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVFNS---DEERYRYREYAER 439
             RE++RDR+RDR +ERDRDRDRER+R R+RER  D +    S         D ER R RE  ER
Sbjct:   235 RERERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKDRSRSREKSRDRERERERE-RER 293

Query:   440 GYERHRA-SREKE-ERHRER-RHREKEETRHKSS-------RSNSRRRHESEEGDSHRRH 489
               ER R    RE+E ER RER R REK++ R +             R     R+     +E      R
Sbjct:   294 ERERERERERERERERERERERERERKDKKRDREEDEEDAYERRKLERKLREKEAAYQERL 353

Query:   490 KHKKSKRSKEGKEAGSEPAPEQE 512
             K+ + +  K+ +E   E   E+E
Sbjct:   354 KNWEIRERKKTREYEKEAEREEE 376

 Score = 205 (30.8 bits), Expect = 4.4e-13, Sum P(2) = 4.4e-13
 Identities = 59/149 (39%), Positives = 83/149 (55%)

Query:   372 DTSKQWDYYARREKDRDR--ERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEE 429
             +  K+ +     R++DRDR  ERDRDR+R+RDRDR+RER+ +R ++R  S   S     D E
Sbjct:   228 EKEKERERERERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKDRSRSREKS---RDRE 284

Query:   430 RYRYREYAERGYERHRA-SREKE-ERHRER-RHREKEETRHKSS-------RSNSRRRHE 479
             R R RE   ER   ER R    RE+E ER RER R REK++ R +             R     R+
Sbjct:   285 RERE-RERERERERERERERERERERERERERERERKDKKRDREEDEEDAYERRKLERKLR 343

Query:   480 SEEGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE 512
             +E       R K+ + +  K+ +E   E   E+E
Sbjct:   344 EKEAAYQERLKNWEIRERKKTREYEKEAEREEE 376

 Score = 202 (30.3 bits), Expect = 9.6e-13, Sum P(2) = 9.6e-13
 Identities = 49/117 (41%), Positives = 70/117 (59%)

Query:   383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEERYRYREYAERGYE 442
             REK RDRER+R+RER+R+R+RERER RERERER+                D++R R  E  E  YE
Sbjct:   277 REKSRDRERERERERERERERERERERERERERERERERER-EKDKKRDR-EEDEEDAYE 334

Query:   443 RHRASREKEERHRERRHREKEETRHKSSRSNSRR-RHESEEGDSHRRHKHKKSKRSKE 499
             R +    E++ R +E  ++E+ +        R +R     E+E   +  RR    K++KR KE
Sbjct:   335 RRKL--ERKLREKEAAYQERLKNWEIRERKKTREYEKEAEREEERRREMAKEAKRLKE 390

 Score = 183 (27.5 bits), Expect = 1.2e-10, Sum P(2) = 1.2e-10
 Identities = 52/141 (36%), Positives = 79/141 (56%)

Query:   372 DTSKQWDYY-ARREKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEE 429
             DT K+ +      ++EK+R  E++R RER+R+R+RERER RERERER+              ++E
Sbjct:   178 DTHKKLEEEKGKKEKERQEIEKER-RERERERERER-RERERERER-----EREKE 230

Query:   430 RYRYREYAERGYERHRASREKEERHRER---RHREKEETRHKSSRSNSRRRHESEEGDSH 486
             + R RE  ER  +R R         +R RER    R RE+     R+K  RS SR +       E +
Sbjct:   231 KERERE-RERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKD-RSRSREKSRDRERERE 288

Query:   487 RRHKHKKSKRSKEGKEAGSEPAPEQE 512
             R  + ++ +  +   +E    E   E+E
Sbjct:   289 RERERERERERERERERERERERERE 314

 Score = 171 (25.7 bits), Expect = 2.5e-09, Sum P(2) = 2.5e-09
 Identities = 49/150 (32%), Positives = 78/150 (52%)

Query:   383 REKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEERYRYREYAERGYE 442
             RE++R+RER+R+RER+R+R+RERER RERERER+               +E+ Y  R+    +  E
Sbjct:   285 RERERERERERERERERERERERERERERERERERKDKKRDREEDEEDAYERRKLERKLRE 344

Query:   443 RHRASREK------EERHRERRHR---EKEETRHKSSRSNSRRRHES-EEGDSHRRH-KH 491
             +  A +E++        ER + R +    E+EE R +       ++R  E   E+ D  R    K+
Sbjct:   345 KEAAYQERLKNWEIRERKKTREYEKEAEREEERRREMAKEAKRLKEFLEDYDDDRDDPKY 404
```

```
Query:   492 ------KKSKRSKEGKEAGSEPAPEQESTE 515
               +K  R +E +    E   ++E  E
Sbjct:   405 YRGSALQKRLRDREKEMEADERDRKREKEE 434

 Score = 162 (24.3 bits), Expect = 2.4e-08, Sum P(2) = 2.4e-08
 Identities = 45/141 (31%), Positives = 74/141 (52%)

Query:   372 DTSKQWDYYARREKDRDRERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEERY 431
             + SK  D + + E+++ ++    +E +++R RERER RERERER           + ER
Sbjct:   172 EISKFRDTHKKLEEEKGKKEKERQEIEKER-RERERERERERRERERER--ERERERE 228

Query:   432 RYREYAERGYERHRASREKEERHRER-RHREKEETRHKSSRSNSRRRHESEEGDSHRRHK 490
             + +E  ER  ER R     +ER R+R R R+++  R +SS  N  R    E+     R +
Sbjct:   229 KEKE-RERERERDRDRDRTKERDRDRDRERDRDRDRERSSDRNKDRSRSREKSRDRERER 287

Query:   491 HKKSKRSKEGKEAGSEPAPEQE 512
              ++ +R +E +E   E   E+E
Sbjct:   288 ERERERERE-RERERERERERE 308

 Score = 137 (20.6 bits), Expect = 1.2e-05, Sum P(2) = 1.2e-05
 Identities = 48/152 (31%), Positives = 68/152 (44%)

Query:   364 APSWPSLVDTSKQWDYYARREKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPS 422
             AP  P  + T +  +     E  RD   R+  + RD  +  E E+ + +E+ER
Sbjct:   143 APLIPYPLITKEDINAIEMEEDKRDLISREISKFRDTHKKLEEEKGK-KEKERQEIEKER 201

Query:   423 VFNSDEERYRYREYAERGYERHRA-SREKE-ERHRER-RHREKEETRHKS-SRSNSRRRH 478
                 + ER R RE  ER  ER R   REKE ER RER R R+++ T+ +   R   R R
Sbjct:   202 R-ERERERERERRERERERERERERKEKERERERDRDRDRTKERDRDRDRERDRD 260

Query:   479 ESEEGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE 512
                E  S R     +S+     +E   E   E+E
Sbjct:   261 RDRERSSDRNKDRSRSREKSRDRERERERERERE 294

 Score = 126 (18.9 bits), Expect = 1.8e-04, Sum P(2) = 1.8e-04
 Identities = 41/149 (27%), Positives = 66/149 (44%)

Query:   375 KQWDYYARREKDRDRERDRDRERDRDRDRERERTRERERERDHSPT---PSVFNSD--EE 429
             K W+    R+K R+ E++ +RE +R R+  +E  R +E   D+      P  +     ++
Sbjct:   354 KNWEI-RERKKTREYEKEAEREEERRREMAKEAKRLKEFLEDYDDDRDDPKYYRGSALQK 412

Query:   430 RYRYREYAERGYERHRASREKEERHRERR------HREKEETRHKSSRSNSRRRHES--E 481
             R R RE      ER R  REKEE    R+      H + +    +  +   RRR     +
Sbjct:   413 RLRDREKEMEADERDR-KREKEELEEIRQRLLAEGHPDPDAELQRMEQEAERRRQPQIKQ 471

Query:   482 EGDSHRRHKHKKSKRSKEGKEAGSEPAPEQE 512
             E +S    + K+ K  K  +    E  PEQ+
Sbjct:   472 EPESEEEEEEKQEKEEKREEPMEEEEEPEQK 502

 Score = 124 (18.6 bits), Expect = 3.0e-04, Sum P(2) = 3.0e-04
 Identities = 41/141 (29%), Positives = 65/141 (46%)

Query:   380 YARREKDRD-RERDRDRERDRDRDRERERTRERERERDHSPTPSVFNSDEERYRYREYAE 438
             Y  R K+ + RER + RE +++ +RE ER RE  +E        + + D++R   + Y
Sbjct:   349 YQERLKNWEIRERKKTREYEKEAEREEERRREMAKEAKRLKE-FLEDYDDDRDDPKYYRG 407

Query:   439 RGYERHRASREKEERHRER-RHREKEETRHKSSRSNSRRRHESEEGDSHRRHKHKKSKRS 497
                ++    REKE    ER R REKEE      R  +   H   + +  R  +  + +R
Sbjct:   408 SALQKRLRDREKEMEADERDRKREKEELEEIRQRLLAEG-HPDPDAELQRMEQEAERRRQ 466

Query:   498 KEGKEAGSEPAPEQESTEATPAE 520
              + K+   EP  E+E  E    E
Sbjct:   467 PQIKQ---EPESEEEEEEKQEKE 486

 Score = 121 (18.2 bits), Expect = 6.2e-04, Sum P(2) = 6.2e-04
 Identities = 43/149 (28%), Positives = 67/149 (44%)

Query:   364 APSWPSLVDTSKQWDYYARREKDRDR-ERDRDRERDRDRDRERERTRERERERDHSPTPS 422
             AP  P  + T +  +     E  RD   R+  + RD  +  E E+ + +E+ER
Sbjct:   143 APLIPYPLITKEDINAIEMEEDKRDLISREISKFRDTHKKLEEEKGK-KEKERQEIEKE- 200

Query:   423 VFNSDEERYRYREYAERGYERHRASREKEERHRERRHREKEETRHKSSRSNSRRRHESEE 482
                 + ER R RE   R  ER R  RE+E    + R RE+E  R +  R+  R R    E
Sbjct:   201 --RRERERERERERRERERER-EREREKEKERERERDRDRD-RTKERDRDRDRE 256

Query:   483 GDSHRRHKHKKSKRSKEGKEAGSEPAPEQE 512
              D  R  + + S R+K+ +    E + ++E
Sbjct:   257 RDRDR-DRERSSDRNKD-RSRSREKSRDRE 284

 Score = 105 (15.8 bits), Expect = 3.1e-02, Sum P(2) = 3.1e-02
```

```
 Identities = 25/73 (34%), Positives = 33/73 (45%)

Query:   428 EERYRYREYAERGYERHRASREKE-ERHRERRHREKEETRHKSSRSNSRRRHESEEGDSH 486
             EE    +E   +  E+ R  RE+E ER RERR RE+E  R +        R  E E
Sbjct:   184 EEEKGKKEKERQEIEKERRERERERERERRERERERERERERERERERERERERERDRDR 243

Query:   487 RRHKHKKSKRSKE 499
             R K +    R +E
Sbjct:   244 DRTKERDRDRDRE 256

 Score = 105 (15.8 bits), Expect = 3.1e-02, Sum P(2) = 3.1e-02
 Identities = 31/87 (35%), Positives = 45/87 (51%)

Query:   382 RREKDRDRERDRDRERDRDRDRER-ERTRERERERDHSPTPSVFNSDEERYRYREYAERG 440
             +R +DR++E + D ERDR R++E  E  R+R      H P P     D E  R  + AER
Sbjct:   412 KRLRDREKEMEAD-ERDRKREKEELEEIRQRLLAEGH-PDP-----DAELQRMEQEAERR 464

Query:   441 YERHRASREKEERHRERRHREKEETRHK 468
               + +  +E E    E   +EKEE R +
Sbjct:   465 -RQPQIKQEPESEEEEEEKQEKEEKREE 491

 Score = 46 (6.9 bits), Expect = 1.5e-16, Sum P(2) = 1.5e-16
 Identities = 13/49 (26%), Positives = 21/49 (42%)

Query:    54 AENGVPKPKVTETEDDSDSDSDDDEDDVHVTIGDIKTGAPQYGSYGTAP 102
             A NG  +P+    +D+    D +     D  + G I+    +Y S    AP
Sbjct:    70 ASNGNARPETVTNDDEEALDEETKRRDQMIK-GAIEVLIREYSSELNAP 117

 Score = 46 (6.9 bits), Expect = 1.8e-04, Sum P(2) = 1.8e-04
 Identities = 14/53 (26%), Positives = 21/53 (39%)

Query:    30 ENEVERPEEENASANPPSGIEDETAENGVPKPKVTETEDDSDSDSDDDEDDVH 82
             + E ER  E              E E  E    + +  E E D  D ++DE+D +
Sbjct:   282 DRERERERERERERERERERER-ERERERERERERERERERKDKKRDREEDEEDAY 333

 Score = 44 (6.6 bits), Expect = 2.0e-13, Sum P(2) = 2.0e-13
 Identities = 13/60 (21%), Positives = 21/60 (35%)

Query:    20 DEEEEWLYGDENEVERPEEENASANPPSGIEDETAENGVPKPKVTETEDDSDSDSDDDED 79
             ++E + + +  +  E ER E                     +  E   K +  E E D D D  + D
Sbjct:   191 EKERQEIEKERRERERERERERRERERERERERERERERERKEKERERERERDRDRDRTKERD 250
```

Pedant information for DKFZphutel_17k7, frame 3

Report for DKFZphutel_17k7.3

```
[LENGTH]      520
[MW]          58375.30
[pI]          5.41
[HOMOL]       PIR:S62454 hypothetical protein SPAC22G7.10 - fission yeast
(Schizosaccharomyces pombe) 3e-18
[FUNCAT]      04.05.05 mrna processing (5'-end, 3'-end processing and mrna degradation)  [S.
cerevisiae, YJR093c] 2e-13
[FUNCAT]      30.10 nuclear organization    [S. cerevisiae, YJR093c] 2e-13
[PROSITE]     MYRISTYL       9
[PROSITE]     AMIDATION      1
[PROSITE]     CK2_PHOSPHO_SITE      18
[PROSITE]     TYR_PHOSPHO_SITE      2
[PROSITE]     PKC_PHOSPHO_SITE      12
[PROSITE]     ASN_GLYCOSYLATION     2
[KW]          Alpha_Beta
[KW]          LOW_COMPLEXITY    35.00 %

SEQ    MSAGEVERLVSELSGGTGGDEEEEWLYGDENEVERPEEENASANPPSGIEDETAENGVPK
SEG    ........................xxxxxxxxxx..........................
PRD    ccchhhhhhhhccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ    PKVTETEDDSDSDSDDDEDDVHVTIGDIKTGAPQYGSYGTAPVNLNIKTGGRVYGTTGTK
SEG    ...xxxxxxxxxxxxxxxxx........................................
PRD    cceeeecccccccccccccccceeeeeccccccccccccccccccceeeeeeccccceeeccccc

SEQ    VKGVDLDAPGSINGVPLLEVDLDSFEDKPWRKPGADLSDYFNYGFNEDTWKAYCEKQKRI
SEG    ............................................................
PRD    ceeeccccccccccceeeeccccccccccccccccccccccccccccchhhhhhhhhhh

SEQ    RMGLEVIPVTSTTNKITVQQGRTGNSEKETALPSTKAEFTSPPSLFKTGLPPSRRLPGAI
SEG    ............................................................
```

```
PRD   hhhheeeeecccccceeeeeeeccccccccccccccceeeecccccceeeecccccccccccc

SEQ   DVIGQTITISRVEGRRRANENSNIQVLSERSATEVDNNFSKPPPFFPPGAPPTHLPPPPF
SEG   ......................................xxxxxxxxxxxxxxxxxxxxx
PRD   ccccceeeeeecccccccccccccceeeccccccccccccccccccccccccccccccccc

SEQ   LPPPPTVSTAPPLIPPPGFPPPPGAPPPSLIPTIESGHSSGYDSRSARAFPYGNVAFPHL
SEG   xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.............................
PRD   cccccccccccccccccccccccccccccccccccccccccccccccccccceeeccc

SEQ   PGSAPSWPSLVDTSKQWDYYARREKDRDRERDRDRERDRDRDRERERTREREREERDHSPT
SEG   .....................xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx....
PRD   ccccccccceeeccccchhhhhhhhhcccccccccccccchhhhhhhhhhhcccccc

SEQ   PSVFNSDEERYRYREYAERGYERHRASREKEERHRERRHREKEETRHKSSRSNSRRRHES
SEG   .......xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
PRD   cccccccchhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccc

SEQ   EEGDSHRRHKHKKSKRSKEGKEAGSEPAPEQESTEATPAE
SEG   xx..xxxxxxxxxxxxxx......................
PRD   cccccccccccccccccccccccccccccccccccccccc
```

Prosite for DKFZphutel_17k7.3

PS00001	40->44	ASN_GLYCOSYLATION	PDOC00001
PS00001	278->282	ASN_GLYCOSYLATION	PDOC00001
PS00005	169->172	PKC_PHOSPHO_SITE	PDOC00005
PS00005	193->196	PKC_PHOSPHO_SITE	PDOC00005
PS00005	206->209	PKC_PHOSPHO_SITE	PDOC00005
PS00005	214->217	PKC_PHOSPHO_SITE	PDOC00005
PS00005	233->236	PKC_PHOSPHO_SITE	PDOC00005
PS00005	268->271	PKC_PHOSPHO_SITE	PDOC00005
PS00005	346->349	PKC_PHOSPHO_SITE	PDOC00005
PS00005	373->376	PKC_PHOSPHO_SITE	PDOC00005
PS00005	469->472	PKC_PHOSPHO_SITE	PDOC00005
PS00005	474->477	PKC_PHOSPHO_SITE	PDOC00005
PS00005	485->488	PKC_PHOSPHO_SITE	PDOC00005
PS00005	494->497	PKC_PHOSPHO_SITE	PDOC00005
PS00006	2->6	CK2_PHOSPHO_SITE	PDOC00006
PS00006	17->21	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	64->68	CK2_PHOSPHO_SITE	PDOC00006
PS00006	66->70	CK2_PHOSPHO_SITE	PDOC00006
PS00006	70->74	CK2_PHOSPHO_SITE	PDOC00006
PS00006	72->76	CK2_PHOSPHO_SITE	PDOC00006
PS00006	74->78	CK2_PHOSPHO_SITE	PDOC00006
PS00006	84->88	CK2_PHOSPHO_SITE	PDOC00006
PS00006	144->148	CK2_PHOSPHO_SITE	PDOC00006
PS00006	206->210	CK2_PHOSPHO_SITE	PDOC00006
PS00006	215->219	CK2_PHOSPHO_SITE	PDOC00006
PS00006	250->254	CK2_PHOSPHO_SITE	PDOC00006
PS00006	271->275	CK2_PHOSPHO_SITE	PDOC00006
PS00006	273->277	CK2_PHOSPHO_SITE	PDOC00006
PS00006	340->344	CK2_PHOSPHO_SITE	PDOC00006
PS00006	369->373	CK2_PHOSPHO_SITE	PDOC00006
PS00006	426->430	CK2_PHOSPHO_SITE	PDOC00006
PS00007	434->442	TYR_PHOSPHO_SITE	PDOC00007
PS00007	152->161	TYR_PHOSPHO_SITE	PDOC00007
PS00008	15->21	MYRISTYL	PDOC00008
PS00008	96->102	MYRISTYL	PDOC00008
PS00008	115->121	MYRISTYL	PDOC00008
PS00008	130->136	MYRISTYL	PDOC00008
PS00008	154->160	MYRISTYL	PDOC00008
PS00008	229->235	MYRISTYL	PDOC00008
PS00008	244->250	MYRISTYL	PDOC00008
PS00008	289->295	MYRISTYL	PDOC00008
PS00008	362->368	MYRISTYL	PDOC00008
PS00009	253->257	AMIDATION	PDOC00009

(No Pfam data available for DKFZphutel_17k7.3)

DKFZphutel_18c12
----

group: uterus derived

DKFZphutel_18c12 encodes a novel 378 amino acid protein nearly identical to human WUGSC:H_DJ0872F07.1 protein.

The novel protein has an additional N-terminal domain, which is not present in WUGSC:H_DJ0872F07.1.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

nearly identical to human WUGSC:H_DJ0872F07.1 protein

on genomic level encoded by AC004537, 10 exons the predicted
protein sequence AC004537_1 is only partialy o.k. first exon wasn't
predicted there are additional exons predicted
(BLASTX/EST-BLAST shows that the cDNA is only party spliced)
intron ~1216-3540//~3577-5059

Sequenced by AGOWA

Locus: map="7q31"

Insert length: 6005 bp
Poly A stretch at pos. 5980, polyadenylation signal at pos. 5968

```
   1 AGCGGGTGCT GCTAGCGGAG GCGCCATATT GGAGGGGACA AAACTCCGGC
  51 GACAGCGAGT GACACAAATA AACCCCTGGA CCCCCTTGTT CCCTCAGCTC
 101 TAAGGGCCGC GATGTTGTAC CTAGAAGACT ATCTGGAAAT GATTGAGCAG
 151 CTTCCTATGG ATCTGCGGGA CCGCTTCACG GAAATGCGCG AGATGGACCT
 201 GCAGGTGCAG AATGCAATGG ATCAACTAGA ACAAAGAGTC AGTGAATTCT
 251 TTATGAATGC AAAGAAAAAT AAACCTGAGT GGAGGGAAGA GCAAATGGCA
 301 TCCATCAAAA AAGACTACTA TAAAGCTTTG GAAGATGCAG ATGAGAAGGT
 351 TCAGTTGGCA AACCAGATAT ATGACTTGGT AGATCGACAC TTGAGAAAGC
 401 TGGATCAGGA ACTGGCTAAG TTTAAAATGG AGCTGGAAGC TGATAATGCT
 451 GGAATTACAG AAATATTAGA GAGGCGATCT TTGGAATTAG ACACTCCTTC
 501 ACAGCCAGTG AACAATCACC ATGCTCATTC ACATACTCCA GTGGAAAAAA
 551 GGAAATATAA TCCAACTTCT CACCATACGA CAACAGATCA TATTCCTGAA
 601 AAGAAATTTA AATCTGAAGC TCTTCTATCC ACCCTTACGT CAGATGCCTC
 651 TAAGGAAAAT ACACTAGGTT GTCGAAATAA TAATTCCACA GCCTCTTCTA
 701 ACAATGCCTA CAATGTGAAT TCCTCCCAAC CTCTGGGATC CTATAACATT
 751 GGCTCGTTAT CTTCAGGAAC TGGTGCAGGG GCAATTACCA TGGCAGCTGC
 801 TCAAGCAGTT CAGGCTACAG CTCAGATGAA GGAGGGACGA AGAACATCAA
 851 GTTTAAAAGC CAGTTATGAA GCATTTAAGA ATAATGACTT TCAGTTGGGA
 901 AAAGAATTTT CAATGGCCAG GGAAACAGTT GGCTATTCAT CATCTTCGGC
 951 ACTTATGACA ACATTAACAC AGAATGCCAG TTCATCAGCA GCCGACTCAC
1001 GGAGTGGTCG AAAGAGCAAA AACAACAACA AGTCTTCAAG CCAGCAGTCA
1051 TCATCTTCCT CCTCCTCTTC TTCCTTATCA TCGTGTTCTT CATCATCAAC
1101 TGTTGTACAA GAAATCTCTC AACAAACAAC TGTAGTGCCA GAATCTGATT
1151 CAAATAGTCA GGTTGATTGG ACTTACGACC CAAATGAACC TCGATACTGC
1201 ATTTGTAATC AGGTAAAAGT CTGTTATATC TATAAAAGTA TAATCTGAAT
1251 AAACTAGAAG GAAGAGAACT ATTTCATTTT TAAGCACTTT TTTAAACTCA
1301 CTTAAAATAC CTTTGCTTTA TTTGTATACT TTTCTCCCCC TTCTTACAAA
1351 AGTGACATTT GCTGTAAATA CTGAGTATAA AGAAAAATGT TACCCATAAT
1401 CCTAGCCCTC AGATACAACC TGTAACTAAA CATTTTTGGT ATACCACTAC
1451 CATATACCTC ATGTGCACAT TGGCTGCCTT AATAAAATAC AACAGACTGG
1501 GTAGCTTAAA CAACAGAAAA TAATTTTCTC ACAGGTATGA AGGCTGGGAA
1551 GTCCAAGATC AAGGTGTCCA CTGACTCAGT TCTGGAGGAG GGCTCCCTTC
1601 CTAGATGGAG ACTGCTGCCT TCTCACCGGG TCCTCACATG ATAGAGGGAG
1651 AAAGAGTGTG CTCTGGTGTC TTTTCTTATA AGGGCACCAG CCTTGTCAGA
1701 GTAGGACCCC ACTCTATGAC CTCATTTAAC CTTTACCACC TCCTCACAGG
1751 CCCTGTTTCC AATTATAGTC ACGTTGGGGG TTAGGGCTTC AACATATGAT
1801 TTTGAGACAT AAGCTTGCAT TTCATAACAC GTGTCTATGC AGATTTGCAC
1851 ATGCATGTGT GTATAAGTTT GTCAGTAGGA ACCACAGTGT ATACTTTCTT
1901 GTTACTGGCT TTTTTCTCTA AATCAGGTAT ACCGAACATG ATTTTTCTTT
1951 AAGATCATAT TTTTAATTTT CACATAGTTA TCTCTTATGC CATCCAGTGT
2001 AGTTTTCTTA ACCAATACCT AGCTATAGAT TATATTAGTG GTTTTAATTT
2051 GTTTGAAATT AGGGATAATA TTACGATAGG CATTTTTTAA ATGTAATCCA
2101 TTTTATACAT CTAATTTCTT GGATAATCTT TTAGAAATAA AATTAGGCTG
2151 TAAATATTTG ACAGACACCA AAATATATTT TCTAGAAATT TATTACCAAA
2201 AATTAATAAA CATACCGGTT TACTAAACCC TGTCCAACAC TGGATATTAT
2251 TTTCTTTTAA AAACTAAGTA CCAATTTGGT AGTTTTATAT TATGATTGTT
2301 TTAAATACAC TAGTATTATT GAAGTTGGAC ATTTTTTGAC CATTTTTGTT
2351 TTTTACATTA TGAATCGACT CCTAATGGTG TCGGCTGATT TTTCTATTGT
```

2401 TTTTGTTATG TACTCTAAAT ATTTGCTTGA TTTAGTTTTT TAAAAATAAT
2451 TCTAAAATTT TAATTTTATG TAGTTATGAC TGTTAATTTT TTTTTATGAA
2501 GCAAGCCATG GATTATATAC TTAGAAGGGC TTTCTCTTTG GCTCTTCTTT
2551 CTACAAAAAA TTGTCTTGTA TAATATTTTC TCCTAGTTTT TATATGGTTT
2601 TGTCTAGTTC TTTGCATGCT TCAGTTTCTT CACATTTAAG ACTTAGTCTA
2651 TCAGCAGATT ATTGTGTCTA ACAGTATGAG TTGCCAGTCT GATTTTTAAA
2701 AATTTTAACA ATTTGTTAGC TGTTCCACTA TCACCCGATA AACATTTTTC
2751 AGTACAAATG ATAGAAAAGC ATATCCTGTA TCCTGACAAC AAAAGTAGAT
2801 TACTTGCAAA AGAACAAAAT CAGACTGAAC CTAGAGTTTT CCTCTGTAAC
2851 ACTAAAAAAC TAGAAGGTGA TGGAATATGT CTGTAGAGCT TTCAGGGAAA
2901 AATTAAGAGC CCCCAAAAAC TTGATATTCA GAGAAGTTAT TTCTCTGCAT
2951 AGGACCATGT AAATATATTT TCACTCATGC AGAGAATCAG AAGATATGCC
3001 ATCTAGTTAA TCCTGTCTGA AAAATTATTC AATCCACTGA GAACTTCAGT
3051 GAACTCAAGA ATTAGCAAGT TATGCCCTAA AGTGCTGGTG ATGAAGAGCA
3101 AAAGAAAAAT GAGAAAGGAC ATAAAATAGA TAAGTTTAGA AGTTTCAAGG
3151 AAGGAGACTA TTAATTGCAA AAATATATAT GACCTAATGT GACCCAAGAA
3201 GTAAAAACTT TCAGTAAGTA AATAATCAAG AAAGGAACTT AAAATTTTTA
3251 CAATAAGAAC TACCCAGAAA GATGACTCCT TCATCCGGGT GATTTATATG
3301 TCAAGTTCTT CCAGACTTCT GAAGGGCAGA TAATTCCTGT GCATTTCTTC
3351 CCACCCTTGC CCCACCCTGC CCAAAAGAGT ATTTCAGGAA AAAATTATTA
3401 TACCTTGATT CTCAATGTAA TTGTATATTC AGTGTATTTC CCTTTATTTT
3451 CCAGCAGTAT CATACATAAA CAGTTAATTG GTATCTAGGT GTTTGTTACA
3501 TAGTCATAAT AAAGACATTT AATTTTTTTT AACTAGGTAT CTTATGGTGA
3551 GATGGTGGGA TGTGATAACC AAGATGTAAG TATTACATTT TTCTATTTAG
3601 GAATGAAAAA AATCACAGGT TGTTATTACT TGAATATTTG TCTTATTTGC
3651 TGTATGGTTT GGTCTAAGAA AACAGGTTTG CAGGTATATT AGTTATGTTA
3701 TGCTAATGCT AGAATATTCC TCTTCAAAAT AGGGTAGTGT CCCTTAATGT
3751 GTTCCCTATT TTAATTTTTA AAGCTAATTT TATGGTTTTA TGTGCAGATT
3801 GTCTCAGAAG TGTTATGTTG TATGAAAATT ATAAATACCC TCCTTTCCCT
3851 TTACTAAAAA ATACTGTGTT TACTAGAATC CAGTTCATTT ATCACATTGA
3901 AGAAATGGAA TTTTAAAACA ATTCATTCTT TCAGGCTGCA CCGTGCTAAA
3951 GTGAAGGGTG GGATAATTGA GGATCTAATG TGAGATTATC TTCCTCTCAT
4001 GAGTATAATA TTTTTTCCTG TACTCTGCAG GTGTCAGCTG ATAAGAGCCA
4051 CCCCTGATCT AAAAAGTAAA GGAAATTTGA AAGGAAGGAA TTCTTGGTTT
4101 TTAGGAGACT TAATTTTAGT TAGAGATACG TTTTTTATTC AATACTGAGA
4151 ATATTGTTGT CTAGTAATTT TGACTCCCTC CTTATTTAGT AGTGACAGGA
4201 TCCTAAGATT AACAAGAGTT TTAAATTTGT AAAACAATCT GAAGATTGAG
4251 GGAGCTGGCT AGGTGCATTA AAATGTGTAC TTTTCCTAGA CCTGATAGGG
4301 TTACAGCAAC ATGCTCACGT AGATTGGGAC AGAGCCTCCT TCTGTTTCCC
4351 TGTCTAGAAT CCCTTGTAGG CTGTTTGTGG TTGTTGCAAA AACAATATTG
4401 CCCAACCATT TCAAGAACAT CACTGTAAAC TCTTCTGGGG CAGTTAGTGA
4451 AAATGATGAA TGAGATTTCT ATGAGTACCA GCATCATGCT TCTCTGATTC
4501 TTCTTATTCC CAGTTGTGCT CTTCTGAGTG CTAAGACTTT CATGAAAGAG
4551 TTTTCTGCTT AATATGTTTC AAAGAGGAAT AATTTTTCTC TACATTTCAA
4601 GGAATAGAAA CACCCACGTA GGAAATGCAG GGCATAAGAC ATAAATTAAT
4651 GTCTTTAATT ACAATCAGCT TATTCTACTT TATGAGACAG CAAATAAGGC
4701 TGACTATTAA ATAAAATCTT AAGTTATATT TACCTTCTAC ATAGAAGATT
4751 CATCCCACTT CTTTTTGCCC TTGAAAGCTG AAAACTAGTG AATTTTCATT
4801 CATTAGGATG AGGGGACTAG ATTACATGGA CCTCAGGATT CTTGAAGATG
4851 CATAATTTTT CTGTGCCTTC ATTTCCTCAT TCCTGAAGCT TATCATTTAG
4901 TCTAAATGAT GTCTAAATAA TCTAGATCTA AAAATTCTGA TGTCACACAT
4951 CTAATTATTG TTAAATTAAA TGGATTATTC AGTCTCCTGA GCATATTTTA
5001 ATATACTCTC TTGTCTTCAG AAGTACTGAA AACTTGTTTT TTGCAATTTT
5051 GCTTTCTAGT GCCCTATAGA ATGGTTCCAT TATGGCTGCG TTGGATTGAC
5101 AGAGGCACCA AAAGGCAAAT GGTACTGTCC ACAGTGCACT GCTGCAATGA
5151 AGAGAAGAGG CAGCAGACAC AAATAAAGGT GGTCCTTTTG TTTGATGAAG
5201 AAATAAACTT CAGCTGAAGA TTTTATATAG GACTTTAAAA AGAAGAGAAG
5251 AGAAAGAAGA AACAATGCAT TTCCAGGCAA CCACTTAAAG GATTTACATA
5301 GACAATCCTA TAAGATCTTG AACTTGAATT TTATGGGTTG TATTTTAATA
5351 ATGTAAGTAA ATTATTTATG CACTCCTGGT GTGCTATGAA TATTATTCCA
5401 GTTAGCCTTG GATTATTTCA GTGGCCAACA TATGCAGACA TTTGTACTCC
5451 TCAACCATTT TCTCAAAGTA ATGGGCATTC TATGATTTAG ACTTCAAGGA
5501 ATTCCAATGA TGAAGATTTT AAGGAAAGTA TTTTATATTC AACAGGTATA
5551 TTCTGCTGCA TGTACTGTAC TCCAGAGCTG TTATGTAACA CTGTATATAA
5601 ATGGTTGCAA AAAAAAAAAA AAGTCAGTGC TTCTAAAAAG AATTTAAGAT
5651 AATGGTTTTT AAAATGCCTT TATAATAAGC TTTGTTTCTT TGTGAAACTA
5701 ATTCAGCAGG CTGAAGGAAA TGGTTCATGT GATAATGTGG GCTGGTATCC
5751 TCTAGAGTAC CTGGGTACAT AAACAGAAAC TCCTGTAGGT AAAAAGTAAT
5801 TTGTGCCATT AGTCTTTCTA TGTTTCTGCA TCCAGATAGA GTGCAGTTCA
5851 TGAGGGAGGG GGCGGGGGAC TGAAGGGGAA AGGGCGTTAA AGTGATACAT
5901 TTTTATACCA AATGTGTTTA TTTTTTTGTG CAAGTAATCC TTAAAATTGC
5951 AATTGTATTA GGTGTTAAAA TAAAGTTTTT AAAAAATTAA AAAAAAAAAA
6001 AAAAA

BLAST Results

Entry HSG20547 from database EMBL:
HSG20547| human STS A005W09.
Length = 154

```
Minus Strand HSPs:
Score = 770 (115.5 bits), Expect = 2.9e-26, P = 2.9e-26
Identities = 154/154 (100%)
```

Medline entries

```
98101645:
The candidate tumour suppressor p33ING1 cooperates with p53 in cell
growth control.
```

Peptide information for frame 1

```
ORF from 112 bp to 1245 bp; peptide length: 378
Category: similarity to known protein


  1 MLYLEDYLEM IEQLPMDLRD RFTEMREMDL QVQNAMDQLE QRVSEFFMNA
 51 KKNKPEWREE QMASIKKDYY KALEDADEKV QLANQIYDLV DRHLRKLDQE
101 LAKFKMELEA DNAGITEILE RRSLELDTPS QPVNNHHAHS HTPVEKRKYN
151 PTSHHTTTDH IPEKKFKSEA LLSTLTSDAS KENTLGCRNN NSTASSNNAY
201 NVNSSQPLGS YNIGSLSSGT GAGAITMAAA QAVQATAQMK EGRRTSSLKA
251 SYEAFKNNDF QLGKEFSMAR ETVGYSSSSA LMTTLTQNAS SSAADSRSGR
301 KSKNNNKSSS QQSSSSSSSS SLSSCSSSST VVQEISQQTT VVPESDSNSQ
351 VDWTYDPNEP RYCICNQVKV CYIYKSII
```

BLASTP hits

```
Entry AF044076_1 from database TREMBL:
"ING1"; product: "candidate tumor suppressor p33ING1";      Homo
sapiens candidate tumor suppressor p33ING1 (ING1) mRNA, complete
cds. Homo sapiens (human)
Length = 279
Score = 162 (57.0 bits), Expect = 1.1e-09, P = 1.1e-09
Identities = 48/183 (26%), Positives = 92/183 (50%)

Entry AC004537_1 from database TREMBL:
gene: "WUGSC:H_DJ0872F07.1"; Homo sapiens PAC clone DJ0872F07 from
7q31, complete sequence.
Score = 1814, P = 3.7e-187, identities = 358/358, positives = 358/358

Entry CEY51H1A_1 from database TREMBL:
gene: "Y51H1A.4"; Caenorhabditis elegans cosmid Y51H1A
Score = 213, P = 3.7e-15, identities = 37/123, positives = 82/123
```

Alert BLASTP hits for DKFZphutel_18c12, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphutel_18c12, frame 1

Report for DKFZphutel_18c12.1

```
[LENGTH]        378
[MW]            42275.72
[pI]            5.72
[HOMOL]         TREMBL:AC004537_1 gene: "WUGSC:H_DJ0872F07.1"; Homo sapiens PAC clone DJ0872F07
from 7q31, complete sequence. 1e-157
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YHR090c] 8e-05
[FUNCAT]        04.05.01.04 transcriptional control   [S. cerevisiae, YNL097c] 2e-04
[PROSITE]       MYRISTYL        3
[PROSITE]       AMIDATION       2
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        4
[PROSITE]       PROKAR_LIPOPROTEIN      1
[PROSITE]       GLYCOSAMINOGLYCAN       1
[PROSITE]       PKC_PHOSPHO_SITE        3
[PROSITE]       ASN_GLYCOSYLATION       5
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY    20.63 %
```

```
[KW]          COILED_COIL          7.94 %

SEQ      MLYLEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFFMNAKKNKPEWREE
SEG      ............................................................
PRD      ccchhhhhhhhhhhccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhh
COILS    ............................................................

SEQ      QMASIKKDYYKALEDADEKVQLANQIYDLVDRHLRKLDQELAKFKMELEADNAGITEILE
SEG      ............................................................
PRD      hhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccchhhhh
COILS    ............CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC..................

SEQ      RRSLELDTPSQPVNNHHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDAS
SEG      ............................................................
PRD      hhcccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhcccc
COILS    ............................................................

SEQ      KENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAGAITMAAAQAVQATAQMK
SEG      ........xxxxxxxxxxxxxxxxx.............xxxxxxxxxxxxxxxxxxxx..
PRD      cccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhh
COILS    ............................................................

SEQ      EGRRTSSLKASYEAFKNNDFQLGKEFSMARETVGYSSSSALMTTLTQNASSSAADSRSGR
SEG      ................................................xxxxxxxxxxxx
PRD      hccccccccchhhhhcccccccccccccccccccccccceeeeeccccccccccccccccc
COILS    ............................................................

SEQ      KSKNNNKSSSQQSSSSSSSSSLSSCSSSSTVVQEISQQTTVVPESDSNSQVDWTYDPNEP
SEG      xxxxxxxxxxxxxxxxxxxxxxxxxxxx................................
PRD      ccccccccccccccccccccceeecccccccccccccccccccccccccceeeecccccc
COILS    ............................................................

SEQ      RYCICNQVKVCYIYKSII
SEG      ..................
PRD      eeeeceeeeeeeeeeccc
COILS    ..................
```

Prosite for DKFZphutel_18c12.1

PS00001	190->194	ASN_GLYCOSYLATION	PDOC00001
PS00001	191->195	ASN_GLYCOSYLATION	PDOC00001
PS00001	203->207	ASN_GLYCOSYLATION	PDOC00001
PS00001	288->292	ASN_GLYCOSYLATION	PDOC00001
PS00001	306->310	ASN_GLYCOSYLATION	PDOC00001
PS00002	218->222	GLYCOSAMINOGLYCAN	PDOC00002
PS00004	243->247	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	64->67	PKC_PHOSPHO_SITE	PDOC00005
PS00005	247->250	PKC_PHOSPHO_SITE	PDOC00005
PS00005	298->301	PKC_PHOSPHO_SITE	PDOC00005
PS00006	142->146	CK2_PHOSPHO_SITE	PDOC00006
PS00006	156->160	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00006	349->353	CK2_PHOSPHO_SITE	PDOC00006
PS00008	186->192	MYRISTYL	PDOC00008
PS00008	214->220	MYRISTYL	PDOC00008
PS00008	219->225	MYRISTYL	PDOC00008
PS00009	241->245	AMIDATION	PDOC00009
PS00009	298->302	AMIDATION	PDOC00009
PS00013	315->326	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphutel_18c12.1)

DKFZphutel_18i19
----

group: transcription factors

DKFZphutel_18i19 encodes a novel 759 amino acid protein with similarity to the SREBP-2 mutant sterol regulatory element binding protein-2 of Cricetulus griseus.

The SREBP-2 protein is embedded in the membranes of the nucleus and endoplasmic reticulum. In cholesterol-depleted cells the proteins are cleaved to release soluble NH2-terminal fragments that enter the nucleus and activate genes encoding the low density lipoprotein receptor and enzymes of cholesterol synthesis. The new protein is a putative transcription factor capable of protein-protein interaction via a lim domain and additionally shows similarity to the common sunflower transcription factor SF3.

The new protein can find application in modulating/blocking the expression of genes involved in lipid metabolism.

similarity to transcription factor SF3

complete cDNA, complete cds, EST hits
strong similarity to mutated SREBP-2 of hamster,
similarity is not to SREP-2 part of protein but to the unknown part of
the fusion protein

Sequenced by AGOWA

Locus: /map=12

Insert length: 3664 bp
Poly A stretch at pos. 3647, polyadenylation signal at pos. 3636

```
   1 GCGCTAGGTA GAGCGCCGGG ACCTGTGACA GGGCTGGTAG CAGCGCAGAG
  51 GAAAGGCGGC TTTTAGCCAG GTATTTCAGT GTCTGTAGAC AAGATGGAAT
 101 CATCTCCATT TAATAGACGG CAATGGACCT CACTATCATT GAGGGTAACA
 151 GCCAAAGAAC TTTCTCTTGT CAACAAGAAC AAGTCATCGG CTATTGTGGA
 201 AATATTCTCC AAGTACCAGA AAGCAGCTGA AGAAACAAAC ATGGAGAAGA
 251 AGAGAAGTAA CACCGAAAAT CTCTCCCAGC ACTTTAGAAA GGGGACCCTG
 301 ACTGTGTTAA AGAAGAAGTG GGAGAACCCA GGGCTGGGAG CAGAGTCTCA
 351 CACAGACTCT CTACGGAACA GCAGCACTGA GATTAGGCAC AGAGCAGACC
 401 ATCCTCCTGC TGAAGTGACA AGCCACGCTG CTTCTGGAGC CAAAGCTGAC
 451 CAAGAAGAAC AAATCCACCC CAGATCTAGA CTCAGGTCAC CTCCTGAAGC
 501 CCTCGTTCAG GGTCGATATC CCCACATCAA GGACGGTGAG GATCTTAAAG
 551 ACCACTCAAC AGAAAGTAAA AAAATGGAAA ATTGTCTAGG AGAATCCAGG
 601 CATGAAGTAG AAAAATCAGA AATCAGTGAA AACACAGATG CTTCGGGCAA
 651 AATAGAGAAA TATAATGTTC CGCTGAACAG GCTTAAGATG ATGTTTGAGA
 701 AAGGTGAACC AACTCAAACT AAGATTCTCC GGGCCCAAAG CCGAAGTGCA
 751 AGTGGAAGGA AGATCTCTGA AAACAGCTAT TCTCTAGATG ACCTGGAAAT
 801 AGGCCCAGGT CAGTTGTCAT CTTCTACATT TGACTCGGAG AAAAATGAGA
 851 GTAGACGAAA TCTGGAACTT CCACGCCTCT CAGAAACCTC TATAAAGGAT
 901 CGAATGGCCA AGTACCAGGC AGCTGTGTCC AAACAAAGCA GCTCAACCAA
 951 CTATACAAAT GAGCTGAAAG CCAGTGGTGG CGAAATCAAA ATTCATAAAA
1001 TGGAGCAAAA GGAGAATGTG CCCCCAGGTC CTGAGGTCTG CATCACCCAT
1051 CAGGAAGGGG AAAAGATTTC TGCAAATGAG AATAGCCTGG CAGTCCGTTC
1101 CACCCCTGCC GAAGATGACT CCCGTGACTC CCAGGTTAAG AGTGAGGTTC
1151 AACAGCCTGT CCATCCCAAG CCACTAAGTC CAGATTCCAG AGCCTCCAGT
1201 CTTTCTGAAA GTTCTCCTCC CAAAGCAATG AAGAAGTTTC AGGCACCTGC
1251 AAGAGAGACC TGCGTGGAAT GTCAGAAGAC AGTCTATCCA ATGGAGCGTC
1301 TCTTGGCCAA CCAGCAGGTG TTTCACATCA GCTGCTTCCG TTGCTCCTAT
1351 TGCAACAACA AACTCAGTCT AGGAACATAT GCATCTTTAC ATGGAAGAAT
1401 CTATTGTAAG CCTCACTTCA ATCAACTCTT TAAATCTAAG GGCAACTATG
1451 ATGAAGGCTT TGGGCACAGA CCACACAAGG ATCTATGGGC AAGCAAAAAT
1501 GAAAACGAAG AGATTTTGGA GAGACCAGCC CAGCTTGCAA ATGCAAGGGA
1551 GACCCCTCAC AGCCCAGGGG TAGAAGATGC CCCTATTGCT AAGGTGGGTG
1601 TCCTGGCTGC AAGTATGGAA GCCAAGGCCT CCTCTCAGCA GGAGAAGGAA
1651 GACAAGCCAG CTGAAACCAA GAAGCTGAGG ATCGCCTGGC CACCCCCCAC
1701 TGAACTTGGA AGTTCAGGAA GTGCCTTGGA GGAAGGGATC AAAATGTCAA
1751 AGCCCAAATG GCCTCCTGAA GACGAAATCA GCAAGCCCGA AGTTCCTGAG
1801 GATGTCGATC TAGATCTGAA GAAGCTAAGA CGATCTTCTT CACTGAAGGA
1851 AAGAAGCCGC CCATTCACTG TAGCAGCTTC ATTTCAAAGC ACCTCTGTCA
1901 AGAGCCCAAA AACTGTGTCC CCACCTATCA GGAAAGGCTG GAGCATGTCA
1951 GAGCAGAGTG AAGAGTCTGT GGGTGGAAGA GTTGCAGAAA GGAAACAAGT
2001 GGAAAATGCC AAGGCTTCTA AGAAGAATGG GAATGTGGGA AAAACAACCT
2051 GGCAAAACAA AGAATCTAAA GGAGAGACAG GGAAGAGAAG TAAGGAAGGT
2101 CATAGTTTGG AGATGGAGAA TGAGAATCTT GTAGAAAATG GTGCAGACTC
2151 CGATGAAGAT GATAACAGCT TCCTCAAACA ACAATCTCCA CAAGAACCCA
2201 AGTCTCTGAA TTGGTCGAGT TTTGTAGACA ACACCTTTGC TGAAGAATTC
2251 ACTACTCAGA ATCAGAAATC CCAGGATGTG GAACTCTGGG AGGGAGAAGT
```

```
2301 GGTCAAAGAG CTCTCTGTGG AAGAACAGAT AAAGAGAAAT CGGTATTATG
2351 ATGAGGATGA GGATGAAGAG TGACAAATTG CAATGATGCT GGGCCTTAAA
2401 TTCATGTTAG TGTTAGCGAG CCACTGCCCT TTGTCAAAAT GTGATGCACA
2451 TAAGCAGGTA TCCCAGCATG AAATGTAATT TACTTGGAAG TAACTTTGGA
2501 AAAGAATTCC TTCTTAAAAT CAAAAACAAA ACAAAAAAAC ACAAAAAACA
2551 CATTCTAAAT ACTAGAGATA ACTTTACTTA AATTCTTCAT TTTAGCAGTG
2601 ATGATATGCG TAAGTGCTGT AAGGCTTGTA ACTGGGGAAA TATTCCACCT
2651 GATAATAGCC CAGATTCTAC TGTATTCCCA AAAGGCAATA TTAAGGTAGA
2701 TAGATGATTA GTAGTATATT GTTACACACT ATTTTGGAAT TAGAGAACAT
2751 ACAGAAGGAA TTTAGGGGCT TAAACATTAC GACTGAATGC ACTTTAGTAT
2801 AAAGGGCACA GTTTGTATAT TTTTAAATGA ATACCAATTT AATTTTTTAG
2851 TATTTACCTG TTAAGAGATT ATTTAGTCTT TAAATTTTTT AGGTTAATTT
2901 TCTTGCTGTG ATATATATGA GGAATTTACT ACTTTATGTC CTGCTCTCTA
2951 AACTACATCC TGAACTCGAC GTCCTGAGGT ATAATACAAC AGAGCACTTT
3001 TTGAGGCAAT TGAAAAACCA ACCTACACTC TTCGGTGCTT AGAGAGATCT
3051 GCTGTCTCCC AAATAAGCTT TTGTATCTGC CAGTGAATTT ACTGTACTCC
3101 AAATGATTGC TTTCTTTTCT GGTGATATCT GTGCTTCTCA TAATTACTGA
3151 AAGCTGCAAT ATTTTAGTAA TACCTTCGGG ATCACTGTCC CCCATCTTCC
3201 GTGTTAGAGC AAAGTGAAGA GTTTAAAGGA GGAAGAAGAA AGAACTGTCT
3251 TACACCACTT GAGCTCAGAC CTCTAAACCC TGTATTTCCC TTATGATGTC
3301 CCCTTTTTGA GACACTAATT TTTAAATACT TACTAGCTCT GAAATATATT
3351 GATTTTTATC ACAGTATTCT CAGGGTGAAA TTAAACCAAC TATAGGCCTT
3401 TTTCTTGGGA TGATTTTCTA GTCTTAAGGT TTGGGGACAT TATAAACTTG
3451 AGTACATTTG TTGTACACAG TTGATATTCC AAATTGTATG GATGGGAGGG
3501 AGAGGTGTCT TAAGCTGTAG GCTTTTCTTT GTACTGCATT TATAGAGATT
3551 TAGCTTTAAT ATTTTTTAGA GATGTAAAAC ATTCTGCTTT CTTAGTCTTA
3601 CCTAGTCTGA AACATTTTTA TTCAATAAAG ATTTTAATTA AAATTTGAAA
3651 AAAAAAAAAA AAAA
```

BLAST Results

Entry HS512217 from database EMBL:
human STS SHGC-14654.
Length = 250
Minus Strand HSPs:
Score = 1202 (180.3 bits), Expect = 1.8e-46, P = 1.8e-46
Identities = 242/244 (99%)

Medline entries

95263566:
Three different rearrangements in a single intron truncate sterol regulatory element binding protein-2 and produce sterol-resistant phenotype in three cell lines. Role of introns in protein evolution.

93258417:
Characterization of a pollen-specific cDNA from sunflower encoding a zinc finger protein.

Peptide information for frame 1

ORF from 94 bp to 2370 bp; peptide length: 759
Category: similarity to known protein

```
  1 MESSPFNRRQ WTSLSLRVTA KELSLVNKNK SSAIVEIFSK YQKAAEETNM
 51 EKKRSNTENL SQHFRKGTLT VLKKKWENPG LGAESHTDSL RNSSTEIRHR
101 ADHPPAEVTS HAASGAKADQ EEQIHPRSRL RSPPEALVQG RYPHIKDGED
151 LKDHSTESKK MENCLGESRH EVEKSEISEN TDASGKIEKY NVPLNRLKMM
201 FEKGEPTQTK ILRAQSRSAS GRKISENSYS LDDLEIGPGQ LSSSTFDSEK
251 NESRRNLELP RLSETSIKDR MAKYQAAVSK QSSSTNYTNE LKASGGEIKI
301 HKMEQKENVP PGPEVCITHQ EGEKISANEN SLAVRSTPAE DDSRDSQVKS
351 EVQQPVHPKP LSPDSRASSL SESSPPKAMK KFQAPARETC VECQKTVYPM
401 ERLLANQQVF HISCFRCSYC NNKLSLGTYA SLHGRIYCKP HFNQLFKSKG
451 NYDEGFGHRP HKDLWASKNE NEEILERPAQ LANARETPHS PGVEDAPIAK
501 VGVLAASMEA KASSQQEKED KPAETKKLRI AWPPPTELGS SGSALEEGIK
551 MSKPKWPPED EISKPEVPED VDLDLKKLRR SSSLKERSRP FTVAASFQST
601 SVKSPKTVSP PIRKGWSMSE QSEESVGGRV AERKQVENAK ASKKNGNVGK
651 TTWQNKESKG ETGKRSKEGH SLEMENENLV ENGADSDEDD NSFLKQQSPQ
701 EPKSLNWSSF VDNTFAEEFT TQNQKSQDVE LWEGEVVKEL SVEEQIKRNR
```

751 YYDEDEDEE

BLASTP hits

Entry CG22818_1 from database TREMBL:
"SREBP-2"; product: "mutant sterol regulatory element binding protein-2"; Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds. Cricetulus griseus (Chinese hamster)
Length = 839
Score = 1502 (528.7 bits), Expect = 3.9e-154, P = 3.9e-154
Identities = 290/380 (76%), Positives = 322/380 (84%)

Entry S28507 from database PIR:
transcription factor SF3 - common sunflower
Length = 219
Score = 212 (74.6 bits), Expect = 6.3e-18, Sum P(2) = 6.3e-18
Identities = 36/82 (43%), Positives = 55/82 (67%)

Entry NTLIMDOM_1 from database TREMBL:
"SF3"; product: "LIM-domain SF3 protein"; N.tabacum mRNA for LIM-domain protein Nicotiana tabacum (common tobacco)
Length = 189
Score = 216 (76.0 bits), Expect = 1.0e-16, P = 1.0e-16
Identities = 42/94 (44%), Positives = 57/94 (60%)

Alert BLASTP hits for DKFZphutel_18i19, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphutel_18i19, frame 1

Report for DKFZphutel_18i19.1

[LENGTH] 759
[MW] 85225.57
[pI] 6.41
[HOMOL] TREMBL:CG22818_1 gene: "SREBP-2"; product: "mutant sterol regulatory element binding protein-2"; Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds. 1e-151
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YLR257w] 3e-05
[FUNCAT] 05.04 translation (initiation, elongation and termination) [S. cerevisiae, YGR162w TIF4631 - mRNA cap-binding protein] 1e-04
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YGR162w TIF4631 - mRNA cap-binding protein] 1e-04
[BLOCKS] BL00478B
[PIRKW] zinc finger 9e-16
[PIRKW] DNA binding 9e-16
[SUPFAM] LIM metal-binding repeat homology 9e-16
[PROSITE] MYRISTYL 6
[PROSITE] LIM_DOMAIN_1 1
[PROSITE] AMIDATION 2
[PROSITE] CAMP_PHOSPHO_SITE 4
[PROSITE] CK2_PHOSPHO_SITE 28
[PROSITE] TYR_PHOSPHO_SITE 2
[PROSITE] PKC_PHOSPHO_SITE 15
[PROSITE] ASN_GLYCOSYLATION 6
[PFAM] LIM domain containing proteins
[KW] Irregular
[KW] 3D
[KW] LOW_COMPLEXITY 5.53 %

```
SEQ    MESSPFNRRQWTSLSLRVTAKELSLVNKNKSSAIVEIFSKYQKAAEETNMEKKRSNTENL
SEG    ............................................................
1ctl-  ............................................................

SEQ    SQHFRKGTLTVLKKKWENPGLGAESHTDSLRNSSTEIRHRADHPPAEVTSHAASGAKADQ
SEG    ............................................................
1ctl-  ............................................................

SEQ    EEQIHPRSRLRSPPEALVQGRYPHIKDGEDLKDHSTESKKMENCLGESRHEVEKSEISEN
SEG    ............................................................
1ctl-  ............................................................

SEQ    TDASGKIEKYNVPLNRLKMMFEKGEPTQTKILRAQSRSASGRKISENSYSLDDLEIGPGQ
SEG    ............................................................
```

```
1ctl-   ............................................................

SEQ     LSSSTFDSEKNESRRNLELPRLSETSIKDRMAKYQAAVSKQSSSTNYTNELKASGGEIKI
SEG     ............................................................
1ctl-   ............................................................

SEQ     HKMEQKENVPPGPEVCITHQEGEKISANENSLAVRSTPAEDDSRDSQVKSEVQQPVHPKP
SEG     ...........................................................x
1ctl-   ............................................................

SEQ     LSPDSRASSLSESSPPKAMKKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYC
SEG     xxxxxxxxxxxxxxxx............................................
1ctl-   .............................ETTTTEEETTTCEEEETTEEEETTTTBTTTT

SEQ     NNKLSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWASKNENEEILERPAQ
SEG     ............................................................
1ctl-   TCBCBTTBEEEEETTEEEETTTTTTTTTCCTTTTTTTTCTTT..................

SEQ     LANARETPHSPGVEDAPIAKVGVLAASMEAKASSQQEKEDKPAETKKLRIAWPPPTELGS
SEG     ............................................................
1ctl-   ............................................................

SEQ     SGSALEEGIKMSKPKWPPEDEISKPEVPEDVDLDLKKLRRSSSLKERSRPFTVAASFQST
SEG     ...............................xxxxxxxxxxxxxxxxxx...........
1ctl-   ............................................................

SEQ     SVKSPKTVSPPIRKGWSMSEQSEESVGGRVAERKQVENAKASKKNGNVGKTTWQNKESKG
SEG     ............................................................
1ctl-   ............................................................

SEQ     ETGKRSKEGHSLEMENENLVENGADSDEDDNSFLKQQSPQEPKSLNWSSFVDNTFAEEFT
SEG     ............................................................
1ctl-   ............................................................

SEQ     TQNQKSQDVELWEGEVVKELSVEEQIKRNRYYDEDEDEE
SEG     ................................xxxxxxx
1ctl-   .......................................
```

Prosite for DKFZphutel_18i19.1

PS00001	29->33	ASN_GLYCOSYLATION	PDOC00001
PS00001	59->63	ASN_GLYCOSYLATION	PDOC00001
PS00001	92->96	ASN_GLYCOSYLATION	PDOC00001
PS00001	251->255	ASN_GLYCOSYLATION	PDOC00001
PS00001	286->290	ASN_GLYCOSYLATION	PDOC00001
PS00001	706->710	ASN_GLYCOSYLATION	PDOC00001
PS00004	52->56	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	65->69	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	222->226	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	579->583	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	15->18	PKC_PHOSPHO_SITE	PDOC00005
PS00005	19->22	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	158->161	PKC_PHOSPHO_SITE	PDOC00005
PS00005	184->187	PKC_PHOSPHO_SITE	PDOC00005
PS00005	220->223	PKC_PHOSPHO_SITE	PDOC00005
PS00005	248->251	PKC_PHOSPHO_SITE	PDOC00005
PS00005	253->256	PKC_PHOSPHO_SITE	PDOC00005
PS00005	266->269	PKC_PHOSPHO_SITE	PDOC00005
PS00005	525->528	PKC_PHOSPHO_SITE	PDOC00005
PS00005	583->586	PKC_PHOSPHO_SITE	PDOC00005
PS00005	601->604	PKC_PHOSPHO_SITE	PDOC00005
PS00005	604->607	PKC_PHOSPHO_SITE	PDOC00005
PS00005	642->645	PKC_PHOSPHO_SITE	PDOC00005
PS00005	662->665	PKC_PHOSPHO_SITE	PDOC00005
PS00006	19->23	CK2_PHOSPHO_SITE	PDOC00006
PS00006	48->52	CK2_PHOSPHO_SITE	PDOC00006
PS00006	55->59	CK2_PHOSPHO_SITE	PDOC00006
PS00006	85->89	CK2_PHOSPHO_SITE	PDOC00006
PS00006	93->97	CK2_PHOSPHO_SITE	PDOC00006
PS00006	132->136	CK2_PHOSPHO_SITE	PDOC00006
PS00006	168->172	CK2_PHOSPHO_SITE	PDOC00006
PS00006	230->234	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00006	266->270	CK2_PHOSPHO_SITE	PDOC00006
PS00006	294->298	CK2_PHOSPHO_SITE	PDOC00006
PS00006	318->322	CK2_PHOSPHO_SITE	PDOC00006
PS00006	326->330	CK2_PHOSPHO_SITE	PDOC00006
PS00006	337->341	CK2_PHOSPHO_SITE	PDOC00006

PS00006	369->373	CK2_PHOSPHO_SITE	PDOC00006
PS00006	389->393	CK2_PHOSPHO_SITE	PDOC00006
PS00006	467->471	CK2_PHOSPHO_SITE	PDOC00006
PS00006	514->518	CK2_PHOSPHO_SITE	PDOC00006
PS00006	543->547	CK2_PHOSPHO_SITE	PDOC00006
PS00006	563->567	CK2_PHOSPHO_SITE	PDOC00006
PS00006	583->587	CK2_PHOSPHO_SITE	PDOC00006
PS00006	617->621	CK2_PHOSPHO_SITE	PDOC00006
PS00006	658->662	CK2_PHOSPHO_SITE	PDOC00006
PS00006	686->690	CK2_PHOSPHO_SITE	PDOC00006
PS00006	698->702	CK2_PHOSPHO_SITE	PDOC00006
PS00006	709->713	CK2_PHOSPHO_SITE	PDOC00006
PS00006	714->718	CK2_PHOSPHO_SITE	PDOC00006
PS00006	741->745	CK2_PHOSPHO_SITE	PDOC00006
PS00007	223->230	TYR_PHOSPHO_SITE	PDOC00007
PS00007	222->230	TYR_PHOSPHO_SITE	PDOC00007
PS00008	239->245	MYRISTYL	PDOC00008
PS00008	427->433	MYRISTYL	PDOC00008
PS00008	502->508	MYRISTYL	PDOC00008
PS00008	539->545	MYRISTYL	PDOC00008
PS00008	548->554	MYRISTYL	PDOC00008
PS00008	627->633	MYRISTYL	PDOC00008
PS00009	220->224	AMIDATION	PDOC00009
PS00009	662->666	AMIDATION	PDOC00009
PS00478	390->425	LIM_DOMAIN_1	PDOC00382

Pfam for DKFZphutel_18i19.1

```
HMM_NAME        LIM domain containing proteins

HMM                 *CagCNrpIyDREivMRAMNKvWHpECFrCcdCqqPLtegdeFYErDGrI
                     C  C++++Y+ E++  A+  V+H++CFRC+ C+  L+ G+ + ++ GRI
Query           390  CVECQKTVYPMERLL-ANQQVFHISCFRCSYCNNKLSLGT-YASLHGRI    436

HMM                 YCKhDYYrrFg*
                    YCK+++ ++F+
Query           437 YCKPHFNQLFK     447
```

DKFZphutel_18i4

group: uterus derived

DKFZphutel_18i4 encodes a novel 220 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

weak similarity to C.elegans D2085.2

complete cDNA, complete cds, few EST hits

Sequenced by AGOWA

Locus: /map="7q31"

Insert length: 1568 bp
Poly A stretch at pos. 1551, polyadenylation signal at pos. 1523

```
   1 GCCGAGCGGA GAGGGTAGAG ACGGGGTTTC ACCGTGTTAG CCAAGATGGT
  51 CTCGATCTCC TGACCTCGTG ATCCGCCCGC CTCGGCCTCC CAAAGTGCTG
 101 GGATTACAGG CGTGAGCCAC TGCGCCCGGC CTGTTGTACA GTTATTAAAG
 151 TTATCATTTA ACATGGAAGA AGATGAGTTC ATTGGAGAAA AAACATTCCA
 201 ACGTTATTGT GCAGAATTCA TTAAACATTC ACAACAGATA GGTGATAGTT
 251 GGGAATGGAG ACCATCAAAG GACTGTTCTG ATGGCTACAT GTGCAAAATA
 301 CACTTTCAAA TTAAGAATGG GTCTGTGATG TCACATCTAG GAGCATCTAC
 351 CCATGGACAG ACATGTCTTC CCATGGAGGA GGCTTTCGAG CTACCCTTGG
 401 ATGATTGTGA AGTGATTGAA ACTGCAGCAG CGTCCGAAGT GATTAAATAT
 451 GAGTATCATG TCTTATATTC CTGTAGCTAC CAAGTGCCTG TACTTTACTT
 501 TAGGGCAAGC TTTTTAGATG GGAGACCTTT AACTCTGAAG GACATATGGG
 551 AAGGAGTTCA TGAGTGCTAT AAGATGCGAC TGCTACAGGG ACCATGGGAC
 601 ACTATTACGC AACAGGAACA TCCAATACTT GGGCAACCCT TTTTTGTACT
 651 TCATCCCTGC AAGACGAATG AATTCATGAC TCCTGTATTA AAGAATTCTC
 701 AGAAAATCAA TAAGAATGTC AACTATATCA CATCATGGCT GAGCATTGTA
 751 GGGCCAGTTG TTGGGCTGAA TCTACCTCTG AGTTATGCCA AAGCAACGTC
 801 TCAGGATGAA CGAAATGTCC CTTAACAAGA TTCTTCTATT GAGTTTAGGA
 851 ATTGCGGCAC GAAGAATGCC AAGAGTTTAC CTGGCCAGCC CTGGCTTTAA
 901 TAGGACTGAT ACCATGGAAT ATTTCATCTC ACCAAGATGT GACATGGATT
 951 ATTTTTCCCT TGGACACAAA TGTCTACAGC AACTGATGTT TGATAGGCTG
1001 AATGTTTAGA AGAAACACTT CAAAGGGATA CATCATGGCC AGGCATGGTG
1051 GCTCACACCT GTAATCCAAG CACTTTGGGA GGCCAAGGTG GGAGCATCAC
1101 TTGATCCTGG GAGTTCGAGA CCAGCCTGGG CAACATGGTG AAACCCTGTC
1151 GGTACAAAAA AATACAAAAA TTTGCCTGTT TATGGTGGTG TGTTCCTGTA
1201 GTCCCAGCTC CCCAGGAGGC TGAGGTGGGA GGTTGGCTTT AACCCAGGAG
1251 GCAGAGGTTG CAGTGAGCTG AGACTGTGCC ACTGCAGTCC AGCCTGGGTG
1301 ACAGAGCCAG ACACTGTCTC GGGAAAAAAA AAAAAAAAAA AAAGACACAT
1351 CACTATAAAT AGCAAAAAAA CAAATCTAAC TTATTAATAC TAGGAATACC
1401 AACATTATTA GGGCACTTGC AGGTTATTCT TTTCTAGGCC AAGTACTTCA
1451 CTTCCATTTG TCTGACATGG AGATTGAGGG AGAAATGTAT TTGTGTGTTC
1501 ATTTTAATGT AAGATATATA AAAATTAAAT TACTGGATTT ACCTGTCCCT
1551 GAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 163 bp to 822 bp; peptide length: 220
Category: similarity to unknown protein

```
  1 MEEDEFIGEK TFQRYCAEFI KHSQQIGDSW EWRPSKDCSD GYMCKIHFQI
 51 KNGSVMSHLG ASTHGQTCLP MEEAFELPLD DCEVIETAAA SEVIKYEYHV
101 LYSCSYQVPV LYFRASFLDG RPLTLKDIWE GVHECYKMRL LQGPWDTITQ
151 QEHPILGQPF FVLHPCKTNE FMTPVLKNSQ KINKNVNYIT SWLSIVGPVV
201 GLNLPLSYAK ATSQDERNVP
```

BLASTP hits

Entry CED2085_2 from database TREMBL:
"D2085.2"; Caenorhabditis elegans cosmid D2085
Length = 173
Score = 167 (58.8 bits), Expect = 1.1e-12, P = 1.1e-12
Identities = 36/121 (29%), Positives = 64/121 (52%)

Alert BLASTP hits for DKFZphutel_18i4, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphutel_18i4, frame 1

Report for DKFZphutel_18i4.1

[LENGTH]	220
[MW]	25278.99
[pI]	5.34
[HOMOL]	TREMBL:CED2085_2 gene: "D2085.2"; Caenorhabditis elegans cosmid D2085 2e-11
[BLOCKS]	BL00221E
[PROSITE]	MYRISTYL 2
[PROSITE]	CK2_PHOSPHO_SITE 4
[PROSITE]	PKC_PHOSPHO_SITE 2
[PROSITE]	ASN_GLYCOSYLATION 1
[KW]	Alpha_Beta

```
SEQ     MEEDEFIGEKTFQRYCAEFIKHSQQIGDSWEWRPSKDCSDGYMCKIHFQIKNGSVMSHLG
PRD     cccccccchhhhhhhhhhhhhhhhccccccccccccccceeeeeeeeeeeeccceeeeec

SEQ     ASTHGQTCLPMEEAFELPLDDCEVIETAAASEVIKYEYHVLYSCSYQVPVLYFRASFLDG
PRD     cccccccchhhhhhhhccccceeehhhhhchhhhhhhheeeeccccceeeeeeeeccccc

SEQ     RPLTLKDIWEGVHECYKMRLLQGPWDTITQQEHPILGQPFFVLHPCKTNEFMTPVLKNSQ
PRD     ccccchhhhhhhhhhhhhhhcccccccccccccccceeeeccccccccccccccccc

SEQ     KINKNVNYITSWLSIVGPVVGLNLPLSYAKATSQDERNVP
PRD     cccccccccccceeeeccccccccccceeeecccccccccc
```

Prosite for DKFZphutel_18i4.1

PS00001	52->56	ASN_GLYCOSYLATION	PDOC00001
PS00005	124->127	PKC_PHOSPHO_SITE	PDOC00005
PS00005	179->182	PKC_PHOSPHO_SITE	PDOC00005
PS00006	116->120	CK2_PHOSPHO_SITE	PDOC00006
PS00006	124->128	CK2_PHOSPHO_SITE	PDOC00006
PS00006	149->153	CK2_PHOSPHO_SITE	PDOC00006
PS00006	212->216	CK2_PHOSPHO_SITE	PDOC00006
PS00008	53->59	MYRISTYL	PDOC00008
PS00008	131->137	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_18i4.1)

DKFZphute1_1811

group: nucleic acid management

DKFZphtes3_15j18 encodes a novel 184 amino acid protein with similarity to S. cerevisiae putative ribosomal protein YHR148w.

The novel protein is similar to several 40S ribosomal proteins and therefore seems to part of the corresponding ribosome subunit.

The new protein can find application in modulation of ribosome assembly, structure and function.

strong similarity to S.cerevisiae YHR148w

complete cDNA, complete cds, EST hits,
potential start at Bp 45 matchs kozak consensus ANNatgG
gene disruption of YHR148w is lethal!

Sequenced by AGOWA

Locus: unknown

Insert length: 1076 bp
Poly A stretch at pos. 1035, polyadenylation signal at pos. 1006

```
   1 GCGCGCTCTC AGCTTCGGGT CCTGCGGCTG CGGCTGCCGC CATCATGGTG
  51 CGGAAGCTTA AGTTCCACGA GCAGAAGCTG CTGAAGCAGG TGGACTTCCT
 101 GAACTGGGAG GTCACCGACC ACAACCTGCA CGAGCTGCGC GTGCTGCGGC
 151 GTTACCGGCT GCAGCGGCGG GAGGACTACA CGCGCTACAA CCAGCTGAGC
 201 CGTGCCGTGC GTGAGCTGGC GCGGCGCCTG CGCGACCTGC CCGAACGCGA
 251 CCAGTTCCGC GTGCGCGCTT CGGCCGCGCT GCTGGACAAG CTGTATGCTC
 301 TCGGCTTGGT GCCCACGCGC GGTTCGCTGG AGCTCTGCGA CTTCGTCACG
 351 GCCTCGTCCT TCTGCCGCCG CCGCCTCCCC ACCGTGCTCC TCAAGCTGCG
 401 CATGGCGCAG CACCTTCAGG CTGCCGTGGC CTTTGTGGAG CAAGGGCACG
 451 TACGCGTGGG CCCTGACGTG GTTACCGACC CCGCCTTCCT TGTCACGCGC
 501 AGCATGGAGG ACTTTGTCAC TTGGGTGGAC TCGTCCAAGA TCAAGCGGCA
 551 CGTGCTAGAG TACAATGAGG AGCGCGATGA CTTCGATCTG GAAGCCTAGC
 601 GGATCTCCCA CTTTGCATGG CTGTCTTTTA CAGATGGGAA AACTGAGGCC
 651 TGATGCTGGA GATTCTATGA GGGTGCTCTC CTCAAGGGTA TCAGACGGTC
 701 GTAGGTTCTT AAGAATTTGA TTCATCAGTG GCAGGCCATG CATAGAGCCA
 751 CGGGAGGTGC GTCCTTGTTT TCCAGGAAAT GTTCTTAGAA CTTGGACTAC
 801 TGATTATTAA TTGACTGTGC CTTGGGAAAC AGTGGGAAGT AACTTGGTGC
 851 AGCACTGGGG TATTGTTGGA CTGGTTCAAT TCGTTTAACT CGAATTCTTG
 901 CTCCTGGCCG TGGTTAAGCT GTGTACAGAT GATGGAGAGT TTGGCCTCAA
 951 GTTTTTATAA ACTGAGCGAG ACTAGTGTTC AGGATCTCCT CCCTTGTTTA
1001 AATGTCAATA AATGCCCCAA CTGCTTTGTA AGCTCAAAAA AAAAAAAAAA
1051 AAAAAAAAAA AAAAAAAAAA AAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 45 bp to 596 bp; peptide length: 184
Category: strong similarity to known protein

```
  1 MVRKLKFHEQ KLLKQVDFLN WEVTDHNLHE LRVLRRYRLQ RREDYTRYNQ
 51 LSRAVRELAR RLRDLPERDQ FRVRASAALL DKLYALGLVP TRGSLELCDF
101 VTASSFCRRR LPTVLLKLRM AQHLQAAVAF VEQGHVRVGP DVVTDPAFLV
151 TRSMEDFVTW VDSSKIKRHV LEYNEERDDF DLEA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_1811, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphutel_1811, frame 3

Report for DKFZphutel_1811.3

```
[LENGTH]        184
[MW]            21850.21
[pI]            9.54
[HOMOL]         PIR:S33911 probable ribosomal protein YHR148w - yeast (Saccharomyces
cerevisiae) 4e-47
[FUNCAT]        05.01 ribosomal proteins      [S. cerevisiae, YHR148w] 2e-48
[FUNCAT]        30.03 organization of cytoplasm      [S. cerevisiae, YPL081w] 5e-07
[FUNCAT]        j mrna translation and ribosome biogenesis   [M. jannaschii, MJ0190] 8e-05
[BLOCKS]        BL00632
[PIRKW]         cytosol 1e-07
[PIRKW]         ribosome 1e-07
[PIRKW]         protein biosynthesis 1e-07
[SUPFAM]        rat ribosomal protein S9 1e-07
[PROSITE]       MYRISTYL       1
[PROSITE]       CK2_PHOSPHO_SITE      2
[PROSITE]       TYR_PHOSPHO_SITE      1
[PROSITE]       PKC_PHOSPHO_SITE      1
[PFAM]          Ribosomal protein S4
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY     6.52 %
```

```
SEQ     MVRKLKFHEQKLLKQVDFLNWEVTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELAR
SEG     ..............................xxxxxxxxxxxx..................
PRD     ccchhhhhhhhhhhhhhhhhcccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ     RLRDLPERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRRLPTVLLKLRM
SEG     ............................................................
PRD     hhhhhccccchhhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhh

SEQ     AQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSMEDFVTWVDSSKIKRHVLEYNEERDDF
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhcccccceeeccccceeeeecccccceeeeecccchhhhhhhhcccccc

SEQ     DLEA
SEG     ....
PRD     cccc
```

Prosite for DKFZphutel_1811.3

PS00005	163->166	PKC_PHOSPHO_SITE	PDOC00005
PS00006	153->157	CK2_PHOSPHO_SITE	PDOC00006
PS00006	159->163	CK2_PHOSPHO_SITE	PDOC00006
PS00007	41->49	TYR_PHOSPHO_SITE	PDOC00007
PS00008	87->93	MYRISTYL	PDOC00008

Pfam for DKFZphutel_1811.3

```
HMM_NAME        Ribosomal protein S4

HMM                  *MSR.YRGPRWKIIRRPGElPWLTnK.....tklmrkYC..lRPgQHgWR
                      M+R ++ +++K+++++++L W          ++++R Y     R+++  ++
Query             1   MVRKLKFHEQKLLKQVDFLNWEVTDHNLHELRVLRRYRLQRREDYTRYN    49

HMM                  qRktLsKIRRmSQYrIRLQEKQKLRFMYGNItERQLRRYvRiaEdKRKlD
                     Q +     +R +++ +   L+E + +R      +++++L++++      +++ L
Query            50  QLSR--AVRELARRLRDLPERDQFRVRASAALLDKLYALGLVP-TRGSLE    96

HMM                  YsTGenLMQILEMRLDNIVFRMGMAPTIHHARQLINHRHIRVNdRIVNIP
                        ++ + ++++RL++++ ++ MA    ++A+ +++++H+RV++ +V++P
Query            97  LCDFVTASSFCRRRLPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDP   146

HMM                  SYiCRPNDiISIRDkqrMQsHIkWnieSPegrmRPNHLErNnkkYeGtIN
```

```
                 ++++++     +       +++++W++ S+        ++R+ + Y+    +
Query       147 AFLVTRS---M-------EDFVTWVDSSK--------IKRHVLEYNEERD .  178

HMM             rIIEReWiplkINElLVVEY*
                +++ +
Query       179 DFDLE---------------     183
```

DKFZphutel_19f19
----

group: transmembrane protein

DKFZphutel_19f19 encodes a novel 204 amino acid protein with similarity to murine p24 protein.

Murine p24 is expressed only in brain where it is localized exclusively in neurons. It seems to be a neuron-specific membrane protein localised in intracellular organelles of highly differentiated neural cells and may play a role in the neural organelle transport system. As p24, the novel protein contains 2 transmembrane regions, but it contains not the sequence homologous to the microtubule-binding domain of microtubule-associated proteins present in p24.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

similarity to mouse P24 protein ;
membrane regions: 2
Summary DKFZphutel_19f19 encodes a novel 204 amino acid protein, with similarity to mouse P24 protein.

similarity to mouse P24 protein

complete cDNA, complete cds, EST hits,
2 TM-domains

Sequenced by AGOWA

Locus: /map=14.8 cR from top of Chr20 linkage group

Insert length: 2042 bp
Poly A stretch at pos. 1958, polyadenylation signal at pos. 1940

```
   1 GCAGGCAGAG AGATGAGGAA ACTGAGACCC AGAAAGGTGG AAGCACTTGT
  51 CTAAGGTCAC GCCTCCAGGA AGCAGTGTGT CCACGACTCC AGTCCAAGTG
 101 GTCAGGCTCC AGAGCCCACA GTCCCAGGGG TCCATGATGC CGAGCTGCAA
 151 TCGTTCCTGC AGCTGCAGCC GCGGCCCCAG CGTGGAGGAT GGCAAGTGGT
 201 ATGGGGTCCG CTCCTACCTG CACCTCTTCT ATGAGGACTG TGCAGGCACT
 251 GCTCTCAGCG ACGACCCTGA GGGACCTCCG GTCCTGTGCC CCCGCCGGCC
 301 CTGGCCCTCA CTGTGTTGGA AGATCAGCCT GTCCTCGGGG ACCCTGCTTC
 351 TGCTGCTGGG TGTGGCGGCT CTGACCACTG GCTATGCAGT GCCCCCCAAG
 401 CTGGAGGGCA TCGGTGAGGG TGAGTTCCTG GTGTTGGATC AGCGGGCAGC
 451 CGACTACAAC CAGGCCCTGG GCACCTGTCG CCTGGCAGGC ACAGCGCTCT
 501 GTGTGGCAGC TGGAGTTCTG CTCGCCATCT GCCTCTTCTG GGCCATGATA
 551 GGCTGGCTGA GCCAGGACAC CAAGGCAGAG CCCTTGGACC CCGAAGCCGA
 601 CAGCCACGTG GAGGTCTTCG GGGATGAGCC AGAGCAGCAG TTGTCACCCA
 651 TTTTCCGCAA TGCCAGTGGC CAGTCATGGT TCTCGCCACC CGCCAGCCCC
 701 TTTGGGCAAT CTTCTGTGCA GACTATCCAG CCCAAGAGGG ACTCCTGAGC
 751 TGCCCACATG GCCTAAGATG TGGGTCCTGG ATCCTTCCCC CTTCTCACCA
 801 TAACCCCCTC TCAGTGTTTC CCCAACTTCT CCCTTTAGAG CCCAACTCCA
 851 GGTCAAATCT GGAGCTCAAA TCCCAGTGCT CCCTCCCCAG GAGTGGGGCC
 901 CCAACTCTTC CAAGATACCA GCATTCCTCA AGTCCTCCCA AAACTTCCTA
 951 CCCACACCCT CTTCCCAAGG CCCTCAGGGG CAGAAAACAT CTCCTTCAAC
1001 CCGTCCCCAC TCCTTCCTCT GCATGACCTT GGGCAAACCC TTGCCCTTTC
1051 AAGCCATCAG CTCCTGCCTC TCTGCCATGA GGGCTTTGGA TCAGATTCCT
1101 CTTCTCGCCA GGATGAGGAC ACGCACTGCC CTCCATAGAC ACAGATGAAG
1151 GGGTGGGGGT CATTCAGCTC GAATGGGTCC CAGATGCTCA CTTGGCCTTT
1201 CCCTGCAGGA TGAGTGAAGA CGTTTGCCTC TCACAGTGTG TCTTCTACCT
1251 GCATTTTGGC ATCAGAGCCC CCCAGCCCAC CCACCACAGG CAATTACTAG
1301 CCCTAGTTGA TAGGTGAGGT GGGTGAAGAA GGCTGGAGGT GACATGTCCG
1351 AGGTCACACA ACAAAGCAGC ATGCAGGAAC TAGAAACACA TCTTCAGCCT
1401 CCTCCTGGGC CAGCTCTTGT GCTACAGGTG GGGCGGAGCC AGCCCCTCAC
1451 CTTCCTGGTT CCCTGAGGGT CCTCAGGGTG GAGGACAGGT TTGGCCCAGA
1501 AAGACTAGCC AGAGGCCTGA TGGTCCCAGG TGGCTCTGGA TATACTTTGG
1551 ATATGGATTT AAATGGTCTC TAAGAGCCGG GGGTAGGGGG CAGGAAAAGT
1601 GGGTTGTCTT TGCCCCTCAA AGTCCACCTA CCTAGAAACC AAGCCCACGG
1651 TCTTGGCCGT GACCCTGATA ATAAATGGGC TCTCTCAGAG GCGCCAGCCC
1701 CTCCCTCCCC AGCCGGAGGC GTCATCTCTC TTCTGTACCA CTAGAGGGAG
1751 CTCTGATGCA GCTGGAGAGC AGCGCTCAAG GCTCTCGCCC CTCCCCTCCC
1801 TAACCCTTAC CTTCAGTCTC CACCAGCCTG AAGGGCCTCC TAGGGGATCC
1851 TCAGGCGGCC CCCACCAGGG CACACCCTAC TGTCCTTGTG CCTCACGCCC
1901 CCTCCTCATC CTGCACCCCT TCCATCCCAC CTTCCCTTTC AATAAACAGC
1951 TGGGATGGAA AAAAAAAAAA AGAAAAAAAA AAAAAAAAAA AAAAAAAAAA
2001 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry HS417348 from database EMBL:
human STS WI-14697.
Length = 290
Minus Strand HSPs:
Score = 1254 (188.2 bits), Expect = 3.0e-50, P = 3.0e-50
Identities = 262/273 (95%)

Medline entries

97334404:
A newly identified membrane protein localized exclusively in intracellular organelles of neurons.

Peptide information for frame 2

ORF from 134 bp to 745 bp; peptide length: 204
Category: similarity to known protein

```
  1 MMPSCNRSCS CSRGPSVEDG KWYGVRSYLH LFYEDCAGTA LSDDPEGPPV
 51 LCPRRPWPSL CWKISLSSGT LLLLLGVAAL TTGYAVPPKL EGIGEGEFLV
101 LDQRAADYNQ ALGTCRLAGT ALCVAAGVLL AICLFWAMIG WLSQDTKAEP
151 LDPEADSHVE VFGDEPEQQL SPIFRNASGQ SWFSPPASPF GQSSVQTIQP
201 KRDS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_19f19, frame 2

TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein, complete cds., N = 1, Score = 295, P = 3.8e-26

```
>TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein,
     complete cds.
          Length = 196

  HSPs:

 Score = 295 (44.3 bits), Expect = 3.8e-26, P = 3.8e-26
 Identities = 58/139 (41%), Positives = 81/139 (58%)

Query:     2 MPSCNRSCSCSRGPSVEDGKW---YGVRSYLHLFYEDCAGTALSDDPEGPPVLCPRRPWP 58
             M SC+ +C   R  +  +G +   YGVRSYLH FYEDC  +     + +       P R W
Sbjct:     1 MTSCSNTCGSRRAQADTEGGYQQRYGVRSYLHQFYEDCTASIWEYEDDFQIQRSPNR-WS 59

Query:    59 SLCWKISLSSGTLLLLLGVAALTTGYAVPPKLEGIGEGEFLVLDQRAADYNQALGTCRLA 118
             S+ WK+ L SGT+ ++LG+  L  G+ VPPK+E  GE +F+V+D  A  YN AL TC+LA
Sbjct:    60 SVFWKVGLISGTVFVILGLTVLAVGFLVPPKIEAFGEADFMVVDTHAVKYNGALDTCKLA 119

Query:   119 GTALCVAAGVLLAICLFWAM 138
             G  L    G  +A CL  ++
Sbjct:   120 GAVLFCIGGTSMAGCLLMSV 139
```

Pedant information for DKFZphutel_19f19, frame 2

Report for DKFZphutel_19f19.2

```
[LENGTH]       204
[MW]           21983.07
[pI]           4.69
[HOMOL]        TREMBL:MMP2000_1 product: "P24 protein"; Mouse mRNA for P24 protein, complete
cds. 7e-19
[PROSITE]      MYRISTYL       4
```

```
[PROSITE]       CAMP_PHOSPHO_SITE      1
[PROSITE]       CK2_PHOSPHO_SITE       3
[PROSITE]       PKC_PHOSPHO_SITE       1
[PROSITE]       ASN_GLYCOSYLATION      2
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY    10.29 %

SEQ     MMPSCNRSCSCSRGPSVEDGKWYGVRSYLHLFYEDCAGTALSDDPEGPPVLCPRRPWPSL
SEG     ............................................................
PRD     cccccccccccccccccccccceeehhhhhccccccccccccccccccccccccccccce
MEM     ..........................................................MM

SEQ     CWKISLSSGTLLLLLGVAALTTGYAVPPKLEGIGEGEFLVLDQRAADYNQALGTCRLAGT
SEG     ....xxxxxxxxxxxxxxxxxxxx....................................
PRD     eeeeeccccceeeccccceeeecccccccccccccccceeeecccccccchhhhhhhhchh
MEM     MMMMMMMMMMMMMMMMMMMMMMMMMMM.........................MMMMMMM

SEQ     ALCVAAGVLLAICLFWAMIGWLSQDTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQ
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhcccccccccccccccceeeeccccccccccccccccccc
MEM     MMMMMMMMMMMMMMMMMMMMMMM.....................................

SEQ     SWFSPPASPFGQSSVQTIQPKRDS
SEG     ........................
PRD     cccccccccccccceeeeccccccc
MEM     ........................
```

Prosite for DKFZphutel_19f19.2

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	176->180	ASN_GLYCOSYLATION	PDOC00001
PS00004	201->205	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	114->117	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	146->150	CK2_PHOSPHO_SITE	PDOC00006
PS00006	157->161	CK2_PHOSPHO_SITE	PDOC00006
PS00008	38->44	MYRISTYL	PDOC00008
PS00008	92->98	MYRISTYL	PDOC00008
PS00008	119->125	MYRISTYL	PDOC00008
PS00008	127->133	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_19f19.2)

DKFZphute1_19g19
----

group: uterus derived

DKFZphute1_19g19 encodes a novel 400 amino acid protein, with strong but partial similarity to a bovine elastin-related protein expressed in fetal calf ligamentum nuchae.

The novel protein contains 2 RGD cell attachment sites.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

similarity to bovine elastin fragment

complete cDNA, complete cds, EST hits

Sequenced by AGOWA

Locus: map=54.9 cR from top of Chr3 linkage group

Insert length: 3244 bp
Poly A stretch at pos. 3227, polyadenylation signal at pos. 3216

```
   1 GTAACTGCAG TAAGTCCCGC TTGGCCCTGG AGTCCACGCG GATTTTCGAA
  51 GCTGGGGCTG GCAAGAGGCC GCTGGACACC ACGCTCCAGT CGTCAGCCCA
 101 CTTCCTAGCT GAACAGCGCG AGGCGGCGGC AGCGAGCCGG GTCCCACCAT
 151 GGCCGCGAAT TATTCCAGTA CCAGTACCCG GAGAGAACAT GTCAAAGTTA
 201 AAACCAGCTC CCAGCCAGGC TTCCTGGAAC GGCTGAGCGA GACCTCGGGT
 251 GGGATGTTTG TGGGGCTCAT GGCCTTCCTG CTCTCCTTCT ACCTAATTTT
 301 CACCAATGAG GGCCGCGCAT TGAAGACGGC AACCTCATTG GCTGAGGGGC
 351 TCTCGCTTGT GGTGTCTCCT GACAGCATCC ACAGTGTGGC TCCGGAGAAT
 401 GAAGGAAGGC TGGTGCACAT CATTGGCGCC TTACGGACAT CCAAGCTTTT
 451 GTCTGATCCA AACTATGGGG TCCATCTTCC GGCTGTGAAA CTGCGGAGGC
 501 ACGTGGAGAT GTACCAATGG GTAGAAACTG AGGAGTCCAG GGAGTACACC
 551 GAGGATGGGC AGGTGAAGAA GGAGACGAGG TATTCCTACA ACACTGAATG
 601 GAGGTCAGAA ATCATCAACA GCAAAAACTT CGACCGAGAG ATTGGCCACA
 651 ATAACCCCAG TGCCATGGCA GTGGAGTCAT TCACGGCAAC AGCCCCCTTT
 701 GTCCAAATTG GCAGGTTTTT CCTCTCGTCA GGCCTCATCG ACAAAGTCGA
 751 CAACTTCAAG TCCCTGAGCC TATCCAAGCT GGAGGACCCT CATGTGGACA
 801 TCATTCGCCG TGGAGACTTT TTCTACCACA GCGAAAATCC CAAGTATCCA
 851 GAGGTGGGAG ACTTGCGTGT CTCCTTTTCC TATGCTGGAC TGAGCGGCGA
 901 TGACCCTGAC CTGGGCCCAG CTCACGTGGT CACTGTGATT GCCCGGCAGC
 951 GGGGTGACCA GCTAGTCCCA TTCTCCACCA AGTCTGGGGA TACCTTACTG
1001 CTCCTGCACC ACGGGGACTT CTCAGCAGAG GAGGTGTTTC ATAGAGAACT
1051 AAGGAGCAAC TCCATGAAGA CCTGGGGCCT GCGGGCAGCT GGCTGGATGG
1101 CCATGTTCAT GGGCCTCAAC CTTATGACAC GGATCCTCTA CACCTTGGTG
1151 GACTGGTTTC CTGTTTTCCG AGACCTGGTC AACATTGGCC TGAAAGCCTT
1201 TGCCTTCTGT GTGGCCACCT CGCTGACCCT GCTGACCGTG GCGGCTGGCT
1251 GGCTCTTCTA CCGACCCCTG TGGGCCCTCC TCATTGCCGG CCTGGCCCTT
1301 GTGCCCATCC TTGTTGCTCG GACACGGGTG CCAGCCAAAA AGTTGGAGTG
1351 AAAAGACCCT GGCACCCGCC CGACACCTGC GTGAGCCCTA GGATCCAGGT
1401 CCTCTCTCAC CTCTGACCCA GCTCCATGCC AGAGCAGGAG CCCCGGTCAA
1451 TTTTGGACTC TGCACCCCCT CTCCTCTTCA GGGGCCAGAC TTGGCAGCAT
1501 GTGCACCAGG TTGGTGTTCA CCAGCTCATG TCTTCCCCAC ATCTCTTCTT
1551 GCCAGTAAGC AGCTTTGGTG GGCAGCAGCA GCCATGAATG GCAAGCTGAC
1601 AGCTTCTCCT GCTGTTTCCT TCCTCTCTTG GACTGAGTGG GTACGGCCAG
1651 CCACTCAGCC CATTGGCAGC TGACAACGCA GACACGCTCT ACGGAGGCCT
1701 GCTGATAAAG GGCTCAGCCT TGCCGTGTGC TGCTTCTCAT CACTGCACAC
1751 AAGTGCCATG CTTTGCCACC ACCACCAAGC ACATCTGTGA TCCTGAAGGG
1801 CGGCCGTTAG TCATTACTGC TGAGTCCTGG GTCACCAGCA GACACACTGG
1851 GCATGGACCC CTCAAAGCAG GCACACCCAA AACACAAGTC TGTGGCTAGA
1901 ACCTGATGTG GTGTTTAAAA GAGAAGAAAC ACTGAAGATG TCCTGAGGAG
1951 AAAAGCTGGA CATATACTGG GCTTCACACT TATCTTATGG CTTGGCAGAA
2001 TCTTTGTAGT GTGTGGGATC TCTGAAGGCC CTATTTAAGT TTTTCTTCGT
2051 TACTTTGCTG CTTCATGTGT ACTTTCCTAC CCCAAGAGGA AGTTTTCTGA
2101 AATAAGATTT AAAAACAAAA CAAAAAAAAC ACTTAATATT TCAGACTGTT
2151 ACAGGAAACA CCCTTTAGTC TGTCAGTTGA ATTCAGAGCA CTGAAAGGTG
2201 TTAAATTGGG GTATGTGGTT TGATTGATAA AAAGTTACCT CTCAGTATTT
2251 TGTGTCACTG AGAAGCTTTA CAATGGATGC TTTTGAAACA AGTATCAGCA
2301 AAAGGATTTG TTTTCACTCT GGGAGGAGAG GGTGGAGAAA GCACTTGCTT
2351 TCATCCTCTG GCATCGGAAA CTCCCCTATG CACTTGAAGA TGGTTTAAAA
2401 GATTAAAGAA ACGATTAAGA GAAAAGGTTG GAAGCTTTAT ACTAAATGGG
2451 CTCCTTCATG GTGACGCCCC GTCAACCACA ATCAAGAACT GAGGCCTGAG
2501 GCTGGTTGTA CAATGCCCAC GCCTGCCTGG CTGCTTTCAC CTGGGAGTGC
2551 TTTCGATGTG GGCACCTGGG CTTCCTAGGG CTGCTTCTGA GTGGTTCTTT
2601 CACGTGTTGT GTCCATAGCT TTAGTCTTCC TAAATAAGAT CCACCCACAC
```

```
2651 CTAAGTCACA GAATTTCTAA GTTCCCCAAC TACTCTCACA CCCTTTTAAA
2701 GATAAAGTAT GTTGTAACCA GGATGTCTTA AATGATTCTT TGTGTACCTT
2751 TTCTGTCATA TTCAGAAACC GTTTTGTGCC TGCTGGGAGT AATTCCTTTA
2801 GCAATTAAGT ATTTGGTAGC TGAATAAGGG GTCAGAACTT CTGAAACCAG
2851 AGATCTGTAA TCATCTCTAT TGGCCTGGGG TGCCTGTGCT ATAAATGAGT
2901 TTCTTCACAT GAAAAACACA GCCAGCCCAA GATGACTTAT CTGGGTTTAG
2951 GATTCAATAG TATTCACTAA CTGCTTATTA CATGAGCAAT TTCATCAAAT
3001 CTCCAAACTC TTAAAGGATG CTTTCGGAAA ACACGCTGTA TACCTAGATG
3051 ATGACTAAAT GCAAAATCCT TGGGCTTTGG TTTTTTTCTA GTAAGGATTT
3101 TAAATAACTG CCGACTTCAA AAGTGTTCTT AAAACGAAAG ATAATGTTAA
3151 GAAAAATTTG AAAGCTTTGG AAAACCAAAT TTGTAATATC ATTGTATTTT
3201 TTATTAAAAG TTTTGTAATA AATTTCTAAA AAAAAAAAAA AAAA
```

BLAST Results

Entry HS545355 from database EMBL:
human STS WI-14815.
Length = 436
Minus Strand HSPs:
Score = 2040 (306.1 bits), Expect = 6.2e-86, P = 6.2e-86
Identities = 420/426 (98%)

Entry HS932147 from database EMBL:
human STS WI-8531.
Length = 341
Minus Strand HSPs:
Score = 1705 (255.8 bits), Expect = 4.7e-70, P = 4.7e-70
Identities = 341/341 (100%)

Medline entries

86051793:
Bovine elastin cDNA clones: evidence for the occurrence of a new elastin-related protein in fetal calf ligamentum nuchae.

Peptide information for frame 2

ORF from 149 bp to 1348 bp; peptide length: 400
Category: similarity to known protein

```
  1 MAANYSSTST RREHVKVKTS SQPGFLERLS ETSGGMFVGL MAFLLSFYLI
 51 FTNEGRALKT ATSLAEGLSL VVSPDSIHSV APENEGRLVH IIGALRTSKL
101 LSDPNYGVHL PAVKLRRHVE MYQWVETEES REYTEDGQVK KETRYSYNTE
151 WRSEIINSKN FDREIGHNNP SAMAVESFTA TAPFVQIGRF FLSSGLIDKV
201 DNFKSLSLSK LEDPHVDIIR RGDFFYHSEN PKYPEVGDLR VSFSYAGLSG
251 DDPDLGPAHV VTVIARQRGD QLVPFSTKSG DTLLLLHHGD FSAEEVFHRE
301 LRSNSMKTWG LRAAGWMAMF MGLNLMTRIL YTLVDWFPVF RDLVNIGLKA
351 FAFCVATSLT LLTVAAGWLF YRPLWALLIA GLALVPILVA RTRVPAKKLE
```

BLASTP hits

Entry I45887 from database PIR:
elastin - bovine (fragment)
Length = 40
Score = 131 (46.1 bits), Expect = 4.9e-08, P = 4.9e-08
Identities = 31/41 (75%), Positives = 34/41 (82%)

Alert BLASTP hits for DKFZphutel_19g19, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphutel_19g19, frame 2

Report for DKFZphutel_19g19.2

[LENGTH] 400

[MW]	44831.53
[pI]	7.23
[HOMOL]	PIR:I45887 elastin - bovine (fragment) 1e-06
[PROSITE]	RGD 2
[PROSITE]	MYRISTYL 3
[PROSITE]	CAMP_PHOSPHO_SITE 1
[PROSITE]	CK2_PHOSPHO_SITE 6
[PROSITE]	TYR_PHOSPHO_SITE 2
[PROSITE]	PKC_PHOSPHO_SITE 5
[PROSITE]	ASN_GLYCOSYLATION 1
[KW]	TRANSMEMBRANE 4

```
SEQ  MAANYSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
PRD  ccceeecccceeeeeeeeeccccccceeeecccccccchhhhhhhhhhheeeeeccccchhhh
MEM  ............................MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM..

SEQ  ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPAVKLRRHVE
PRD  hhhhhccceeeeccccceeeecccccceeeeeeeeeceeeccccccccccchhhhhhhhh
MEM  ............................................................

SEQ  MYQWVETEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHNNPSAMAVESFTA
PRD  hheeehhhhheeeccccccccceeecccccccceeeeeeccccceeeccccccceeeeeeecc
MEM  ...........................................................M

SEQ  TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
PRD  ccceeeeeeeeeccccccccccccceeeeeeeccccceeeeecccceeecccccccccccee
MEM  MMMMMMMMMMMMMMMMM...........................................

SEQ  VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAEEVFHRE
PRD  eeccccccccccccccceeeeeeeeecccccccccccccceeeeeeecccccchhhhhhh
MEM  ............................................................

SEQ  LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFAFCVATSLT
PRD  hhccccccccchhhhhhhhhhhchhhhhhhhheeecccccccccccceeeeeeeeeehhhh
MEM  ........MMMMMMMMMMMMMMMMMMMMMMMMM......................MMMM

SEQ  LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE
PRD  hhhhhccceeehhhhhhhhhhhhchhhhhhhhcccccccc
MEM  MMMMMMMMMMMMMMMMMMMMMMMMMM..............
```

Prosite for DKFZphutel_19g19.2

PS00001	4->8	ASN_GLYCOSYLATION	PDOC00001
PS00004	140->144	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	9->12	PKC_PHOSPHO_SITE	PDOC00005
PS00005	10->13	PKC_PHOSPHO_SITE	PDOC00005
PS00005	97->100	PKC_PHOSPHO_SITE	PDOC00005
PS00005	276->279	PKC_PHOSPHO_SITE	PDOC00005
PS00005	305->308	PKC_PHOSPHO_SITE	PDOC00005
PS00006	10->14	CK2_PHOSPHO_SITE	PDOC00006
PS00006	63->67	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00006	249->253	CK2_PHOSPHO_SITE	PDOC00006
PS00006	292->296	CK2_PHOSPHO_SITE	PDOC00006
PS00006	332->336	CK2_PHOSPHO_SITE	PDOC00006
PS00007	220->227	TYR_PHOSPHO_SITE	PDOC00007
PS00007	99->107	TYR_PHOSPHO_SITE	PDOC00007
PS00008	35->41	MYRISTYL	PDOC00008
PS00008	93->99	MYRISTYL	PDOC00008
PS00008	310->316	MYRISTYL	PDOC00008
PS00016	221->224	RGD	PDOC00016
PS00016	268->271	RGD	PDOC00016

(No Pfam data available for DKFZphutel_19g19.2)

DKFZphutel_19g22
----

group: cell structure and motility

DKFZphutel_19g22 encodes a novel 390 amino acid protein with very strong similarity to tuftelin/enamelin.

Tuftelin/enamelin are matrix proteins of the teeth. As other proteins involved in calcification, these proteins are also expressed in the uterus matrix.

The new protein can find application in modulation of tissue-calcification, especially the uterus.

complete cDNA, complete cds start at Bp 51, EST hits in 3' UTR,
human homolog of mouse tuftelin
tuftelin is descriebed as a matrix protein of teeth but it seems also
to be pressend in the uterus matrix

Sequenced by AGOWA

Locus: unknown

Insert length: 3110 bp
Poly A stretch at pos. 3093, polyadenylation signal at pos. 3071

```
   1 GCAGACAGCG GGGTGGACAA GTGGCGTGTG TGCTGCGACC CCGAGGGAAG
  51 ATGAACGGGA CGCGGAACTG GTGTACCCTG GTGGACGTGC ACCCAGAGGA
 101 CCAGGCGGCG GGCAGCGTGG ACATTCTCAG GCTGACTCTC CAGGGTGAAC
 151 TGACAGGAGA TGAACTTGAA CACATAGCCC AGAAGGCGGG CAGGAAGACC
 201 TATGCCATGG TGTCCAGCCA CTCAGCTGGT CATTCTCTGG CTTCAGAACT
 251 GGTGGAGTCC CATGATGGAC ATGAGGAGAT CATTAAGGTG TACTTGAAGG
 301 GGAGGTCTGG AGACAAGATG ATTCACGAGA AGAATATTAA CCAGCTGAAG
 351 AGTGAGGTCC AGTACATCCA GGAGGCCAGG AACTGCCTAC AGAAGCTCCG
 401 GGAGGATATA AGTAGCAAGC TTGACAGGAA CCTAGGAGAT TCTCTCCATC
 451 GACAGGAGAT ACAGGTGGTG CTAGAAAAGC CAAATGGCTT TAGTCAGAGT
 501 CCCACAGCCC TGTACAGCAG CCCACCTGAG GTGGACACCT GTATAAATGA
 551 GGATGTTGAG AGCTTGAGGA AGACGGTGCA GGACTTGCTG GCCAAGCTTC
 601 AGGAGGCCAA GCGGCAACAC CAGTCAGACT GTGTGGCTTT TGAGGTCACA
 651 CTCAGCCGGT ACCAGAGGGA AGCAGAACAA AGTAATGTGG CCCTTCAGAG
 701 AGAGGAGGAC AGAGTGGAGC AGAAAGAGGC AGAAGTCGGA GAGCTGCAGA
 751 GGCGCTTGCT AGGGATGGAG ACGGAGCATC AGGCCTTACT GGCGAAAGTG
 801 AGGGAAGGGG AGGTGGCCCT AGAGGAACTT CGGAGCAACA ATGCTGACTG
 851 CCAAGCAGAA CGAGAAAAGG CTGCTACCCT GGAAAAGGAA GTGGCCGGGT
 901 TGCGGGAGAA GATCCACCAC TTGGATGACA TGCTCAAGAG CCAGCAGCGG
 951 AAAGTCCGGC AAATGATAGA GCAGCTCCAG AATTCAAAAG CTGTGATCCA
1001 GTCAAAGGAC GCCACCATCC AGGAGCTCAA GGAGAAAATC GCCTATCTGG
1051 AGGCAGAGAA TTTAGAGATG CATGACCGGA TGGAACACCT GATAGAAAAA
1101 CAAATCAGTC ATGGCAACTT CAGCACCCAG GCCCGGGCCA AGACAGAGAA
1151 CCCGGGCAGT ATTAGGATAT CCAAGCCGCC TAGCCCGAAG CCCATGCCTG
1201 TCATCCGAGT GGTGGAAACC TGAGCTGCCT GGAGATGGTT GCTGCCATTG
1251 CTGCTGCCTC TGCCTCGGAG AAGCCCACTG CCCCTGTTGG CTGTTAACAC
1301 TGCCTTTGAC TTCCTGACTG TCCCCTGGCT GCACCCAGGA CTTCGGGCTC
1351 CTGTGTCTCA CCATTCCCAA GCCCCTGGCC ACTCTAAGCT GGGCAGACGG
1401 AGCACGAGCA CCTATTCAAG GCACTGCAGC CCTTTGGAAG ACATTGTCCT
1451 GCAAGCAGGA GCCAGGGCAA TATCTATATT CCTACAGTGA CTATTTTTCT
1501 CTGTAGAGAG CCTCCCTTCT GTTGTAGACT GGACTCTGGC TGCGCCATAA
1551 GCCAGGCCTT CATCAGATTG GGAGAGGTGA CAAGATTTGC CTCAGCCCTA
1601 AAAGCTGGAG ACACAGATGT CCAGAGTGAT TGGAGAATGT CCTGGGGGAA
1651 TGAAGTTCCT TCCACAAACA CAGCTCAGTT CTTAGCAACA AACTGTTTGT
1701 TTTTCTACTT GCTCCATCTG CAGCCTACGC TGCCCTGGCC TCCTGCAGAC
1751 AGATAGTGGG GTTACCTGGC AAGGCCTGGT GAGAGCCAGT GAACCTAAGC
1801 TTTGACTGGG TGGCCTTGTC TTTCTGGGGA GGAGGGAATG TACATTCAGG
1851 GAGTAGCCTT TTGCGGAAAA ATTCTCTAGG GCTACAGACA GTCATGTGTG
1901 ACTTCTCTCT GCTGTGAAAA CTCCCAGAGT CTCTTTAGGG ATTTTCCCTA
1951 AGGTGTACCA CCAGGCACAC CTCAGTCTTC TTGACCCAGA GCCTGAAAAC
2001 TGTTTTCACT GGGTTCCACC AGTCCCAGCA AAATCCTCTT TGTATTTATT
2051 TTGCTAAGTT ATTGGTGGTT TTGCTTACAT CTCATGATTG ATATAATACC
2101 AAAGTTCTAT AGCCTTCTCT TGCAGTATTT GGATTTGCTT GAAACCGGGA
2151 AAACTGTTCC CATTAGGCTT GTTAATGTCA GAGTGACACT ATTATGAATC
2201 TTTCTCTCCC TTTCCTCTGC CTGTTTCTTC TCTCTTTCTC CTTCAAACTT
2251 GCTCTGCAGC TAAGGAAGGT GAGTCTACTT TCCCTGAGGC TTTGGGGTCA
2301 GAGTATATGT TGTTTGGAGA AAGAGGGCAA TCAGGACTCT TCTGGGACCC
2351 AGATGAGTTC TTCACTAGCC CTTCTGAACC CCTTGCTCCA TAATTGGTCT
2401 TTTATCCTGG CTCTGAATGA CCCTGCAGGT CATCATGGTT TTCTTTTTTT
2451 ATTGTTTTTT TTTTTTTCTG AGACAGAGTC TCACTCTGTC ACCCAGGCTG
2501 GAGTGCAGTG GCGCGATCTC AGCTCACTGC AACCTCTGCC TCCCGGATTT
2551 AAGCGATTCT TCTGCCTCAG CCTCCCGAGT AGCTGGGACT ACAGGTGTGC
```

```
2601 CACCACGCCT GGCTGATTTT TGTATTTTTA GTAGAGATGG GGTTTCACCA
2651 TACTGGCTAG GCTGGTCTCG AATTCCTGAC CTCAGGTGAT CCACCCACCT
2701 CGGCTTCCCA AAGTGCTAGG ATTATAGGCT TGAGCTACTG TGCCCGGCCC
2751 ATGGTGTTTT TCTTTAGGGC TCTTCCTACA GCCTTGAGAA GTAGATAGGC
2801 ATCAGAGTAT GGTACTATAG GAATCAGAAA AATTCAAAAC AAATGTGGAT
2851 TAAGTGTTTA GGCTCTATGT GGCTCACGCA GCCAGAATCC TTAAGTCTGT
2901 GTGTTTCTGT GTCTCAAGAC TGGGCTCACA TTCTGGCTTT GTCCATAACA
2951 ATGCTCTGGG ATTTCAGGGA GTTCCCTCAT TTGTAAAATG AGGGGGTCAG
3001 AGCAGGTGAT ATCCATGTTT CTTCCCTTTC TGATATTGTT GTCTGTGGCA
3051 TATTCTTTGT ATGGCGAATT TAATAAATTA TATTAATGTG TCTAAAAAAA
3101 AAAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

98200312:
Tuftelin--aspects of protein and gene structure

97228909:
Timing of the expression of enamel gene products during mouse tooth development.

91340750:
Sequencing of bovine enamelin ("tuftelin") a novel acidic enamel protein.

Peptide information for frame 3

ORF from 51 bp to 1220 bp; peptide length: 390
Category: strong similarity to known protein

```
  1 MNGTRNWCTL VDVHPEDQAA GSVDILRLTL QGELTGDELE HIAQKAGRKT
 51 YAMVSSHSAG HSLASELVES HDGHEEIIKV YLKGRSGDKM IHEKNINQLK
101 SEVQYIQEAR NCLQKLREDI SSKLDRNLGD SLHRQEIQVV LEKPNGFSQS
151 PTALYSSPPE VDTCINEDVE SLRKTVQDLL AKLQEAKRQH QSDCVAFEVT
201 LSRYQREAEQ SNVALQREED RVEQKEAEVG ELQRRLLGME TEHQALLAKV
251 REGEVALEEL RSNNADCQAE REKAATLEKE VAGLREKIHH LDDMLKSQQR
301 KVRQMIEQLQ NSKAVIQSKD ATIQELKEKI AYLEAENLEM HDRMEHLIEK
351 QISHGNFSTQ ARAKTENPGS IRISKPPSPK PMPVIRVVET
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_19g22, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphutel_19g22, frame 3

Report for DKFZphutel_19g22.3

[LENGTH] 390
[MW] 44264.09
[pI] 5.68
[HOMOL] TREMBL:AF047704_1 product: "tuftelin"; Mus musculus tuftelin mRNA, complete cds. 0.0
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YDL058w] 2e-11
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YDL058w] 2e-11
[FUNCAT] 1 genome replication, transcription, recombination and repair [M. jannaschii, MJ1643] 7e-11
[FUNCAT] 09.13 biogenesis of chromosome structure [S. cerevisiae, YLR086w] 1e-08
[FUNCAT] 03.22.01 cell cycle check point proteins [S. cerevisiae, YGL086w] 6e-08
[FUNCAT] 30.10 nuclear organization [S. cerevisiae, YGL086w] 6e-08
[FUNCAT] 03.13 meiosis [S. cerevisiae, YNL250w] 7e-08

[FUNCAT] 03.19 recombination and dna repair [S. cerevisiae, YNL250w] 7e-08
[FUNCAT] 11.04 dna repair (direct repair, base excision repair and nucleotide excision repair) [S. cerevisiae, YKR095w] 1e-07
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YDR285w] 2e-07
[FUNCAT] 30.13 organization of chromosome structure [S. cerevisiae, YDR285w] 2e-07
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YOR216c] 1e-05
[FUNCAT] 01.03.16 polynucleotide degradation [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 03.07 pheromone response, mating-type determination, sex-specific proteins [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 08.19 cellular import [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 06.10 assembly of protein complexes [S. cerevisiae, YNL243w] 1e-04
[FUNCAT] 08.22 cytoskeleton-dependent transport [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 4e-04
[FUNCAT] 03.25 cytokinesis [S. cerevisiae, YHR023w MYO1 - myosin-1 isoform] 4e-04
[FUNCAT] 09.10 nuclear biogenesis [S. cerevisiae, YDR356w] 4e-04
[FUNCAT] 30.05 organization of centrosome [S. cerevisiae, YMR294w] 7e-04
[EC] 3.6.1.32 Myosin ATPase 8e-09
[PIRKW] blocked amino end 1e-07
[PIRKW] nucleus 1e-06
[PIRKW] citrulline 1e-07
[PIRKW] tandem repeat 8e-09
[PIRKW] heterodimer 3e-06
[PIRKW] DNA repair 2e-06
[PIRKW] heart 8e-09
[PIRKW] endocytosis 3e-07
[PIRKW] transmembrane protein 4e-10
[PIRKW] zinc finger 3e-07
[PIRKW] metal binding 3e-07
[PIRKW] muscle contraction 8e-09
[PIRKW] acetylated amino end 1e-06
[PIRKW] actin binding 8e-09
[PIRKW] microtubule binding 1e-06
[PIRKW] cell division control 1e-06
[PIRKW] ATP 8e-09
[PIRKW] chromosomal protein 3e-06
[PIRKW] thick filament 8e-09
[PIRKW] phosphoprotein 1e-145
[PIRKW] skeletal muscle 8e-09
[PIRKW] calcium binding 1e-07
[PIRKW] meiosis 2e-06
[PIRKW] alternative splicing 7e-08
[PIRKW] DNA condensation 3e-06
[PIRKW] coiled coil 4e-10
[PIRKW] P-loop 8e-09
[PIRKW] heptad repeat 1e-07
[PIRKW] methylated amino acid 8e-09
[PIRKW] immunoglobulin receptor 2e-06
[PIRKW] peripheral membrane protein 3e-07
[PIRKW] cardiac muscle 8e-09
[PIRKW] hydrolase 8e-09
[PIRKW] muscle 7e-08
[PIRKW] EF hand 1e-07
[PIRKW] cytoskeleton 7e-08
[PIRKW] hair 1e-07
[PIRKW] smooth muscle 7e-08
[PIRKW] calmodulin binding 3e-07
[SUPFAM] conserved hypothetical P115 protein 2e-09
[SUPFAM] myosin heavy chain 8e-09
[SUPFAM] RAD50 protein 2e-06
[SUPFAM] calmodulin repeat homology 1e-07
[SUPFAM] myosin motor domain homology 8e-09
[SUPFAM] alpha-actinin actin-binding domain homology 1e-06
[SUPFAM] tropomyosin 7e-08
[SUPFAM] protein-tyrosine kinase ret 3e-07
[SUPFAM] plectin 1e-06
[SUPFAM] trichohyalin 1e-07
[SUPFAM] pleckstrin repeat homology 2e-06
[SUPFAM] ribosomal protein S10 homology 1e-06
[SUPFAM] protein kinase homology 3e-07
[SUPFAM] protein kinase C zinc-binding repeat homology 2e-06
[SUPFAM] giantin 4e-06
[SUPFAM] kinesin-related protein KLPA 1e-06
[SUPFAM] kinesin motor domain homology 1e-06
[SUPFAM] human early endosome antigen 1 3e-07
[SUPFAM] M5 protein 2e-06
[PROSITE] MYRISTYL 1
[PROSITE] AMIDATION 1
[PROSITE] CK2_PHOSPHO_SITE 6

```
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       2
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY       4.62 %
[KW]            COILED_COIL         35.13 %

SEQ    MNGTRNWCTLVDVHPEDQAAGSVDILRLTLQGELTGDELEHIAQKAGRKTYAMVSSHSAG
SEG    ............................................................
PRD    cccccceeeeeeecccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ............................................................

SEQ    HSLASELVESHDGHEEIIKVYLKGRSGDKMIHEKNINQLKSEVQYIQEARNCLQKLREDI
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ............................................................

SEQ    SSKLDRNLGDSLHRQEIQVVLEKPNGFSQSPTALYSSPPEVDTCINEDVESLRKTVQDLL
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ..........................................CCCCCCCCCCCCCCCCCC

SEQ    AKLQEAKRQHQSDCVAFEVTLSRYQREAEQSNVALQREEDRVEQKEAEVGELQRRLLGME
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  CCCCCCCCCCCC.....................CCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ    TEHQALLAKVREGEVALEELRSNNADCQAEREKAATLEKEVAGLREKIHHLDDMLKSQQR
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  CC.....................CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

SEQ    KVRQMIEQLQNSKAVIQSKDATIQELKEKIAYLEAENLEMHDRMEHLIEKQISHGNFSTQ
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS  CCCCCCCCCCC........CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC..........

SEQ    ARAKTENPGSIRISKPPSPKPMPVIRVVET
SEG    .........xxxxxxxxxxxxxxxxxx...
PRD    hhcccccccceeeecccccccccccceeeccc
COILS  ..............................
```

Prosite for DKFZphutel_19g22.3

PS00001	2->6	ASN_GLYCOSYLATION	PDOC00001
PS00001	356->360	ASN_GLYCOSYLATION	PDOC00001
PS00005	121->124	PKC_PHOSPHO_SITE	PDOC00005
PS00005	171->174	PKC_PHOSPHO_SITE	PDOC00005
PS00005	370->373	PKC_PHOSPHO_SITE	PDOC00005
PS00005	378->381	PKC_PHOSPHO_SITE	PDOC00005
PS00006	9->13	CK2_PHOSPHO_SITE	PDOC00006
PS00006	35->39	CK2_PHOSPHO_SITE	PDOC00006
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	157->161	CK2_PHOSPHO_SITE	PDOC00006
PS00006	175->179	CK2_PHOSPHO_SITE	PDOC00006
PS00006	322->326	CK2_PHOSPHO_SITE	PDOC00006
PS00008	355->361	MYRISTYL	PDOC00008
PS00009	46->50	AMIDATION	PDOC00009

(No Pfam data available for DKFZphutel_19g22.3)

DKFZphutel_19h17
----

group: intracellular transport and trafficking

DKFZphutel_19h17 encodes a novel 879 amino acid protein, with similarity to N.crassa osbP oxysterol-binding protein.

The novel protein contains a oxysterol-binding protein family signature. Mammalian oxysterol-binding protein (OSBP) is a protein binds a variety of oxysterols (oxygenated derivatives of cholesterol). OSBP seems to play a complex role in the regulation of sterol metabolism. OSBP is a cytosolic/Golgi receptor for oxysterols such as 25-hydroxycholesterol, and thus a potential target of siphingomyelin turnover and cholesterol mobilization at the plasma membrane and/or Golgi apparatus. Therefore, the new protein seems to be involved in oxysterol metabolism.

The new protein can find application in modulating the response of cells to oxysterols. The protein can be used as marker for the golgi system. The Protein might be used to direct drugs to the golgi system in response to oxidative stess.

strong similarity to C.elegans ZK1086.1 and oxysterol-binding proteins

complete cDNA, complete cds, few EST hits
similarity to proteins involved in steroid biosynthesis

Sequenced by AGOWA

Locus: unknown

Insert length: 3828 bp
Poly A stretch at pos. 3811, polyadenylation signal at pos. 3784

```
   1 GCCCGCGCGC CCGGCCGGCC CGGAGCACCG AGCTCGCGGC ACGGTAGGAG
  51 AAGCCCCCGA GCGCCCACAG CATGAAGGAG GAGGCCTTCC TCCGGCGCCG
 101 CTTCTCCCTG TGTCCACCTT CCTCCACCCC TCAGAAAGTC GACCCCCGGA
 151 AGCTCACCCG GAACTTGCTC CTCAGCGGAG ACAATGAGCT CTACCCACTC
 201 AGCCCAGGGA AGGACATGGA GCCCAACGGC CCGTCGCTGC CCAGGGATGA
 251 AGGGCCCCCG ACCCCAAGCT CTGCCACGAA GGTGCCACCG GCAGAGTACA
 301 GGCTGTGCAA CGGGTCAGAC AAGGAATGTG TGTCCCCCAC CGCCAGGGTC
 351 ACCAAGAAGG AGACTCTCAA GGCGCAGAAG GAGAACTACC GGCAGGAGAA
 401 GAAGCGCGCC ACACGGCAGC TGCTCAGCGC TCTGACAGAC CCCAGCGTGG
 451 TCATCATGGC TGACAGCCTG AAGATCCGCG GCACCCTGAA GAGCTGGACC
 501 AAGCTGTGGT GCGTGCTGAA GCCGGGGGTG CTGCTCATCT ACAAGACGCC
 551 CAAGGTGGGC CAGTGGGTGG GCACGGTGCT GCTGCACTGC TGCGAGCTCA
 601 TCGAGCGGCC CTCCAAGAAG GACGGCTTCT GCTTCAAGCT CTTCCACCCG
 651 CTGGATCAGT CCGTCTGGGC CGTGAAGGGC CCCAAAGGTG AGAGCGTGGG
 701 CTCCATCACA CAGCCCCTGC CCAGCAGCTA CCTGATCTTC AGGGCCGCCT
 751 CCGAGTCAGA TGGTCGCTGC TGGCTGGACG CCCTGGAGCT GGCCCTGCGC
 801 TGCTCTAGCC TACTGAGACT GGGCACCTGC AAGCCGGGCC GAGACGGGGA
 851 GCCAGGGACC TCGCCAGACG CATCACCCTC ATCGCTCTGT GGGCTGCCAG
 901 CCTCAGCCAC TGTCCACCCA GACCAAGACC TGTTCCCACT GAACGGGTCT
 951 TCCCTGGAGA ACGATGCATT CTCAGACAAG TCGGAGAGAG AGAACCCTGA
1001 GGAGTCAGAT ACCGAGACCC AGGACCATAG CCGGAAGACG GAGAGTGGCA
1051 GCGACCAGTC AGAGACCCCT GGGGCCCCGG TGCGGAGAGG GACCACCTAT
1101 GTGGAGCAGG TCCAGGAGGA GCTGGGGGAG CTGGGCGAGG CGTCCCAGGT
1151 GGAGACAGTG TCAGAGGAGA ACAAGAGTCT GATGTGGACC CTGCTGAAGC
1201 AGCTACGGCC AGGCATGGAC CTGTCCCGCG TGGTGCTACC CACGTTCGTA
1251 CTGGAGCCGC GCTCCTTCCT GAACAAGCTC TCCGACTACT ACTACCACGC
1301 AGACCTGCTC TCCAGGGCTG CGGTGGAGGA GGATGCCTAC AGCCGCATGA
1351 AGCTGGTGCT GCGGTGGTAC CTGTCTGGCT TCTACAAGAA GCCCAAGGGA
1401 ATCAAGAAGC CGTACAACCC CATCCTGGGG GAGACCTTCC GCTGCTGCTG
1451 GTTCCACCCG CAGACTGACA GCCGCACATT CTACATAGCA GAGCAGGTGT
1501 CCCACCACCC GCCCGTGTCT GCCTTCCACG TCAGCAACCG GAAGGACGGC
1551 TTCTGCATCA GTGGCAGCAT CACAGCCAAG TCCAGGTTTT ATGGGAACTC
1601 GCTGTCGGCG CTGCTGGACG GCAAAGCCAC GCTCACCTTC CTGAACCGAG
1651 CCGAGGATTA CACCCTTACC ATGCCCTACG CCCACTGCAA AGGAATCCTG
1701 TATGGCACGA TGACCCTGGA GCTGGGTGGG AAGGTCACCA TCGAGTGTGC
1751 GAAGAACAAC TTCCAGGCCC AGCTGGAATT CAAACTCAAG CCCTTCTTCG
1801 GGGGTAGCAC CAGCATCAAC CAGATCTCGG GAAAGATCAC GTCGGGAGAG
1851 GAAGTCCTGG CGAGCCTCAG TGGCCACTGG GACAGGGACG TGTTTATCAA
1901 GGAGGAAGGG AGCGGAAGCA GTGCGCTTTT CTGGACCCCG AGCGGGGAGG
1951 TCCGCAGACA GAGGCTGAGG CAGCACACGG TGCCGCTGGA GGAGCAGACG
2001 GAGCTGGAGT CCGAGAGGCT CTGGCAGCAC GTCACCAGGG CCATCAGCAA
2051 GGGCGACCAG CACAGGGCCA CACAGGAGAA GTTTGCACTG GAGGAGGCAC
2101 AGCGGCAGCG GGCCCGTGAG CGGCAGGAGA GCCTCATGCC CTGGAAGCCG
2151 CAGCTGTTCC ACCTGGACCC CATCACCCAG GAGTGGCACT ACCGATACGA
2201 GGACCACAGC CCCTGGGACC CCCTGAAGGA CATCGCCCAG TTTGAGCAAG
2251 ACGGGATCCT GCGGACCTTG CAGCAGGAGG CCGTGGCCCG CCAGACCACC
```

```
2301 TTCCTGGGCA GCCCAGGGCC CAGGCACGAG AGGTCTGGCC CAGACCAGCG
2351 GCTTCGCAAG GCCAGCGACC AGCCCTCCGG CCACAGCCAG GCCACGGAGA
2401 GCAGCGGATC CACGCCTGAG TCCTGCCCAG AGCTCTCAGA CGAGGAGCAG
2451 GATGGTGACT TTGTCCCTGG CGGTGAGAGC CCATGCCCTC GGTGCAGGAA
2501 GGAGGCGCGG CGGCTGCAGG CCCTGCACGA GGCCATCCTC TCCATCCGAG
2551 AGGCCCAGCA GGAGCTGCAC AGGCACCTCT CGGCCATGCT GAGCTCCACG
2601 GCACGGGCAG CACAGGCACC GACCCCAGGC CTCCTGCAGA GCCCCCGATC
2651 CTGGTTCCTG CTCTGCGTGT TCCTGGCGTG TCAGCTGTTC ATTAACCACA
2701 TCCTCAAATA GGAGCCCTGG GGGCAGAGCT CCTGGCCAGT CCCGAGCCCT
2751 CCCTCCCAGG CACCCAGCAC TTTAAGCCTG CTCCATGGAG GCAGAGAGGC
2801 CCGGCAAGCA CAGCCACTGT GACGGGGAGT CCAGGCGCAG GAGGGACCCG
2851 GGGCCACAAG GCGCTGCGGG CCCAGGTGTG CTGGGCCCCT CTCAGGGGCA
2901 CTGGCCTCTC TGCAGGGCCT TCCGCCCAGC GCTGGCCTTA ATGCTAAAGC
2951 CAAATGCAGC TTCTGCTGTG CGACGCACTC CTGGCCATCT TGCCGTGTCA
3001 CCCCCTGTCC GGCCTCCACT TGCCATGGGG GATGGATGGA TTTAGGGTGG
3051 GAGGGCCTGT GGGGGCCCTG GACAGTCACA CCCCAGCAGC AGTGAGTGGG
3101 CAGGTTTGGA GGAGCAGCCA GGGAGCCCCG AGTGGCCCAG GAGTCCCCCC
3151 ACACACAGAT GCATAGGCCT GCCTTCCGGA GACCCTGTCC ACATTGCCGG
3201 GACCACCCTG GTGGGGCCAC TGGTGGGTGC CAGGGACAGG TTAGGGCCAC
3251 TCTGGGGAAG GCATTTTGGT TTTTTATTCC ACGCTCTGCT GTTTGGATGG
3301 GAGCCCCACA GAGGCAGGTC CTGGAACCAC CCCACCCCCA CACCTGGACG
3351 CTCGCTCTGG TGGGGGCACA CGCAGGTGGA GGTGGTTGTG GGTGCAGGTG
3401 TGTGCAGGGG TGTGGGGGGC GCAGGGGTGT GGCTTAGCTG GCCCCGCACC
3451 CAGGCCGGGG AGGCTCAAGT TCGCCACTTT ACTCAGACCG ATGCACAGTC
3501 TTCCCATTTT ACACTTTTTT AATAAACATA ATTGCAATAT TTTAGGTGGG
3551 CTGCGAGCTG CAGTCAGCCT TCACGTCTGG CCTCAGTCCC CGTGTCAGTG
3601 CCGCTCTGCG TGTGCGTGTG CGCGTGTGTG AGCCTCTACA CATATATATA
3651 TGTACAGAGC CTTAAACCAC ATCGTGGCGG TGCCGTCTGA GCTGTAGCGG
3701 GTGGCTTTGT TTCCAGTTTT TGTACCCGTG TCCTTGTCTC CCCTCCTCCC
3751 CCATCTGGGG ATGTGTCTGT GTTCCACACC TTGAAATAAA CAGACACATA
3801 CGTGTTCTCT TAAAAAAAAA AAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

98315477:
The pleckstrin homology domain of oxysterol-binding protein recognises a determinant specific to Golgi membranes.

98146266:
A Drosophila homologue of oxysterol binding protein (OSBP)--implications for the role of OSBP.

98146266:
A Drosophila homologue of oxysterol binding protein (OSBP)--implications for the role of OSBP.

Peptide information for frame 3

ORF from 72 bp to 2708 bp; peptide length: 879
Category: strong similarity to known protein

```
  1 MKEEAFLRRR FSLCPPSSTP QKVDPRKLTR NLLLSGDNEL YPLSPGKDME
 51 PNGPSLPRDE GPPTPSSATK VPPAEYRLCN GSDKECVSPT ARVTKKETLK
101 AQKENYRQEK KRATRQLLSA LTDPSVVIMA DSLKIRGTLK SWTKLWCVLK
151 PGVLLIYKTP KVGQWVGTVL LHCCELIERP SKKDGFCFKL FHPLDQSVWA
201 VKGPKGESVG SITQPLPSSY LIFRAASESD GRCWLDALEL ALRCSSLLRL
251 GTCKPGRDGE PGTSPDASPS SLCGLPASAT VHPDQDLFPL NGSSLENDAF
301 SDKSERENPE ESDTETQDHS RKTESGSDQS ETPGAPVRRG TTYVEQVQEE
351 LGELGEASQV ETVSEENKSL MWTLLKQLRP GMDLSRVVLP TFVLEPRSFL
401 NKLSDYYYHA DLLSRAAVEE DAYSRMKLVL RWYLSGFYKK PKGIKKPYNP
451 ILGETFRCCW FHPQTDSRTF YIAEQVSHHP PVSAFHVSNR KDGFCISGSI
501 TAKSRFYGNS LSALLDGKAT LTFLNRAEDY TLTMPYAHCK GILYGTMTLE
551 LGGKVTIECA KNNFQAQLEF KLKPFFGGST SINQISGKIT SGEEVLASLS
601 GHWDRDVFIK EEGSGSSALF WTPSGEVRRQ RLRQHTVPLE EQTELESERL
```

```
651 WQHVTRAISK GDQHRATQEK FALEEAQRQR ARERQESLMP WKPQLFHLDP
701 ITQEWHYRYE DHSPWDPLKD IAQFEQDGIL RTLQQEAVAR QTTFLGSPGP
751 RHERSGPDQR LRKASDQPSG HSQATESSGS TPESCPELSD EEQDGDFVPG
801 GESPCPRCRK EARRLQALHE AILSIREAQQ ELHRHLSAML SSTARAAQAP
851 TPGLLQSPRS WFLLCVFLAC QLFINHILK
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphute1_19h17, frame 3

TREMBL:CEZK1086_2 gene: "ZK1086.1"; Caenorhabditis elegans cosmid ZK1086, N = 1, Score = 1495, P = 2.7e-153

PIR:S25324 hypothetical protein YKR003w - yeast (Saccharomyces cerevisiae), N = 2, Score = 574, P = 8.5e-57

TREMBL:CEAF195_7 gene: "C32F10.1"; Caenorhabditis elegans cosmid C32F10., N = 1, Score = 588, P = 8.6e-57

PIR:S46796 hypothetical protein YKR003w homolog YHR001w - yeast (Saccharomyces cerevisiae), N = 1, Score = 585, P = 1.9e-56

TREMBL:NCOSBP_1 gene: "osbP"; product: "oxysterol-binding protein"; N.crassa mRNA for putative oxysterol-binding protein, N = 1, Score = 571, P = 7e-55

TREMBL:AB017026_1 product: "oxysterol-binding protein"; Mus musculus mRNA for oxysterol-binding protein, complete cds., N = 2, Score = 328, P = 3e-35

```
>TREMBL:CEZK1086_2 gene: "ZK1086.1"; Caenorhabditis elegans cosmid ZK1086
          Length = 751

  HSPs:

 Score = 1495 (224.3 bits), Expect = 2.7e-153, P = 2.7e-153
 Identities = 327/663 (49%), Positives = 430/663 (64%)

Query:   129 MADSLKIRGTLKSWTKLWCVLKPGVLLIYKTPKV--GQWVGTVLLHCCELIERPSKKDGF 186
             MAD+LKIRG LK W + +CVLKPG+L++YK  K   G WVGTVLL+ CELIERPSKKDGF
Sbjct:     1 MADTLKIRGALKRWNRYYCVLKPGLLILYKHKKADRGDWVGTVLLNHCELIERPSKKDGF 60

Query:   187 CFKLFHPLDQSVWAVKGPKGESVGSIT-QPLPSSYLIFRAASESDGRCWLDALELALRCS 245
             CFKLFHP+D S+W  +GP G+S GS T  PL +S+LI RA S+  GRCW+DALEL+ +C+
Sbjct:    61 CFKLFHPMDMSIWGNRGPLGQSFGSFTLNPLNTSFLICRAPSDQAGRCWMDALELSFKCT 120

Query:   246 SLLRLGTCKPGRDGEPGTSPDASPSSLCGLPASATVHPDQDLFPLNGSSLENDAFSDK-S 304
              LL+  T     D + G   D+S +   G    + +  D D     G      A S+  +
Sbjct:   121 GLLKK-TMNE-LDDKNG---DSSMND--GQRDESRMSRDSD-----GDDTRELAVSETDA 168

Query:   305 ERENPEESDTETQDHSRKTESGSDQSETPGAPVRRGTT---YVEQVQEELGELGEASQVE 361
             E+   E  D + +DH    E G   SET    +R   T   ++   +E  G  G  S  E
Sbjct:   169 EKHFQEIDDVQDEDH----EDGK-MSETSDT-IREAFTESAWIPSPKEVFGPDG--SLTE 220

Query:   362 TVSEENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYHADLLSRAAVEED 421
              V EENKSL+WTLLKQ+RPGMDLS+VVLPTF+LEPRSFL KL+DYYYHADL+S A  E D
Sbjct:   221 EVGEENKSLIWTLLKQIRPGMDLSKVVLPTFILEPRSFLEKLADYYYHADLISEAVAEPD 280

Query:   422 AYSRMKLVLRWYLSGFYKKPKGIKKPYNPILGETFRCCWFHPQTDSRTFYIAEQVSHHPP 481
              + R+  V +++LSGFYKKPKG+KKPYNPILGETFRC W HP   S TFY+AEQVSHHPP
Sbjct:   281 PFQRIVKVTKFFLSGFYKKPKGLKKPYNPILGETFRCKWEHPD-GSTTFYMAEQVSHHPP 339

Query:   482 VSAFHVSNRKDGFCISGSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCKG 541
             VS+  ++NRK GF ISG+I AKS++YGNSLSA+L GK  LT LN  E Y + +PYA+CKG
Sbjct:   340 VSSLFITNRKAGFNISGTILAKSKYYGNSLSAILAGKLRLTLLNLGETYIVNLPYANCKG 399

Query:   542 ILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQISGKITSGEEVLASLSG 601
             I+ GTMT+ELGG+V IEC K  ++  L+FKLKP  GG+   NQI G I  G + LAS+ G
Sbjct:   400 IMIGTMTMELGGEVNIECEKTGYRTTLDFKLKPMLGGA--YNQIEGSIKYGSDRLASIEG 457

Query:   602 HWDRDVFIKEEGSGSSALFWTPSGEVRRQRLRQHTVPLEEQTELESERLWQHVTRAISKG 661
              WD  + IK  G       W P+ EV + RL ++ + ++EQ E ES +LW+HVT AIS
Sbjct:   458 AWDGVIRIK--GPDGKKELWNPTPEVIKTRLPRYEINMDEQGEWESAKLWRHVTEAISNE 515

Query:   662 DQHRATQEKFALEEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDPLKDI 721
             DQ++AT+EK ALE  QR RA+    S +P + + F       ++ Y + D+ PWD   DI
Sbjct:   516 DQYKATEEKTALENDQRARAK----SGIPHETKFFKKQH-GDDYVYIHADYRPWDNNNDI 570
```

```
Query:  722 AQFEQDGILRTLQQEAVAR--QTTFLGSPGPRHERSGPDQRLRKASDQPSGHSQATESSG 779
            Q E + +++T+ + +  +   + LGS     E S  D+ +     +P    +    +
Sbjct:  571 QQIENNYVVKTISRHSKRKTGNSEQLGSDNTS-EASESDEEVI----EPKIKKKEIVPAK 625

Query:  780 STPESCPELSDE 791
            S P + PE++DE
Sbjct:  626 SKPIT-PEVADE 636
```

Pedant information for DKFZphutel_19h17, frame 3

Report for DKFZphutel_19h17.3

```
[LENGTH]      879
[MW]          98616.79
[pI]          7.29
[HOMOL]       TREMBL:CEZK1086_2 gene: "ZK1086.1"; Caenorhabditis elegans cosmid ZK1086 1e-157

[FUNCAT]      01.06.16 lipid and fatty-acid binding       [S. cerevisiae, YHR001w] 3e-55
[FUNCAT]      01.06.01 lipid, fatty-acid and sterol biosynthesis   [S. cerevisiae, YHR001w]
3e-55
[FUNCAT]      30.03 organization of cytoplasm      [S. cerevisiae, YPL145c] 3e-23
[FUNCAT]      08.07 vesicular transport (golgi network, etc.)     [S. cerevisiae, YPL145c]
3e-23
[FUNCAT]      04.05.01.07 chromatin modification    [S. cerevisiae, YAR044w] 5e-20
[BLOCKS]      BL00168F
[BLOCKS]      BL01013D Oxysterol-binding protein family proteins
[BLOCKS]      BL01013C Oxysterol-binding protein family proteins
[BLOCKS]      BL01013B Oxysterol-binding protein family proteins
[BLOCKS]      BL01013A Oxysterol-binding protein family proteins
[PIRKW]       transmembrane protein 1e-19
[SUPFAM]      pleckstrin repeat homology 8e-18
[SUPFAM]      ankyrin repeat homology 1e-19
[SUPFAM]      unassigned ankyrin repeat proteins 1e-19
[PROSITE]     MYRISTYL      12
[PROSITE]     CAMP_PHOSPHO_SITE      6
[PROSITE]     OSBP   1
[PROSITE]     CK2_PHOSPHO_SITE      21
[PROSITE]     PROKAR_LIPOPROTEIN     1
[PROSITE]     TYR_PHOSPHO_SITE       2
[PROSITE]     PKC_PHOSPHO_SITE      20
[PROSITE]     ASN_GLYCOSYLATION      3
[PFAM]        PH (pleckstrin  homology) domain
[KW]          TRANSMEMBRANE  1
[KW]          LOW_COMPLEXITY     2.96 %
[KW]          COILED_COIL        3.53 %

SEQ    MKEEAFLRRRFSLCPPSSTPQKVDPRKLTRNLLLSGDNELYPLSPGKDMEPNGPSLPRDE
SEG    ............................................................
PRD    ccchhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccccc
COILS  ............................................................
MEM    ............................................................

SEQ    GPPTPSSATKVPPAEYRLCNGSDKECVSPTARVTKKETLKAQKENYRQEKKRATRQLLSA
SEG    ............................................................
PRD    cccccccccccccceeeeccccccceeeecccccchhhhhhhhhhhhhhhhhhhhhhhhh
COILS  ...............................ccccccccccccccccccccccccccccc
MEM    ............................................................

SEQ    LTDPSVVIMADSLKIRGTLKSWTKLWCVLKPGVLLIYKTPKVGQWVGTVLLHCCELIERP
SEG    ............................................................
PRD    hccccceeeeccccccccccccccceeeeeeecccceeeeecccccccceeeeecccccccccc
COILS  ccc.........................................................
MEM    ............................................................

SEQ    SKKDGFCFKLFHPLDQSVWAVKGPKGESVGSITQPLPSSYLIFRAASESDGRCWLDALEL
SEG    ............................................................
PRD    cccccceeeeccccccceeeeeccccccceeecccccccccceeeeeeehhhhhhhhhhhhh
COILS  ............................................................
MEM    ............................................................

SEQ    ALRCSSLLRLGTCKPGRDGEPGTSPDASPSSLCGLPASATVHPDQDLFPLNGSSLENDAF
SEG    ............................................................
PRD    hhhhhhhhhhhhcccccccccccccccccccccccccccccccccccccccccccccccc
COILS  ............................................................
MEM    ............................................................

SEQ    SDKSERENPEESDTETQDHSRKTESGSDQSETPGAPVRRGTTYVEQVQEELGELGEASQV
```

```
SEG      ...........................................xxxxxxxxxxxxx....
PRD      cccccccccccccccccccccccccccccccccccccccccccchhhhhhhhhccccccc
COILS    ............................................................
MEM      ............................................................

SEQ      ETVSEENKSLMWTLLKQLRPGMDLSRVVLPTFVLEPRSFLNKLSDYYYHADLLSRAAVEE
SEG      ............................................................
PRD      ccccccchhhhhhhhhhcccccceeeeccceeeeccccchhhhhhhhhcccccccccccc
COILS    ............................................................
MEM      ............................................................

SEQ      DAYSRMKLVLRWYLSGFYKKPKGIKKPYNPILGETFRCCWFHPQTDSRTFYIAEQVSHHP
SEG      ............................................................
PRD      chhhhhhhhhhhhhhcccccccccccccccccceeeeeeecccccccceeeeeecccccc
COILS    ............................................................
MEM      ............................................................

SEQ      PVSAFHVSNRKDGFCISGSITAKSRFYGNSLSALLDGKATLTFLNRAEDYTLTMPYAHCK
SEG      ............................................................
PRD      cceeeeecccccccccccccccccccccccccccccceeeeeeccccceeeecccccceee
COILS    ............................................................
MEM      ............................................................

SEQ      GILYGTMTLELGGKVTIECAKNNFQAQLEFKLKPFFGGSTSINQISGKITSGEEVLASLS
SEG      ............................................................
PRD      eeeecccccccccceeeeecccccccceeeecccccccccccccceeeeeecccccceeeeec
COILS    ............................................................
MEM      ............................................................

SEQ      GHWDRDVFIKEEGSGSSALFWTPSGEVRRQRLRQHTVPLEEQTELESERLWQHVTRAISK
SEG      ............................................................
PRD      cccccceeeeecccccceeeeeccccccccccccccccccccchhhhhhhhhhhhhhhhhhh
COILS    ............................................................
MEM      ............................................................

SEQ      GDQHRATQEKFALEEAQRQRARERQESLMPWKPQLFHLDPITQEWHYRYEDHSPWDPLKD
SEG      .............xxxxxxxxxxxxx..................................
PRD      cchhhhhhhhhhhhhhhhhhhhhhhhhhhccccccccccccccccccceeeecccccccchh
COILS    ............................................................
MEM      ............................................................

SEQ      IAQFEQDGILRTLQQEAVARQTTFLGSPGPRHERSGPDQRLRKASDQPSGHSQATESSGS
SEG      ............................................................
PRD      hhhhhhhhhhhhhhhhhhhhhhhhcccccccccccccchhhhhccccccccccccccccccc
COILS    ............................................................
MEM      ............................................................

SEQ      TPESCPELSDEEQDGDFVPGGESPCPRCRKEARRLQALHEAILSIREAQQELHRHLSAML
SEG      ............................................................
PRD      ccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhh
COILS    ............................................................
MEM      ............................................................

SEQ      SSTARAAQAPTPGLLQSPRSWFLLCVFLACQLFINHILK
SEG      .......................................
PRD      hhhhhhcccccccccccccceeeeehhhhhhhhhhhhccc
COILS    .......................................
MEM      .....................MMMMMMMMMMMMMMMMM.
```

Prosite for DKFZphutel_19h17.3

PS00001	80->84	ASN_GLYCOSYLATION	PDOC00001
PS00001	291->295	ASN_GLYCOSYLATION	PDOC00001
PS00001	367->371	ASN_GLYCOSYLATION	PDOC00001
PS00004	9->13	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	26->30	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	95->99	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	111->115	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	338->342	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	762->766	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	90->93	PKC_PHOSPHO_SITE	PDOC00005
PS00005	94->97	PKC_PHOSPHO_SITE	PDOC00005
PS00005	98->101	PKC_PHOSPHO_SITE	PDOC00005
PS00005	132->135	PKC_PHOSPHO_SITE	PDOC00005
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00005	159->162	PKC_PHOSPHO_SITE	PDOC00005
PS00005	181->184	PKC_PHOSPHO_SITE	PDOC00005
PS00005	252->255	PKC_PHOSPHO_SITE	PDOC00005

PS00005	301->304	PKC_PHOSPHO_SITE	PDOC00005
PS00005	304->307	PKC_PHOSPHO_SITE	PDOC00005
PS00005	320->323	PKC_PHOSPHO_SITE	PDOC00005
PS00005	455->458	PKC_PHOSPHO_SITE	PDOC00005
PS00005	488->491	PKC_PHOSPHO_SITE	PDOC00005
PS00005	501->504	PKC_PHOSPHO_SITE	PDOC00005
PS00005	586->589	PKC_PHOSPHO_SITE	PDOC00005
PS00005	647->650	PKC_PHOSPHO_SITE	PDOC00005
PS00005	824->827	PKC_PHOSPHO_SITE	PDOC00005
PS00005	843->846	PKC_PHOSPHO_SITE	PDOC00005
PS00005	857->860	PKC_PHOSPHO_SITE	PDOC00005
PS00006	82->86	CK2_PHOSPHO_SITE	PDOC00006
PS00006	94->98	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	227->231	CK2_PHOSPHO_SITE	PDOC00006
PS00006	263->267	CK2_PHOSPHO_SITE	PDOC00006
PS00006	293->297	CK2_PHOSPHO_SITE	PDOC00006
PS00006	304->308	CK2_PHOSPHO_SITE	PDOC00006
PS00006	312->316	CK2_PHOSPHO_SITE	PDOC00006
PS00006	325->329	CK2_PHOSPHO_SITE	PDOC00006
PS00006	342->346	CK2_PHOSPHO_SITE	PDOC00006
PS00006	358->362	CK2_PHOSPHO_SITE	PDOC00006
PS00006	362->366	CK2_PHOSPHO_SITE	PDOC00006
PS00006	590->594	CK2_PHOSPHO_SITE	PDOC00006
PS00006	643->647	CK2_PHOSPHO_SITE	PDOC00006
PS00006	659->663	CK2_PHOSPHO_SITE	PDOC00006
PS00006	713->717	CK2_PHOSPHO_SITE	PDOC00006
PS00006	755->759	CK2_PHOSPHO_SITE	PDOC00006
PS00006	780->784	CK2_PHOSPHO_SITE	PDOC00006
PS00006	784->788	CK2_PHOSPHO_SITE	PDOC00006
PS00006	789->793	CK2_PHOSPHO_SITE	PDOC00006
PS00006	824->828	CK2_PHOSPHO_SITE	PDOC00006
PS00007	402->409	TYR_PHOSPHO_SITE	PDOC00007
PS00007	415->424	TYR_PHOSPHO_SITE	PDOC00007
PS00008	137->143	MYRISTYL	PDOC00008
PS00008	163->169	MYRISTYL	PDOC00008
PS00008	274->280	MYRISTYL	PDOC00008
PS00008	326->332	MYRISTYL	PDOC00008
PS00008	381->387	MYRISTYL	PDOC00008
PS00008	498->504	MYRISTYL	PDOC00008
PS00008	508->514	MYRISTYL	PDOC00008
PS00008	541->547	MYRISTYL	PDOC00008
PS00008	552->558	MYRISTYL	PDOC00008
PS00008	577->583	MYRISTYL	PDOC00008
PS00008	613->619	MYRISTYL	PDOC00008
PS00008	728->734	MYRISTYL	PDOC00008
PS00013	860->871	PROKAR_LIPOPROTEIN	PDOC00013
PS01013	474->485	OSBP	PDOC00774

Pfam for DKFZphutel_19h17.3

```
HMM_NAME       PH (pleckstrin  homology) domain

HMM                *dvIREGWMyKWgswrkstgnWqrRWFvLrndpnrLiYYkddkdekPrYM
                    +VI+  +++++G  +      W + W+VL++   ++L+ YK + +   + ++
Query          126  VVIMADSLKIRGTLKS----WTKLWCVLKP--GVLLIYKTP-KVGQWVG   167

HMM                lIdldcWrMidVEidWmmdndHCFiIWtrq....................
                      L+C+  +I+ ++ ++     +CF+++ +
Query          168 TVLLHCCELIERPSKKD---GFCFKLFHPLDQSVWAVKGPKGESVGSITQ   214

HMM                ....rtYYFQAeNeEEMmeWMsaIrRaIw*
                       + ++F+A++E++ + W++A++ A++
Query          215 PLPSSYLIFRAASESDGRCWLDALELALR    243
```

DKFZphutel_19j11
----

group: uterus derived

DKFZphutel_19j11 encodes a novel 708 amino acid protein with C-terminal similarity to several known proteins, such as human KIAA0231 or murine ras binding protein Sur8.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

Strong similarity to KIAA0231, similarity to ras binding protein Sur8

EST AA854189 extendes the sequence (294 Bp), with this sequence complete cDNA,

Sequenced by AGOWA

Locus: unknown

Insert length: 2343 bp
Poly A stretch at pos. 2323, polyadenylation signal at pos. 2295

```
   1 GCTCCTGCTA ACCCCATCAC TGTGGAAATG AAAGGCCTGA AGACAGATTT
  51 GGACCTTCAG CAGTACAGCT TTATAAATCA GATGTGTTAT GAGCGAGCCC
 101 TCCACTGGTA TGCCAAGTAT TTCCCTTACC TTGTCCTCAT CCATACCCTG
 151 GTCTTTATGC TCTGCAGTAA CTTTTGGTTC AAATTCCCTG GTTCCAGCTC
 201 CAAAATAGAA CATTTCATCT CCATTCTGGG GAAGTGTTTT GACTCTCCTT
 251 GGACCACACG GGCTTTATCT GAAGTGTCTG GGGAGGACTC AGAAGAAAAG
 301 GACAACAGGA AGAACAACAT GAACAGGTCC AACACCATCC AATCTGGTCC
 351 AGAAGGCAGC CTGGTCAACT CTCAGTCTTT AAAGTCCATT CCTGAGAAGT
 401 TTGTAGTTGA TAAATCCACT GCAGGGGCTC TGGATAAAAA GGAAGGTGAG
 451 CAGGCTAAGG CCTTATTTGA GAAGGTGAAG AAGTTCAGGC TGCATGTGGA
 501 AGAAGGTGAT ATTCTATATG CCATGTATGT TCGCCAGACT GTACTTAAAG
 551 TTATCAAATT CCTAATCATC ATTGCATATA ATAGTGCTCT GGTTTCCAAG
 601 GTCCAGTTTA CAGTGGACTG TAATGTGGAC ATTCAGGACA TGACTGGATA
 651 TAAAAACTTT TCTTGCAATC ATACCATGGC ACACTTGTTC TCAAAACTGT
 701 CCTTTTGCTA TCTGTGCTTT GTTAGTATCT ATGGATTGAC GTGCCTTTAT
 751 ACCTTATACT GGCTGTTCTA CCGTTCTCTA CGGGAATATT CCTTTGAGTA
 801 TGTCCGTCAG GAGACTGGAA TTGATGATAT TCCAGATGTG AAAAATGACT
 851 TTGCTTTTAT GCTTCATATG ATAGATCAGT ATGACCCTCT CTATTCCAAG
 901 AGATTTGCAG TGTTCCTGTC TGAAGTCAGT GAAAACAAAT TAAAGCAGCT
 951 GAACTTAAAT AACGAATGGA CTCCTGATAA ACTGAGGCAG AAGCTACAGA
1001 CAAATGCCCA TAATCGACTG GAATTGCCTC TTATCATGCT CTCTGGCCTT
1051 CCAGACACTG TTTTTGAAAT CACAGAGTTG CAATCTCTAA AACTTGAAAT
1101 CATTAAGAAC GTAATGATAC CAGCCACCAT TGCACAGCTA GACAATCTTC
1151 AAGAGCTCTC TCTGCACCAG TGTTCTGTCA AAATCCACAG TGCGGCGCTC
1201 TCTTTCCTGA AGGAAAACCT CAAGGTCTTG AGCGTCAAGT TTGATGACAT
1251 GAGGGAACTC CCCCCCTGGA TGTATGGGCT CCGAAATCTG GAAGAGCTGT
1301 ACCTAGTTGG CTCTCTAAGT CATGATATTT CCAGAAATGT CACCCTTGAG
1351 TCTCTGCGGG ATCTCAAAAG CCTTAAAATT CTCTCTATCA AAAGCAACGT
1401 TTCCAAAATC CCTCAGGCAG TGGTTGATGT TTCCAGCCAT CTCCAGAAGA
1451 TGTGCATACA TAATGATGGC ACCAAGCTGG TGATGCTCAA CAACTTAAAG
1501 AAGATGACCA ATCTGACAGA GCTGGAGCTG GTCCACTGTG ACCTGGAGCG
1551 TATTCCTCAT GCTGTGTTCA GCCTACTCAG CCTCCAGGAA TTGGACCTGA
1601 AGGAAAACAA TCTGAAATCT ATAGAAGAAA TCGTTAGCTT TCAGCACTTA
1651 AGAAAGTTGA CAGTGCTAAA ACTGTGGCAT AACAGCATCA CCTACATCCC
1701 AGAGCATATA AAGAAACTCA CCAGCCTGGA ACGCCTGTCC TTTAGTCACA
1751 ATAAAATAGA GGTGCTGCCT TCCCACCTCT TCCTATGCAA CAAGATCCGA
1801 TACTTGGACT TATCGTACAA TGACATTCGA TTTATCCCCC CTGAAATTGG
1851 AGTTCTACAA AGTTTACAGT ATTTTTCCAT CACATGTAAC AAAGTGGAAA
1901 GCCTTCCAGA TGAACTCTAC TTCTGCAAGA AACTTAAAAC TCTGAAGATT
1951 GGAAAAAACA GCCTATCTGT ACTTTCACCG AAAATTGGAA ATTTGCTATT
2001 TCTTTCCTAC TTAGATGTAA AAGGTAATCA CTTTGAAATC CTCCCTCCTG
2051 AACTGGGTGA CTGTCGGGCT CTGAAGCGAG CTGGTTTAGT TGTAGAAGAT
2101 GCTCTGTTTG AAACTCTGCC TTCTGACGTC CGGGAGCAAA TGAAAACAGA
2151 ATAACTTATT TTTCGTTAAA GTTTGACTGA AACACGCTTC TACCAAATAC
2201 AGTATAAATA ATTAGGTAGT CTTAATGCCT TTCCTATTTT TTTTTCCTTT
2251 TCACACAAAA TGTACACAAA GATCGCGTAA GGAGTATGTA TTTTTAATAA
2301 AAATTTAATT GTATTTTTTC AATATTAAAA AAAAAAAAAA AAA
```

BLAST Results

No BLAST result

Medline entries

96421675:
Characterization of densin-180, a new brain-specific synaptic protein of the
O-sialoglycoprotein family.

98337190:
SUR-8, a conserved Ras-binding protein with leucine-rich repeats, positively regulates Ras-mediated signaling in C. elegans.

Peptide information for frame 1

ORF from 28 bp to 2151 bp; peptide length: 708
Category: similarity to known protein
Classification: Cell signaling/communication

```
  1 MKGLKTDLDL QQYSFINQMC YERALHWYAK YFPYLVLIHT LVFMLCSNFW
 51 FKFPGSSSKI EHFISILGKC FDSPWTTRAL SEVSGEDSEE KDNRKNNMNR
101 SNTIQSGPEG SLVNSQSLKS IPEKFVVDKS TAGALDKKEG EQAKALFEKV
151 KKFRLHVEEG DILYAMYVRQ TVLKVIKFLI IIAYNSALVS KVQFTVDCNV
201 DIQDMTGYKN FSCNHTMAHL FSKLSFCYLC FVSIYGLTCL YTLYWLFYRS
251 LREYSFEYVR QETGIDDIPD VKNDFAFMLH MIDQYDPLYS KRFAVFLSEV
301 SENKLKQLNL NNEWTPDKLR QKLQTNAHNR LELPLIMLSG LPDTVFEITE
351 LQSLKLEIIK NVMIPATIAQ LDNLQELSLH QCSVKIHSAA LSFLKENLKV
401 LSVKFDDMRE LPPWMYGLRN LEELYLVGSL SHDISRNVTL ESLRDLKSLK
451 ILSIKSNVSK IPQAVVDVSS HLQKMCIHND GTKLVMLNNL KKMTNLTELE
501 LVHCDLERIP HAVFSLLSLQ ELDLKENNLK SIEEIVSFQH LRKLTVLKLW
551 HNSITYIPEH IKKLTSLERL SFSHNKIEVL PSHLFLCNKI RYLDLSYNDI
601 RFIPPEIGVL QSLQYFSITC NKVESLPDEL YFCKKLKTLK IGKNSLSVLS
651 PKIGNLLFLS YLDVKGNHFE ILPPELGDCR ALKRAGLVVE DALFETLPSD
701 VREQMKTE
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_19j11, frame 1

TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene, partial cds., N = 1, Score = 1408, P = 4.5e-144

TREMBL:AF054827_1 gene: "soc-2"; product: "leucine-rich repeat protein SOC-2"; Caenorhabditis elegans leucine-rich repeat protein SOC-2 (soc-2) mRNA, complete cds., N = 1, Score = 304, P = 5.7e-24

TREMBL:RNU66707_1 product: "densin-180"; Rattus norvegicus densin-180 mRNA, complete cds., N = 1, Score = 311, P = 7.4e-24

TREMBL:AF068921_1 product: "Ras-binding protein SUR-8"; Mus musculus Ras-binding protein SUR-8 mRNA, complete cds., N = 1, Score = 302, P = 1.1e-23

>TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene, partial cds.
Length = 476

HSPs:

Score = 1408 (211.3 bits), Expect = 4.5e-144, P = 4.5e-144
Identities = 265/471 (56%), Positives = 361/471 (76%)

```
Query:   237 LTCLYTLYWLFYRSLREYSFEYVRQETGIDDIPDVKNDFAFMLHMIDQYDPLYSKRFAVF 296
             LT  Y+L+W+   SL++YSFE +R+++   DIPDVKNDFAF+LH+ DQYDPLYSKRF++F
Sbjct:     1 LTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFILHLADQYDPLYSKRFSIF 60

Query:   297 LSEVSENKLKQLNLNNEWTPDKLRQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKL 356
             LSEVSENKLKQ+NLNNEWT +KL+ KL  NA +++EL L ML+GLPD VFE+TE++ L L
Sbjct:    61 LSEVSENKLKQINLNNEWTVEKLKSKLVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSL 120
```

```
Query:  357 EIIKNVMIPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDDMRELPPWMY 416
            E+I  V +P+ ++QL NL+EL ++  S+ +   AL+FL+ENLK+L +KF +M ++P W++
Sbjct:  121 ELIPEVKLPSAVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGKIPRWVF 180

Query:  417 GLRNLEELYLVGSLSHDISRNVTLESLRDLKSLKILSIKSNVSKIPQAVVDVSSHLQKMC 476
             L+NL+ELYL G +  +    + LE  +DLK+L+ L +KS++S+IPQ V D+   LQK+
Sbjct:  181 HLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYLKSSLSRIPQVVTDLLPSLQKLS 240

Query:  477 IHNDGTKLVMLNNLKKMTNLTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIV 536
            + N+G+KLV+LNNLKKM NL  LEL+ CDLERIPH++FSL +L ELDL+ENNLK++EEI+
Sbjct:  241 LDNEGSKLVVLNNLKKMVNLKSLELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEII 300

Query:  537 SFQHLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSHLFLCNKIRYLDLS 596
            SFQHL+ L+ LKLWHN+I YIP  I  L++LE+LS  HN IE LP  LFLC K+ YLDLS
Sbjct:  301 SFQHLQNLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFLCTKLHYLDLS 360

Query:  597 YNDIRFIPPEIGVLQSLQYFSITCNKVESLPDELYFCKKLKTLKIGKNSLSVLSPKIGNL 656
            YN + FIP EI  L +LQYF++T N +E LPD L+ CKKL+ L +GKNSL  LSP +G L
Sbjct:  361 YNHLTFIPEEIQYLSNLQYFAVTNNNIEMLPDGLFQCKKLQCLLLGKNSLMNLSPHVGEL 420

Query:  657 LFLSYLDVKGNHFEILPPELGDCRALKRAGLVVEDALFETLPSDVREQMKT 707
            L++L++ GN+ E LPPEL  C++LKR  L+VE+ L  TLP  V E+++T
Sbjct:  421 SNLTHLELIGNYLETLPPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQT 471
```

Pedant information for DKFZphute1_19j11, frame 1

Report for DKFZphute1_19j11.1

```
[LENGTH]        708
[MW]            81812.82
[pI]            7.55
[HOMOL]         TREMBL:HSD984_1 gene: "KIAA0231"; Human mRNA for KIAA0231 gene, partial cds.
1e-149
[FUNCAT]        30.02 organization of plasma membrane       [S. cerevisiae, YJL005w] 3e-17
[FUNCAT]        03.22 cell cycle control and mitosis [S. cerevisiae, YJL005w] 3e-17
[FUNCAT]        10.04.03 second messenger formation  [S. cerevisiae, YJL005w] 3e-17
[FUNCAT]        01.03.10 metabolism of cyclic and unusual nucleotides      [S. cerevisiae,
YJL005w] 3e-17
[FUNCAT]        03.10 sporulation and germination    [S. cerevisiae, YJL005w] 3e-17
[FUNCAT]        30.10 nuclear organization    [S. cerevisiae, YKL193c] 3e-09
[FUNCAT]        06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)        [S. cerevisiae, YKL193c] 3e-09
[FUNCAT]        04.05.01.04 transcriptional control  [S. cerevisiae, YAL021c] 9e-08
[FUNCAT]        01.05.04 regulation of carbohydrate utilization      [S. cerevisiae, YAL021c]
9e-08
[FUNCAT]        01.01.04 regulation of amino-acid metabolism        [S. cerevisiae, YAL021c]
9e-08
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YOR353c] 3e-07
[BLOCKS]        BL00868F
[BLOCKS]        BL00985B Spermadhesins family proteins
[EC]            3.4.17.3 Lysine carboxypeptidase 1e-08
[EC]            4.6.1.1 Adenylate cyclase 3e-18
[PIRKW]         blocked amino end 1e-10
[PIRKW]         phosphotransferase 1e-09
[PIRKW]         nucleus 6e-08
[PIRKW]         duplication 3e-18
[PIRKW]         platelet 1e-10
[PIRKW]         tandem repeat 7e-16
[PIRKW]         keratan sulfate 7e-07
[PIRKW]         metallo-carboxypeptidase 1e-08
[PIRKW]         transmembrane protein 1e-10
[PIRKW]         serine/threonine-specific protein kinase 1e-09
[PIRKW]         autophosphorylation 1e-09
[PIRKW]         cartilage 7e-07
[PIRKW]         connective tissue 7e-07
[PIRKW]         magnesium 1e-09
[PIRKW]         cAMP biosynthesis 3e-18
[PIRKW]         ATP 1e-09
[PIRKW]         receptor 1e-09
[PIRKW]         leucine zipper 3e-13
[PIRKW]         glycoprotein 5e-12
[PIRKW]         extracellular matrix 7e-07
[PIRKW]         chondroitin sulfate proteoglycan 7e-07
[PIRKW]         cell adhesion 1e-08
[PIRKW]         hydrolase 1e-08
[PIRKW]         sulfoprotein 7e-07
[PIRKW]         membrane protein 1e-08
[PIRKW]         phosphorus-oxygen lyase 3e-18
```

```
[PIRKW]         collagen binding 7e-07
[SUPFAM]        leucine-rich alpha-2-glycoprotein repeat homology 3e-21
[SUPFAM]        chaoptin 1e-08
[SUPFAM]        gelsolin repeat homology 3e-21
[SUPFAM]        protein kinase homology 1e-09
[SUPFAM]        protein kinase Xa21 1e-09
[SUPFAM]        fibromodulin 4e-12
[SUPFAM]        yeast adenylate cyclase catalytic domain homology 3e-18
[SUPFAM]        yeast adenylate cyclase 3e-18
[KW]            TRANSMEMBRANE  3
[KW]            LOW_COMPLEXITY     1.41 %
```

```
SEQ   MKGLKTDLDLQQYSFINQMCYERALHWYAKYFPYLVLIHTLVFMLCSNFWFKFPGSSSKI
SEG   ............................................................
PRD   ccccchhhhhhhhhhhhhhhhhhhhhhhhhcchhhhhhhhhhhhccceeeecccccccee
MEM   .................................MMMMMMMMMMMMMMMMMM.........

SEQ   EHFISILGKCFDSPWTTRALSEVSGEDSEEKDNRKNNMNRSNTIQSGPEGSLVNSQSLKS
SEG   ............................................................
PRD   eeeeeeeecccccccceeeeeccccccccccccccccccccccccccccceeeeccccc
MEM   ............................................................

SEQ   IPEKFVVDKSTAGALDKKEGEQAKALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLI
SEG   ............................................................
PRD   cccceeecccccccccchhhhhhhhhhhhhhhhhhhhhhcccceeeehhhhhhhhhhhhhh
MEM   ...................................................MMMMMMMMM

SEQ   IIAYNSALVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCFVSIYGLTCL
SEG   ............................................................
PRD   hhhhcchhhheeeeecccccccccccccccccchhhhhhhhheeeeeeeeeeeeccceee
MEM   MMMMMMMM...................................MMMMMMMMMMMMMMMMM

SEQ   YTLYWLFYRSLREYSFEYVRQETGIDDIPDVKNDFAFMLHMIDQYDPLYSKRFAVFLSEV
SEG   ............................................................
PRD   hhhhhhhhhhhhhhhhhhhhhhhccccccccccchhhhhhhhhhhccchhhhhhhhhhhh
MEM   ............................................................

SEQ   SENKLKQLNLNNEWTPDKLRQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIK
SEG   ..xxxxxxxxxx................................................
PRD   hhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhh
MEM   ............................................................

SEQ   NVMIPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDDMRELPPWMYGLRN
SEG   ............................................................
PRD   hccccccchhhhhhhhhhhccccccccccccchhhhhhhhhhcccccccccccccchhhh
MEM   ............................................................

SEQ   LEELYLVGSLSHDISRNVTLESLRDLKSLKILSIKSNVSKIPQAVVDVSSHLQKMCIHND
SEG   ............................................................
PRD   hhhhhhccccccccccccccchhhhhhhhhhhhcccccccccccchhhhhhhhhhhcccc
MEM   ............................................................

SEQ   GTKLVMLNNLKKMTNLTELELVHCDLERIPHAVFSLLSLQELDLKENNLKSIEEIVSFQH
SEG   ............................................................
PRD   ceeeeccccccccchhhhhhhhhcccccccccccchhhhhhhhhhcccccccccccccccch
MEM   ............................................................

SEQ   LRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSHLFLCNKIRYLDLSYNDI
SEG   ............................................................
PRD   hhhhhhhcccccceeeccccccchhhhhheeecccccceeeccccccchhhhhhhhhccccc
MEM   ............................................................

SEQ   RFIPPEIGVLQSLQYFSITCNKVESLPDELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLS
SEG   ............................................................
PRD   cccccccchhhhhhhhhhhccccccccccccchhhhhcccccccceeecccccccchhhh
MEM   ............................................................

SEQ   YLDVKGNHFEILPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
SEG   ................................................
PRD   hhhcccccccccccccchhhhhhhheeeeccccccccccccccccccc
MEM   ................................................
```

(No Prosite data available for DKFZphutel_19j11.1)

(No Pfam data available for DKFZphutel_19j11.1)

DKFZphutel_1i2
----

group: transcription factor

DKFZphutel_1i2 encodes a novel 594 amino acid protein similar to signal transducing proteins.

The protein contains 2 WD-40 repeats, which is typical for the beta-transducin subunit of G-proteins. In addition, the protein contains a C3HC4 zinc finger and a leucine zipper. The beta subunits seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. Due to the zinc finger the novel protein seems to be a new molecule involved in signal transduction and transcription.

The new protein can find application in modulating/blocking gene expression of genes controlled by this molecule.

similarity to Dictostelium myosin heavy chain kinase

complete cDNA, complete cds, EST hits
[PFAM] Zinc finger, C3HC4 type (RING finger)
[PFAM] WD domain, G-beta repeats
[SCOP] d1tbgc_ 2.46.3.1.1 beta1-subunit of the signal-transducing G protei 3e-07

Sequenced by BMFZ

Locus: /map="16p13.3"

Insert length: 3584 bp
Poly A stretch at pos. 3555, polyadenylation signal at pos. 3537

```
   1 GGGCGGGAGG TGCTTCCCAA GGACCGTAGA TGCCTCTCTA GAGCATGAGC
  51 TCAGGCAAGA GTGCCCGCTA CAACCGCTTC TCCGGGGGGC CCAGCAATCT
 101 TCCCACCCCA GACGTCACCA CAGGGACCAG AATGGAAACG ACCTTCGGAC
 151 CCGCCTTTTC AGCCGTCACC ACCATCACAA AAGCTGACGG GACCAGCACC
 201 TACAAGCAGC ACTGCAGGAC AGCATGCCCC CCATCAGCAC TCCCCGCCGC
 251 TCCGACTCCG CCATCTCTGT CCGCTCCCTG CACTCAGAGT CCAGCATGTC
 301 TCTGCGCTCC ACATTCTCAC TGCCCGAGGA GGAGGAGGAG CCGGAGCCAC
 351 TGGTGTTTGC GGAGCAGCCC TCGGTGAAGC TGTGCTGTCA GCTCTGCTGC
 401 AGCGTCTTCA AAGACCCCGT GATCACCACG TGTGGGCACA CGTTCTGTAG
 451 GAGATGCGCC TTGAAGTCAG AGAAGTGTCC CGTGGACAAC GTCAAACTGA
 501 CCGTGGTGGT GAACAACATC GCGGTGGCCG AGCAGATCGG GGAGCTCTTC
 551 ATCCACTGCC GGCACGGCTG CCGGGTAGCG GGCAGCGGGA AGCCCCCCAT
 601 CTTTGAGGTG GACCCCCGAG GGTGCCCCTT CACCATCAAG CTCAGCGCCC
 651 GGAAGGACCA CGAGGGCAGC TGTGACTACA GGCCTGTGCG GTGTCCCAAC
 701 AACCCCAGCT GCCCCCCGCT GCTCAGGATG AACCTGGAGG CCCACCTCAA
 751 GGAGTGCGAG CACATCAAAT GCCCCCACTC CAAGTACGGG TGCACGTTCA
 801 TCGGGAACCA GGACACTTAC GAGACCCACC TGGAGACTTG CCGCTTCGAG
 851 GGCCTGAAGG AGTTTCTGCA GCAGACGGAT GACCGCTTCC ACGAGATGCA
 901 CGTGGCTCTG GCCCAGAAGG ACCAGGAGAT CGCCTTCCTG CGCTCCATGC
 951 TGGGAAAGCT CTCGGAGAAG ATCGACCAGC TAGAGAAGAG CCTGGAGCTC
1001 AAGTTTGACG TCCTGGACGA AAACCAGAGC AAGCTCAGCG AGGACCTCAT
1051 GGAGTTCCGG CGGGACGCAT CCATGTTAAA TGACGAGCTG TCCCACATCA
1101 ACGCGCGGCT GAACATGGGC ATCCTAGGCT CCTACGACCC TCAGCAGATC
1151 TTCAAGTGCA AAGGGACCTT TGTGGGCCAC CAGGGCCCTG TGTGGTGTCT
1201 CTGCGTCTAC TCCATGGGTG ACCTGCTCTT CAGTGGCTCC TCTGACAAGA
1251 CCATCAAGGT GTGGGACACA TGTACCACCT ACAAGTGTCA GAAGACACTG
1301 GAGGGCCATG ATGGCATCGT GCTGGCTCTC TGCATCCAGG GGTGCAAACT
1351 CTACAGCGGC TCTGCAGACT GCACCATCAT TGTGTGGGAC ATCCAGAACC
1401 TGCAGAAGGT GAACACCATC CGGGCCCATG ACAACCCGGT GTGCACGCTG
1451 GTCTCCTCAC ACAACGTGCT CTTCAGCGGC TCCCTGAAGG CCATCAAGGT
1501 CTGGGACATC GTGGGCACTG AGCTGAAGTT GAAGAAGGAG CTCACAGGCC
1551 TCAACCACTG GGTGCGGGCC CTGGTGGCTG CCCAGAGCTA CCTGTACAGC
1601 GGCTCCTACC AGACAATCAA GATCTGGGAC ATCCGAACCC TTGACTGCAT
1651 CCACGTCCTG CAGACGTCTG GTGGCAGCGT CTACTCCATT GCTGTGACAA
1701 ATCACCACAT TGTCTGTGGC ACCTACGAGA ACCTCATCCA CGTGTGGGAC
1751 ATTGAGTCCA AGGAGCAGGT GCGGACCCTC ACGGGCCACG TGGGCACCGT
1801 GTATGCCCTG GCGGTCATCT CGACGCCAGA CCAGACCAAA GTCTTCAGTG
1851 CATCCTACGA CCGGTCCCTC AGGGTCTGGA GTATGGACAA CATGATCTGC
1901 ACGCAGACCC TGCTGCGTCA CCAGGGCAGT GTCACCGCGC TGGCTGTGTC
1951 CCGGGGCCGA CTCTTCTCAG GGGCTGTGGA TAGCACTGTG AAGGTTTGGA
2001 CTTGCTAACA GGATCCAGGC CAGGCTGTGG TTTCCCCTGA ACCAGCCCTG
2051 GACCTTTCTG AGCCAGGCTG GCCACATGGG GTGGTCTCGG GGTTTCTGCC
2101 TGCCCCGTGG GCATAGGTGG ACAGGCTCTG GCAGCCGGGC AGTGCCCTCC
2151 CCGTCCCATG CTCGGCGAGC CTCCCTCTAC TCGGCACTGT CCTTGCTGCC
2201 CAGCCCCTCT CTGGGTGCCA GGTACGACGC TTGCCCCGGC CCACCCTCCA
2251 TCCCCACCCT CCATCCCCAC CCTAGATGGA GCGAGGGCCT TTTTACTCAC
2301 CTTTTCTACC GTTTTTAGAC TGTATGTAGA TTTGGTTACC TCCTGGTTGA
```

```
2351 AATAAATGCT CCACAGACTG TGGCTGTGAG TGGGGACAGC TCCTCGGGAC
2401 AAGGGGGCTG TGTGTGGCCT TGAGGTTGGT GTGCACAGGC ACTGGCTGCT
2451 GTGAGTGGGG GGGCATGGGG CAGTTTCCTT TGGTGGACCC CAGGACTTCG
2501 GCCCACTCCG GGGCCTCCCC TCCCTGCTAG GAGGCAACTC GTCACACCCA
2551 AGCTGCTGGC CTCCAGTCCC ATCTCCCCCA ACACATGTGC CCCCAAAAAG
2601 TGAGCCAGGC ACCTCTGTTT CCTGCTGTTT ATTGACAGCC GACGGCAGCG
2651 CCTTGCCCAG ACCTCCCCTG CCCACCTGCT GGAGCCCAGC CTGTGCCGCC
2701 CTCTGAGGAG AGGCCTGGGG GGACAGCTGG GCACGTCCAC TCGCAGGGAA
2751 ACACGGGGTG AGACAGCAGG AAGGGGCCCT GCACGCCGGG ACGCCACCTC
2801 CGCCAGCCGC CTCCACCCGC CCCACACCAC AATCGCTGGT TTTCGGCATT
2851 TTTTAAATTT TTTTTTTAAG AAACGTCAAA GTTGTGCCCA ACACTGTGGA
2901 TCAGCAAACA CGATAGAGGA GACCAGTCAG TACTTCTTGG AGGGGGCAGG
2951 AGGAGAGAGG AAAAGGGAGG GCGAGAATGA CCACACAACA CAGCCTTGGA
3001 CCATGAGCAG AAGCGTCCGT GGGAACTCCA CTGGGGTGGA TGGGCTGCCT
3051 GCACAGCCCC TGGAGAGGGG GCCAGGCACA CCCTCAGAGG AGCTGCAAGC
3101 CCGTGGCCTG GCCTGCTACA TGCCCTGCTT CCACGTGGCT GCCACGCTGA
3151 CACACCCACA TTCACCAAAC CCACCCGCGC CCTGGGACGC AGCCACGCCA
3201 GGAGGAGGAC ACGGCCGCCG AGAGCAAGGC ACAACCTCGA GTTCTTGGGG
3251 CGCAGAGAAC TTAGGAGAGA AGCACGGAGG AGCCCCCGGC AGAGCACCCG
3301 CCCCCGGGCC CCAGCCTTCC ACCTGTGCTA GCAGCCTGGG GCCTCCACTC
3351 TGGCCGGAGG AAGGACCGCA GGCAGACAGC CTGGGCCTCT AACAGCTTTT
3401 GTCCGGAGCT AGACTTCGTG TCCTTTCAGT TGGTAAATGG TTTTCTATAG
3451 AATCAATAAT ATTTCTTTCT TTAAATATAT ATTTGTTAAA GTTATACCTT
3501 TTTGTTTCTC TGGGGAAATC CGCCTCAGCT CATTCCCAAT AAATTAATAC
3551 TCTTGATAAA AAAAAAAAAA AGAAAAAAAA AAAA
```

BLAST Results

Entry HSBE from database EMBL:
Homo sapiens (clone exon trap d5) chromosome 16p13.3 gene, exon.
Score = 2375, P = 7.1e-101, identities = 475/475

Entry HSBD from database EMBL:
Homo sapiens (clone exon trap d32) chromosome 16p13.3 gene, exon.
Score = 876, P = 3.0e-31, identities = 176/177

Medline entries

95122486:
Structural analysis of myosin heavy chain kinase A from Dictyostelium. Evidence for a highly divergent protein kinase domain, an amino-terminal coiled-coil domain, and a domain homologous to the beta-subunit of heterotrimeric G proteins.

96149460:
Dictyostelium myosin heavy chain kinase A regulates myosin localization during growth and development.

97277316:
Identification of a protein kinase from Dictyostelium with homology to the novel catalytic domain of myosin heavy chain kinase A.

96009891:
A gene responsible for vegetative incompatibility in the fungus Podospora anserina encodes a protein with a GTP-binding motif and G beta homologous domain.

Peptide information for frame 2

ORF from 224 bp to 2005 bp; peptide length: 594
Category: similarity to known protein
Prosite motifs: ZINC_FINGER_C3HC4 (70-80)
LEUCINE_ZIPPER (436-458)
LEUCINE_ZIPPER (436-458)
G_BETA_REPEATS (335-355)
G_BETA_REPEATS (376-391)

```
  1 MPPISTPRRS DSAISVRSLH SESSMSLRST FSLPEEEEEP EPLVFAEQPS
 51 VKLCCQLCCS VFKDPVITTC GHTFCRRCAL KSEKCPVDNV KLTVVVNNIA
101 VAEQIGELFI HCRHGCRVAG SGKPPIFEVD PRGCPFTIKL SARKDHEGSC
151 DYRPVRCPNN PSCPPLLRMN LEAHLKECEH IKCPHSKYGC TFIGNQDTYE
201 THLETCRFEG LKEFLQQTDD RFHEMHVALA QKDQEIAFLR SMLGKLSEKI
251 DQLEKSLELK FDVLDENQSK LSEDLMEFRR DASMLNDELS HINARLNMGI
301 LGSYDPQQIF KCKGTFVGHQ GPVWCLCVYS MGDLLFSGSS DKTIKVWDTC
351 TTYKCQKTLE GHDGIVLALC IQGCKLYSGS ADCTIIVWDI QNLQKVNTIR
401 AHDNPVCTLV SSHNVLFSGS LKAIKVWDIV GTELKLKKEL TGLNHWVRAL
451 VAAQSYLYSG SYQTIKIWDI RTLDCIHVLQ TSGGSVYSIA VTNHHIVCGT
501 YENLIHVWDI ESKEQVRTLT GHVGTVYALA VISTPDQTKV FSASYDRSLR
551 VWSMDNMICT QTLLRHQGSV TALAVSRGRL FSGAVDSTVK VWTC
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphute1_1i2, frame 2

SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B)., N = 1, Score = 419, P = 3.6e-37

SWISSPROT:HET1_PODAN VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1., N = 1, Score = 392, P = 3.1e-33

SWISSPROT:YDJ5_SCHPO HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I., N = 1, Score = 357, P = 4.1e-30

TREMBL:AF032878_1 gene: "slimb"; product: "Slimb"; Drosophila melanogaster Slimb (slimb) mRNA, complete cds., N = 1, Score = 347, P = 1.7e-29

```
>SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
          Length = 732

  HSPs:

 Score = 419 (62.9 bits), Expect = 3.6e-37, P = 3.6e-37
 Identities = 96/268 (35%), Positives = 158/268 (58%)

Query:    325 CLCVYSMGDLLFSGSSDKTIKVWD-TCTTYKCQKTLEGHDGIVLALCIQGCKLYSGSADC 383
              C+C     +LLF+G SD +I+V+D      +C +TL+GH+G V ++C     L+SGS+D
Sbjct:    467 CIC----DNLLFTGCSDNSIRVYDYKSQNMECVQTLKGHEGPVESICYNDQYLFSGSSDH 522

Query:    384 TIIVWDIQNLQKVNTIRAHDNPVCTLVSSHNVLFSGSL-KAIKVWDIVGTELKLKKELTG 442
              +I VWD++ L+ + T+  HD PV T++ +   LFSGS  K IKVWD+    L+ K  L
Sbjct:    523 SIKVWDLKKLRCIFTLEGHDKPVHTVLLNDKYLFSGSSDKTIKVWDL--KTLECKYTLES 580

Query:    443 LNHWVRALVAAQSYLYSGSY-QTIKIWDIRTLDCIHVLQTSGGSVYSIAVTNHHIVCGTY 501
                  V+ L  +  YL+SGS  +TIK+WD++T  C + L+     V +I +   ++  G+Y
Sbjct:    581 HARAVKTLCISGQYLFSGSNDKTIKVWDLKTFRCNYTLKGHTKWVTTICILGTNLYSGSY 640

Query:    502 ENLIHVWDIESKEQVRTLTGHVGTVYALAVISTPDQTKVFSASYDRSLRVWSMDNMICTQ 561
              +  I VW+++S E   TL GH   V  + +    D+  +F+AS D ++++W ++ + C
Sbjct:    641 DKTIRVWNLKSLECSATLRGHDRWVEHMVIC---DKL-LFTASDDNTIKIWDLETLRCNT 696

Query:    562 TLLRHQGSVTALAVSRGR--LFSGAVDSTVKVW 592
              TL  H  +V  LAV   +  + S + D +++VW
Sbjct:    697 TLEGHNATVQCLAVWEDKKCVISCSHDQSIRVW 729

 Score = 415 (62.3 bits), Expect = 1.2e-36, P = 1.2e-36
 Identities = 113/303 (37%), Positives = 166/303 (54%)

Query:    255 KSLEL-KFDVLDENQSKLSEDLMEFRRDASMLNDEL-SHINARLNMGILGS-------YD 305
              KS++L K ++L  N+ K S +L   +   ++    + SH+    N+   G        YD
Sbjct:    427 KSIDLEKPEILINNKKKESINLETIKLIETIKGYHVTSHLCICDNLLFTGCSDNSIRVYD 486

Query:    306 -PQQIFKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVWDTCTTYKCQKTLEGHDG 364
                 Q  +C  T  GH+GPV  +C Y+    LFSGSSD +IKVWD     +C  TLEGHD
Sbjct:    487 YKSQNMECVQTLKGHEGPVESIC-YN-DQYLFSGSSDHSIKVWDL-KKLRCIFTLEGHDK 543

Query:    365 IVLALCIQGCKLYSGSADCTIIVWDIQNLQKVNTIRAHDNPVCTLVSSHNVLFSGSL-KA 423
               V  + +    L+SGS+D TI VWD++ L+   T+ +H   V TL  S   LFSGS  K
Sbjct:    544 PVHTVLLNDKYLFSGSSDKTIKVWDLKTLECKYTLESHARAVKTLCISGQYLFSGSNDKT 603

Query:    424 IKVWDIVGTELKLKKELTGLNHWVRALVAAQSYLYSGSY-QTIKIWDIRTLDCIHVLQTS 482
              IKVWD+     +    L G   WV  +    + LYSGSY +TI++W++++L+C   L+
Sbjct:    604 IKVWDL--KTFRCNYTLKGHTKWVTTICILGTNLYSGSYDKTIRVWNLKSLECSATLRGH 661
```

```
Query:   483 GGSVYSIAVTNHHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVYALAVISTPDQTKVFS 542
             V  + + +  +    + +N I +WD+E+      TL GH  TV  LAV    D+  V S
Sbjct:   662 DRWVEHMVICDKLLFTASDDNTIKIWDLETLRCNTTLEGHNATVQCLAVWE--DKKCVIS 719

Query:   543 ASYDRSLRVW 552
             S+D+S+RVW
Sbjct:   720 CSHDQSIRVW 729

 Score = 262 (39.3 bits), Expect = 3.2e-19, P = 3.2e-19
 Identities = 60/184 (32%), Positives = 109/184 (59%)

Query:   352 TYKCQKTLEGHDGIVLALCIQGCKLYSGSADCTIIVWDI--QNLQKVNTIRAHDNPVCTL 409
             T K  +T++G+  +    LCI    L++G +D +I V+D   QN++  V T++ H+ PV ++
Sbjct:   450 TIKLIETIKGYH-VTSHLCICDNLLFTGCSDNSIRVYDYKSQNMECVQTLKGHEGPVESI 508

Query:   410 VSSHNVLFSGSLK-AIKVWDIVGTELKLKKELTGLNHWVRALVAAQSYLYSGSY-QTIKI 467
              +    LFSGS    +IKVWD+    +L+    L G +  V   ++     YL+SGS  +TIK+
Sbjct:   509 CYNDQYLFSGSSDHSIKVWDL--KKLRCIFTLEGHDKPVHTVLLNDKYLFSGSSDKTIKV 566

Query:   468 WDIRTLDCIHVLQTSGGSVYSIAVTNHHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVY 527
             WD++TL+C + L++    +V ++ ++ ++  G+ +   I VWD+++        TL GH    V
Sbjct:   567 WDLKTLECKYTLESHARAVKTLCISGQYLFSGSNDKTIKVWDLKTFRCNYTLKGHTKWVT 626

Query:   528 ALAVIST 534
             + ++ T
Sbjct:   627 TICILGT 633

 Score = 173 (26.0 bits), Expect = 1.7e-09, P = 1.7e-09
 Identities = 43/118 (36%), Positives = 65/118 (55%)

Query:   310 FKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVWDTCTTYKCQKTLEGHDGIVLAL 369
             F+C  T  GH   V  +C+  +G  L+SGS DKTI+VW+   + +C  TL GHD  V  +
Sbjct:   612 FRCNYTLKGHTKWVTTICI--LGTNLYSGSYDKTIRVWNL-KSLECSATLRGHDRWVEHM 668

Query:   370 CIQGCKLYSGSADCTIIVWDIQNLQKVNTIRAHDNPV-CTLVSSHN--VLFSGSLKAIKV 426
             I    L++  S D TI  +WD++  L+    T+  H+  V C  V       V+    ++I+V
Sbjct:   669 VICDKLLFTASDDNTIKIWDLETLRCNTTLEGHNATVQCLAVWEDKKCVISCSHDQSIRV 728

Query:   427 W 427
             W
Sbjct:   729 W 729
```

Pedant information for DKFZphutel_1i2, frame 2

Report for DKFZphutel_1i2.2

```
[LENGTH]      594
[MW]          66541.94
[pI]          6.64
[HOMOL]       SWISSPROT:KMHB_DICDI MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B). 3e-37

[FUNCAT]      03.22 cell cycle control and mitosis  [S. cerevisiae, YIL046w] 5e-21
[FUNCAT]      06.13.01 cytoplasmic degradation      [S. cerevisiae, YIL046w] 5e-21
[FUNCAT]      04.05.01.04 transcriptional control   [S. cerevisiae, YIL046w] 5e-21
[FUNCAT]      30.10 nuclear organization    [S. cerevisiae, YIL046w] 5e-21
[FUNCAT]      01.01.04 regulation of amino-acid metabolism        [S. cerevisiae, YIL046w]
5e-21
[FUNCAT]      99 unclassified proteins      [S. cerevisiae, YCR072c beta-transducin family]
2e-15
[FUNCAT]      30.04 organization of cytoskeleton    [S. cerevisiae, YFL009w] 1e-14
[FUNCAT]      03.04 budding, cell polarity and filament formation  [S. cerevisiae, YFL009w]
1e-14
[FUNCAT]      03.10 sporulation and germination     [S. cerevisiae, YFL009w] 1e-14
[FUNCAT]      03.16 dna synthesis and replication   [S. cerevisiae, YFL009w] 1e-14
[FUNCAT]      30.09 organization of intracellular transport vesicles      [S. cerevisiae,
YDL145c] 1e-13
[FUNCAT]      08.07 vesicular transport (golgi network, etc.)      [S. cerevisiae, YDL145c]
1e-13
[FUNCAT]      04.05.03 mrna processing (splicing)  [S. cerevisiae, YPR178w] 2e-11
[FUNCAT]      06.10 assembly of protein complexes  [S. cerevisiae, YPR178w] 2e-11
[FUNCAT]      04.05.01.01 general transcription activities        [S. cerevisiae, YBR198c
TAF90 - TFIID subunit] 3e-11
[FUNCAT]      03.13 meiosis  [S. cerevisiae, YLR129w] 8e-09
[FUNCAT]      30.03 organization of cytoplasm      [S. cerevisiae, YCR057c] 2e-07
[FUNCAT]      03.25 cytokinesis      [S. cerevisiae, YCR057c] 2e-07
[FUNCAT]      02.16 fermentation     [S. cerevisiae, YMR116c] 5e-07
[FUNCAT]      05.04 translation (initiation, elongation and termination)  [S. cerevisiae,
YMR116c] 5e-07
```

```
[FUNCAT]        06.13 proteolysis      [S. cerevisiae, YGL003c] 3e-06
[FUNCAT]        03.01 cell growth      [S. cerevisiae, YKL021c] 2e-04
[FUNCAT]        01.03.07 deoxyribonucleotide metabolism      [S. cerevisiae, YOR269w] 2e-04
[FUNCAT]        30.02 organization of plasma membrane      [S. cerevisiae, YOR212w] 0.001
[FUNCAT]        10.05.07 g-proteins    [S. cerevisiae, YOR212w] 0.001
[FUNCAT]        03.07 pheromone response, mating-type determination, sex-specific proteins
        [S. cerevisiae, YOR212w] 0.001
[BLOCKS]        BL00678
[BLOCKS]        BL00518 Zinc finger, C3HC4 type, proteins
[SCOP]          d1tbgd_ 2.46.3.1.1 beta1-subunit of the signal-transducing  3e-10
[EC]            2.7.1.129 Myosin-heavy-chain kinase 3e-26
[PIRKW]         phosphotransferase 3e-26
[PIRKW]         nucleus 1e-06
[PIRKW]         plasma 9e-08
[PIRKW]         duplication 3e-25
[PIRKW]         hormone 9e-08
[PIRKW]         zinc 3e-09
[PIRKW]         cell cycle control 4e-13
[PIRKW]         transmembrane protein 3e-12
[PIRKW]         zinc finger 1e-08
[PIRKW]         stomach 9e-08
[PIRKW]         DNA binding 9e-06
[PIRKW]         autophosphorylation 3e-26
[PIRKW]         phosphoprotein 3e-26
[PIRKW]         signal transduction 5e-08
[PIRKW]         heterotrimer 5e-08
[PIRKW]         coiled coil 3e-26
[PIRKW]         multimer 3e-26
[PIRKW]         transcription regulation 4e-10
[PIRKW]         GTP binding 5e-08
[SUPFAM]        chromobox homology 9e-06
[SUPFAM]        RING finger homology 3e-09
[SUPFAM]        coatomer complex beta' chain 1e-07
[SUPFAM]        WD repeat homology 3e-26
[SUPFAM]        yeast coatomer complex alpha chain 3e-12
[SUPFAM]        GTP-binding regulatory protein beta chain 5e-08
[SUPFAM]        PRL1 protein 2e-09
[PROSITE]       WD_REPEATS      2
[PROSITE]       LEUCINE_ZIPPER 1
[PROSITE]       MYRISTYL        14
[PROSITE]       CK2_PHOSPHO_SITE        4
[PROSITE]       ZINC_FINGER_C3HC4       1
[PROSITE]       PKC_PHOSPHO_SITE        18
[PROSITE]       ASN_GLYCOSYLATION       1
[PFAM]          Zinc finger, C3HC4 type (RING finger)
[PFAM]          WD domain, G-beta repeats
[KW]            Irregular
[KW]            3D
[KW]            LOW_COMPLEXITY      6.23 %
[KW]            COILED_COIL         6.73 %

SEQ    MPPISTPRRSDSAISVRSLHSESSMSLRSTFSLPEEEEEPEPLVFAEQPSVKLCCQLCCS
SEG    .............xxxxxxxxxxxxxx....xxxxxxxxx....................
COILS  ............................................................
1gg2B  ............................................................

SEQ    VFKDPVITTCGHTFCRRCALKSEKCPVDNVKLTVVVNNIAVAEQIGELFIHCRHGCRVAG
SEG    ............................................................
COILS  ............................................................
1gg2B  ............................................................

SEQ    SGKPPIFEVDPRGCPFTIKLSARKDHEGSCDYRPVRCPNNPSCPPLLRMNLEAHLKECEH
SEG    ............................................................
COILS  ............................................................
1gg2B  ............................................................

SEQ    IKCPHSKYGCTFIGNQDTYETHLETCRFEGLKEFLQQTDDRFHEMHVALAQKDQEIAFLR
SEG    ............................................................
COILS  ..............................................CCCCCCCCCCCCCC
1gg2B  ............................................................

SEQ    SMLGKLSEKIDQLEKSLELKFDVLDENQSKLSEDLMEFRRDASMLNDELSHINARLNMGI
SEG    ............................................................
COILS  CCCCCCCCCCCCCCCCCCCCCCCCCC..................................
1gg2B  ............................................................

SEQ    LGSYDPQQIFKCKGTFVGHQGPVWCLCVYSMGDLLFSGSSDKTIKVWDTCTTYKCQKTLE
SEG    ............................................................
COILS  ............................................................
1gg2B  ...........EECCCCCCCEEEEEEETTTTCEEEEEEETTTEEEEEEG-GGCEEEEEEE
```

```
SEQ     GHDGIVLALCIQGCKLYSGSADCTIIVWDIQNLQKVNTIRAHDNPVCTLVSSHNVLFSGS
SEG     ............................................................
COILS   ............................................................
1gg2B   CCCCCEEEEEETTCEEEEEETTTCEEEEETTTTEEEEEE-CTTTTCCCEEE.........

SEQ     LKAIKVWDIVGTELKLKKELTGLNHWVRALVAAQSYLYSGSYQTIKIWDIRTLDCIHVLQ
SEG     ..........xxxxxxxxxxxx......................................
COILS   ............................................................
1gg2B   ............................................................

SEQ     TSGGSVYSIAVTNHHIVCGTYENLIHVWDIESKEQVRTLTGHVGTVYALAVISTPDQTKV
SEG     ............................................................
COILS   ............................................................
1gg2B   ............................................................

SEQ     FSASYDRSLRVWSMDNMICTQTLLRHQGSVTALAVSRGRLFSGAVDSTVKVWTC
SEG     ......................................................
COILS   ......................................................
1gg2B   ......................................................
```

Prosite for DKFZphutel_1i2.2

PS00001	267->271	ASN_GLYCOSYLATION	PDOC00001
PS00005	6->9	PKC_PHOSPHO_SITE	PDOC00005
PS00005	15->18	PKC_PHOSPHO_SITE	PDOC00005
PS00005	26->29	PKC_PHOSPHO_SITE	PDOC00005
PS00005	50->53	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	121->124	PKC_PHOSPHO_SITE	PDOC00005
PS00005	137->140	PKC_PHOSPHO_SITE	PDOC00005
PS00005	141->144	PKC_PHOSPHO_SITE	PDOC00005
PS00005	205->208	PKC_PHOSPHO_SITE	PDOC00005
PS00005	247->250	PKC_PHOSPHO_SITE	PDOC00005
PS00005	340->343	PKC_PHOSPHO_SITE	PDOC00005
PS00005	343->346	PKC_PHOSPHO_SITE	PDOC00005
PS00005	352->355	PKC_PHOSPHO_SITE	PDOC00005
PS00005	398->401	PKC_PHOSPHO_SITE	PDOC00005
PS00005	420->423	PKC_PHOSPHO_SITE	PDOC00005
PS00005	464->467	PKC_PHOSPHO_SITE	PDOC00005
PS00005	548->551	PKC_PHOSPHO_SITE	PDOC00005
PS00005	588->591	PKC_PHOSPHO_SITE	PDOC00005
PS00006	32->36	CK2_PHOSPHO_SITE	PDOC00006
PS00006	201->205	CK2_PHOSPHO_SITE	PDOC00006
PS00006	330->334	CK2_PHOSPHO_SITE	PDOC00006
PS00006	533->537	CK2_PHOSPHO_SITE	PDOC00006
PS00008	115->121	MYRISTYL	PDOC00008
PS00008	133->139	MYRISTYL	PDOC00008
PS00008	194->200	MYRISTYL	PDOC00008
PS00008	299->305	MYRISTYL	PDOC00008
PS00008	314->320	MYRISTYL	PDOC00008
PS00008	364->370	MYRISTYL	PDOC00008
PS00008	379->385	MYRISTYL	PDOC00008
PS00008	419->425	MYRISTYL	PDOC00008
PS00008	460->466	MYRISTYL	PDOC00008
PS00008	484->490	MYRISTYL	PDOC00008
PS00008	499->505	MYRISTYL	PDOC00008
PS00008	524->530	MYRISTYL	PDOC00008
PS00008	568->574	MYRISTYL	PDOC00008
PS00008	583->589	MYRISTYL	PDOC00008
PS00518	70->80	ZINC_FINGER_C3HC4	PDOC00449
PS00029	436->458	LEUCINE_ZIPPER	PDOC00029
PS00678	335->350	WD_REPEATS	PDOC00574
PS00678	376->391	WD_REPEATS	PDOC00574

Pfam for DKFZphutel_1i2.2

```
HMM_NAME      WD domain, G-beta repeats

HMM                *MrGHnnWVWCVaFSPDGrWFIvSGSWDgTCRLWD*
                    ++GH ++VWC+ +   G + ++SGS D+T+++WD
Query         316   FVGHQGPVWCLCVYSMGDL-LFSGSSDKTIKVWD    348

22.93    519   553    1    34 dkfzphutel_1i2.2 similarity to Dictostelium myosin heavy chain
kinase
  Alignment to HMM consensus:
```

```
Query                 *MrGHnnWVWCVaF..SPDGrWFIvSGSWDgTCRLWD*
                       ++GH ++V+++A+  +PD    ++S+S D+++R+W+
  dkfzphutel   519    LTGHVGTVYALAVISTPDQTK-VFSASYDRSLRVWS     553


HMM_NAME       Zinc finger, C3HC4 type (RING finger)

HMM                   *CPICFcTFQlDyPWPFdePmMlPCgHsFCypCIrrW..CPmC*
                       C++C     +      F++P++++CGH+FC+ C +++  CP+
Query            55   CQLC-----CSV---FKDPVITTCGHTFCRRCALKSEKCPVD      88
```

DKFZphutel_20b19
----

group: metabolism

DKFZphutel_20b19 encodes a novel 486 amino acid protein with similarity to bacterial sarcosine oxidases (EC 1.5.3.1.)

The novel protein seems to be a novel enzyme with sarcosine oxidase activity.

The new protein can find application in modulation of sarcosine metabolism and as a new enzyme for biotechnologic production processes.

similarity to sarcosine oxidases
membrane regions: 1
Summary DKFZphutel_20b19 encodes a novel 486 amino acid protein, with similarity to sarcosine oxidases.

similarity to sarcosine oxidases

complete cDNA?, complete cds potential start at Bp 48, EST hits,

Sequenced by AGOWA

Locus: unknown

Insert length: 1967 bp
Poly A stretch at pos. 1950, no polyadenylation signal found

```
   1 AGCGAGGCAG CAGTGCAGCT TTCAGAGGGT CCGGGCTCAG AGGGGTTATG
  51 ATTCGGAGGG TTCTGCCGCA CGGCATGGGC CGGGGCCTCT TGACCCGGAG
 101 GCCAGGCACG CGCAGAGGAG GCTTTTCTCT GGACTGGGAT GGAAAGGTGT
 151 CTGAGATTAA GAAGAAGATC AAGTCGATCC TGCCTGGAAG GTCCTGTGAT
 201 CTACTGCAAG ACACCAGCCA CCTGCCTCCC GAGCACTCGG ATGTGGTGAT
 251 CGTGGGAGGT GGGGTGCTTG GCTTGTCTGT GGCCTATTGG CTGAAGAAGC
 301 TGGAGAGCAG ACGAGGTGCT ATTCGAGTGC TAGTGGTGGA ACGGGACCAC
 351 ACGTATTCAC AGGCCTCCAC TGGGCTCTCA GTAGGTGGGA TTTGTCAGCA
 401 GTTCTCATTG CCTGAGAACA TCCAGCTCTC CCTCTTTTCA GCCAGCTTTC
 451 TACGGAACAT CAATGAGTAC CTGGCCGTAG TCGATGCTCC TCCCCTGGAC
 501 CTCCGGTTCA ACCCCTCGGG CTACCTCTTG CTGGCTTCAG AAAAGGATGC
 551 TGCAGCCATG GAGAGCAACG TGAAAGTGCA GAGGCAGGAG GGAGCCAAAG
 601 TTTCTCTGAT GTCTCCTGAT CAGCTTCGGA ACAAGTTTCC CTGGATAAAC
 651 ACAGAGGGAG TGGCTTTGGC GTCTTATGGG ATGGAGGACG AAGGTTGGTT
 701 TGACCCCTGG TGTCTGCTCC AGGGGCTTCG GCGAAAGGTC CAGTCCTTGG
 751 GAGTCCTTTT CTGCCAGGGA GAGGTGACAC GTTTTGTCTC TTCATCTCAA
 801 CGCATGTTGA CCACAGATGA CAAAGCGGTG GTCTTGAAAA GGATCCATGA
 851 AGTCCATGTG AAGATGGACC GCAGCCTGGA GTACCAGCCT GTGGAATGCG
 901 CCATTGTGAT CAACGCAGCC GGAGCCTGGT CTGCGCAAAT CGCAGCACTG
 951 GCTGGTGTTG GAGAGGGGCC GCCTGGCACC CTGCAGGGCA CCAAGCTACC
1001 TGTGGAGCCG AGGAAAAGGT ATGTGTATGT GTGGCACTGC CCCCAGGGAC
1051 CAGGCCTAGA GACTCCGCTT GTTGCAGACA CCAGTGGAGC CTATTTTCGC
1101 CGGGAAGGAT TAGGTAGCAA CTACCTAGGT GGTCGTAGCC CCACTGAGCA
1151 GGAAGAACCG GACCCGGCGA ACCTGGAAGT GGACCATGAT TTCTTCCAGG
1201 ACAAGGTGTG GCCCCATTTG GCCCTGAGGG TCCCAGCTTT TGAGACTCTG
1251 AAGGTTCAGA GCGCCTGGGC CGGCTATTAC GACTACAACA CCTTTGACCA
1301 GAATGGCGTG GTGGGCCCCC ACCCGCTAGT TGTCAACATG TACTTTGCTA
1351 CTGGCTTCAG TGGTCACGGG CTCCAGCAGG CCCCTGGCAT TGGGCGAGCT
1401 GTAGCAGAGA TGGTACTGAA GGGCAGGTTC CAGACCATCG ACCTGAGCCC
1451 CTTCCTCTTT ACCCGCTTTT ACTTGGGAGA GAAGATCCAG GAGAACAACA
1501 TCATCTGAGC ATGTGTGCTC TGCACTGGCT CCACTGGCTT GCATCCTGGC
1551 TGTGTTCACA GCCTTGTTTG CTGCTTCCAT CTTCCCCAGT ACTGTGCCAG
1601 GCCTTCTCCC CCTCCCCAGT GTCCTCTCCT CTCAGGCAGG CCATTGCACC
1651 CATATGGCTG GGCAGGCACA GGCAGTGAGG CCGAGGCCAA TAGCGAGTGA
1701 TGAGCGGGAT CCTAGGACTG ATCTGTAGCC CATGCTGATG TCACCCACCA
1751 GGGCAATCCA TCTGGAGGCC TGAGCACCCT GGCCCAGGAC TGGCTTCATC
1801 CTGGCACTGA CCAGGAAAGA CTGCCTCTGA CCCTCTTAGC AGACAGAGCC
1851 CAGGCATGGG AGCACTCTGG GGCAGCCTGG CTCAGGTTTA TTGATTTTCG
1901 TCTGTTTACC CTATCCATTA ATCAATACAT GTAATTAACT CCTTCCCTCC
1951 AAAAAAAAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 48 bp to 1505 bp; peptide length: 486
Category: similarity to known protein

```
  1 MIRRVLPHGM GRGLLTRRPG TRRGGFSLDW DGKVSEIKKK IKSILPGRSC
 51 DLLQDTSHLP PEHSDVVIVG GGVLGLSVAY WLKKLESRRG AIRVLVVERD
101 HTYSQASTGL SVGGICQQFS LPENIQLSLF SASFLRNINE YLAVVDAPPL
151 DLRFNPSGYL LLASEKDAAA MESNVKVQRQ EGAKVSLMSP DQLRNKFPWI
201 NTEGVALASY GMEDEGWFDP WCLLQGLRRK VQSLGVLFCQ GEVTRFVSSS
251 QRMLTTDDKA VVLKRIHEVH VKMDRSLEYQ PVECAIVINA AGAWSAQIAA
301 LAGVGEGPPG TLQGTKLPVE PRKRYVYVWH CPQGPGLETP LVADTSGAYF
351 RREGLGSNYL GGRSPTEQEE PDPANLEVDH DFFQDKVWPH LALRVPAFET
401 LKVQSAWAGY YDYNTFDQNG VVGPHPLVVN MYFATGFSGH GLQQAPGIGR
451 AVAEMVLKGR FQTIDLSPFL FTRFYLGEKI QENNII
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_20b19, frame 3

TREMBL:CEM04B2_4 gene: "M04B2.4"; Caenorhabditis elegans cosmid M04B2,
N = 1, Score = 801, P = 9.2e-80

PIR:B71184 probable sarcosine oxidase - Pyrococcus horikoshii, N = 2,
Score = 194, P = 2e-26

PIR:B69284 sarcosine oxidase, subunit beta (soxB) homolog -
Archaeoglobus fulgidus, N = 3, Score = 189, P = 8.2e-22

TREMBL:AF042732_1 gene: "Bb"; product: "unknown protein"; Anopheles
gambiae (Bb) gene, partial cds; and TU37B2 (TU37B2) and diphenol
oxidase-A2 (Dox-A2) genes, complete cds., N = 1, Score = 386, P =
8.7e-36

PIR:F71008 probable sarcosine oxidase - Pyrococcus horikoshii, N = 2,
Score = 200, P = 4e-25

>TREMBL:CEM04B2_4 gene: "M04B2.4"; Caenorhabditis elegans cosmid M04B2
Length = 527

HSPs:

Score = 801 (120.2 bits), Expect = 9.2e-80, P = 9.2e-80
Identities = 171/433 (39%), Positives = 260/433 (60%)

```
Query:    61 PEHSDVVIVGGGVLGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFS 120
             P   +++VI+GGG+ G S A+WLK+    R     +V+VVE +  ++++ST LS GGI QQFS
Sbjct:    91 PYRAEIVIIGGGLSGSSTAFWLKE-RFRDEDFKVVVVENNDVFTKSSTMLSTGGITQQFS 149

Query:   121 LPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLLLA-SEKDAAAMESNVKVQR 179
             +PE + +SLF+  FLR+  E+L ++D+   D+ F P+GYL LA ++++    M S  KVQ
Sbjct:   150 IPEFVDMSLFTTEFLRHAGEHLRILDSEQPDINFFPTGYLRLAKTDEEVEMMRSAWKVQI 209

Query:   180 QEGAKVSLMSPDQLRNKFPWINTEGVALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFC 239
             + GAKV L+S D+L  ++P++N + V LAS G+E+EG  D W LL  +R K  +LGV +
Sbjct:   210 ERGAKVQLLSKDELTKRYPYMNVDDVLLASLGVENEGTIDTWQLLSAIREKNITLGVQYV 269

Query:   240 QGEVTRFVSSSQRM----------LTTDDKAVVLKRIHEVHVKMDRS-LEYQPVECAIVI 288
             +GEV  F     R            T D+  +  +RI  V V+  +     +P+   +++
Sbjct:   270 KGEVEGFQFERHRASSEVHAFGDDATADENKLRAQRISGVLVRPQMNDASARPIRAHLIV 329

Query:   289 NAAGAWSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGLETPLVADTS-G 347
             NAAG W+ Q+A +AG+G+G  G L     +P++PRKR V+V   P  P  + P + D S G
Sbjct:   330 NAAGPWAGQVAKMAGIGKGT-GLL-AVPVPIQPRKRDVFVIFAPDVPS-DLPFIIDPSTG 386

Query:   348 AYFRREGLGSNYLGGRSPTEQEEP--DPANLEVDHDFFQDKVWPHLALRVPAFETLKVQS 405
              + R+    G  +L GR+P+++E+   D +NL+VD+D F  K+WP L  RVP F+T KV+S
Sbjct:   387 VFCRQTDSGQTFLVGRTPSKEEDAKRDHSNLDVDYDDFYQKIWPVLVDRVPGFQTAKVKS 446
```

```
Query:  406 AWAGYYDYNTFDQNGVVGPHPLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTID 465
            AW+GY D NTFD   V+G HPL  N++   GF   G+  +    RA AE +  G +  ++
Sbjct:  447 AWSGYQDINTFDDAPVIGEHPLYTNLHMMCGFGERGVMHSMAAARAYAERIFDGAYINVN 506

Query:  466 LSPFLFTRFYLGEKIQE 482
            L  F   R    + I E
Sbjct:  507 LRKFDMRRIVKMDPITE 523
```

Pedant information for DKFZphutel_20b19, frame 3

Report for DKFZphutel_20b19.3

```
[LENGTH]      486
[MW]          53811.85
[pI]          7.66
[HOMOL]       TREMBL:CEM04B2_4 gene: "M04B2.4"; Caenorhabditis elegans cosmid M04B2 1e-78
[FUNCAT]      c energy conversion   [H. influenzae, HI0499] 8e-05
[BLOCKS]      BL00677A D-amino acid oxidases proteins
[BLOCKS]      BL00623A GMC oxidoreductases proteins
[BLOCKS]      BL01304A
[EC]          1.5.99.2 Dimethylglycine dehydrogenase 2e-07
[PIRKW]       flavoprotein 2e-07
[PIRKW]       oxidoreductase 2e-07
[PROSITE]     MYRISTYL        12
[PROSITE]     CK2_PHOSPHO_SITE       5
[PROSITE]     GLYCOSAMINOGLYCAN      1
[PROSITE]     PKC_PHOSPHO_SITE       6
[KW]          TRANSMEMBRANE  1
[KW]          LOW_COMPLEXITY      7.00 %

SEQ    MIRRVLPHGMGRGLLTRRPGTRRGGFSLDWDGKVSEIKKKIKSILPGRSCDLLQDTSHLP
SEG    .........xxxxxxxxxxxxxxx...........xxxxxxxx................
PRD    ccceeecccccceeeccccccccccccccccchhhhhhhhhcccccceeeccccccc
MEM    ............................................................

SEQ    PEHSDVVIVGGGVLGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICQQFS
SEG    .....xxxxxxxxxxx............................................
PRD    ccccceeeecccccchhhhhhhhhhhhhccccceeeeeeccccccccccccccccceeeec
MEM    .....MMMMMMMMMMMMMMMM.......................................

SEQ    LPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLLLASEKDAAAMESNVKVQRQ
SEG    ............................................................
PRD    ccchhhhhhhhhhhhhhhhhhhhhhhhhcccccceeeccccceeeehhhhhhhhhhhhhhhh
MEM    ............................................................

SEQ    EGAKVSLMSPDQLRNKFPWINTEGVALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQ
SEG    ............................................................
PRD    ccccceeecccchhhhhhccccccccccccccccccccccccchhhhhhhhhhheeeeec
MEM    ............................................................

SEQ    GEVTRFVSSSQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGAWSAQIAA
SEG    ............................................................
PRD    ceeeeecccccccccccchhhhhhhhhheeeeccccccccccceeeeeeeecccchhhhhhh
MEM    ............................................................

SEQ    LAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGLETPLVADTSGAYFRREGLGSNYL
SEG    ............................................................
PRD    hhcccccccccccccccccccceeeeeeeccccccccccceeecccccceeeeccccccee
MEM    ............................................................

SEQ    GGRSPTEQEEPDPANLEVDHDFFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNG
SEG    ............................................................
PRD    ecccccccccccccccccccchhhhhhhhhhhhhhcchhhhhhhhhhheeeeeccccccc
MEM    ............................................................

SEQ    VVGPHPLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPFLFTRFYLGEKI
SEG    ............................................................
PRD    cccccccccceeeeccccccccccchhhhhhhhhhhhhhccceeeecccccccccccccccc
MEM    ............................................................

SEQ    QENNII
SEG    ......
PRD    cccccc
MEM    ......
```

Prosite for DKFZphutel_20b19.3

PS00002	438->442	GLYCOSAMINOGLYCAN	PDOC00002
PS00005	16->19	PKC_PHOSPHO_SITE	PDOC00005
PS00005	21->24	PKC_PHOSPHO_SITE	PDOC00005
PS00005	87->90	PKC_PHOSPHO_SITE	PDOC00005
PS00005	164->167	PKC_PHOSPHO_SITE	PDOC00005
PS00005	250->253	PKC_PHOSPHO_SITE	PDOC00005
PS00005	400->403	PKC_PHOSPHO_SITE	PDOC00005
PS00006	120->124	CK2_PHOSPHO_SITE	PDOC00006
PS00006	164->168	CK2_PHOSPHO_SITE	PDOC00006
PS00006	255->259	CK2_PHOSPHO_SITE	PDOC00006
PS00006	364->368	CK2_PHOSPHO_SITE	PDOC00006
PS00006	366->370	CK2_PHOSPHO_SITE	PDOC00006
PS00008	9->15	MYRISTYL	PDOC00008
PS00008	20->26	MYRISTYL	PDOC00008
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	75->81	MYRISTYL	PDOC00008
PS00008	109->115	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00008	204->210	MYRISTYL	PDOC00008
PS00008	235->241	MYRISTYL	PDOC00008
PS00008	292->298	MYRISTYL	PDOC00008
PS00008	310->316	MYRISTYL	PDOC00008
PS00008	354->360	MYRISTYL	PDOC00008
PS00008	447->453	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_20b19.3)

DKFZphutel_20g21
----

group: signal transduction

DKFZphutel_20g21 encodes a novel 861 amino acid protein with partial similarity to human ras inhibitor and other ras inhibitor proteins.

Ras is a signal transducting molecule involved in the receptor tyrosine kinase/RAS/Map kinase signalling cascade. Ras proteins bind GDP/GTP and show intrinsic GTPase activity. Mutations in ras, which change aa 12, 13 or 61 activate the potential of ras to transform cultured cells and are implicated in a variety of human tumours. The novel protein seems to be a new ras inhibitor protein.

The new protein can find application in modulating/blocking ras dependent signal transduction pathways.

Ras inhibitor

additional 1188 Bp at 5' and 1107 at 3' end in comparison to I22483

Sequenced by AGOWA

Locus: unknown

Insert length: 4137 bp
Poly A stretch at pos. 4116, no polyadenylation signal found

```
   1 GGGAGAACTG AAACAGGAGA TGGTGCGGAC AGATGTCAAC CTGGAAAATG
  51 GCCTGGAACC CGCTGAAACC CACAGCATGG TAAGACACAA GGATGGTGGC
 101 TATTCCGAGG AAGAGGACGT GAAGACCTGT GCCCGGGACT CAGGCTATGA
 151 CAGCCTCTCC AACAGGCTCA GCATCTTGGA CCGGCTCCTC CACACCCACC
 201 CCATATGGCT GCAGCTGAGT CTGAGTGAGG AGGAGGCAGC AGAGGTCCTG
 251 CAGGCCCAGC CTCCGGGGAT CTTCCTGGTT CATAAATCTA CCAAGATGCA
 301 GAAGAAAGTC CTCTCCCTCC GCCTGCCCTG TGAATTTGGG GCCCCACTCA
 351 AGGAATTTGC CATAAAGGAA AGCACATACA CCTTTTCCCT GGAAGGCTCA
 401 GGAATCAGTT TCGCAGATTT ATTCCGGCTC ATTGCTTTCT ACTGCATCAG
 451 CAGGGATGTT CTACCATTTA CCTTGAAGTT GCCTTATGCC ATTTCAACAG
 501 CCAAGTCGGA GGCTCAGCTT GAAGAACTGG CCCAGATGGG ACTAAATTTC
 551 TGGAGCTCCC CAGCTGACAG CAAACCCCCG AACCTTCCAC CTCCCCATAG
 601 GCCTCTTTCC TCCGACGGTG TCTGTCCTGC CTCCCTGCGT CAGCTCTGCC
 651 TTATAAATGG AGTGCATTCT ATCAAAACCA GGACGCCTTC AGAGCTGGAG
 701 TGCAGCCAGA CCAACGGGGC CCTGTGCTTT ATTAATCCCC TTTTCTTGAA
 751 AGTGCACAGC CAGGACCTCA GTGGAGGCCT GAAACGGCCG AGCACAAGGA
 801 CTCCCAACGC GAATGGCACG GAGCGGACTC GGTCCCCCCC ACCCAGGCCC
 851 CCGCCACCCG CTATTAATAG TCTCCACACA AGCCCTCGGC TGGCCAGGAC
 901 TGAAACCCAG ACGAGCATGC CAGAAACAGT CAACCATAAC AAACATGGGA
 951 ACGTAGCTCT GCCTGGAACG AAACCAACTC CCATCCCTCC ACCCCGGCTG
1001 AAGAAGCAGG CTTCTTTTCT GGAAGCAGAG GGCGGTGCAA AGACCTTGAG
1051 CGGCGGCCGG CCGGGCGCAG GCCCGGAGCT GGAGCTGGGC ACAGCTGGCA
1101 GCCCAGGTGG GGCCCCGCCT GAGGCCGCCC CGGGGGATTG CACAAGGGCC
1151 CCGCCGCCCA GCTCTGAATC ACGGCCCCCG TGCCATGGAG GCCGGCAGCG
1201 GCTGAGCGAC ATGAGCATTT CTACTTCCTC CTCCGACTCG CTGGAGTTCG
1251 ACCGGAGCAT GCCTCTGTTT GGCTACGAGG CGGACACCAA CAGCAGCCTG
1301 GAGGACTACG AGGGGGAAAG TGACCAAGAG ACCATGGCGC CCCCCATCAA
1351 GTCCAAAAAG AAAAGGAGCA GCTCCTTCGT GCTGCCCAAG CTCGTCAAGT
1401 CCCAGCTGCA GAAGGTGAGC GGGGTGTTCA GCTCCTTCAT GACCCCGGAG
1451 AAGCGGATGG TCCGCAGGAT CGCCGAGCTT TCCCGGGACA AATGCACCTA
1501 CTTCGGGTGC TTAGTGCAGG ACTACGTGAG CTTCCTGCAG GAGAACAAGG
1551 AGTGCCACGT GTCCAGCACC GACATGCTGC AGACCATCCG GCAGTTCATG
1601 ACCCAGGTCA AGAACTATTT GTCTCAGAGC TCGGAGCTGG ACCCCCCCAT
1651 CGAGTCGCTG ATCCCTGAAG ACCAAATAGA TGTGGTGCTG GAAAAAGCCA
1701 TGCACAAGTG CATCTTGAAG CCCCTCAAGG GGCATGTGGA GGCCATGCTG
1751 AAGGACTTTC ACATGGCCGA TGGCTCATGG AAGCAACTCA AGGAGAACCT
1801 GCAGCTTGTG CGGCAGAGGA ATCCGCAGGA GCTGGGGGTC TTCGCCCCGA
1851 CCCCTGATTT TGTGGATGTG GAGAAAATCA AAGTCAAGTT CATGACCATG
1901 CAGAAGATGT ATTCGCCGGA AAAGAAGGTC ATGCTGCTGC TGCGGGTCTG
1951 CAAGCTCATT TACACGGTCA TGGAGAACAA CTCAGGGAGG ATGTATGGCG
2001 CTGATGACTT CTTGCCAGTC CTGACCTATG TCATAGCCCA GTGTGACATG
2051 CTTGAATTGG ACACTGAAAT CGAGTACATG ATGGAGCTCC TAGACCCATC
2101 GCTGTTACAT GGAGAAGGAG GCTATTACTT GACAAGCGCA TATGGAGCAC
2151 TTTCTCTGAT AAAGAATTTC CAAGAAGAAC AAGCAGCGCG ACTGCTCAGC
2201 TCAGAAACCA GAGACACCCT GAGGCAGTGG CACAAACGGA GAACCACCAA
2251 CCGGACCATC CCCTCTGTGG ACGACTTCCA GAATTACCTC CGAGTTGCAT
2301 TTCAGGAGGT CAACAGTGGT TGCACAGGAA AGACCCTCCT TGTGAGACCT
2351 TACATCACCA CTGAGGATGT GTGTCAGATC TGCGCTGAGA AGTTCAAGGT
2401 GGGGGACCCT GAGGAGTACA GCCTCTTTCT CTTCGTTGAC GAGACATGGC
2451 AGCAGCTGGC AGAGGACACT TACCCTCAAA AAATCAAGGC GGAGCTGCAC
```

```
2501 AGCCGACCAC AGCCCCACAT CTTCCACTTT GTCTACAAAC GCATCAAGAA
2551 CGATCCTTAT GGCATCATTT TCCAGAACGG GGAAGAAGAC CTCACCACCT
2601 CCTAGAAGAC AGGCGGGACT TCCCAGTGGT GCATCCAAAG GGGAGCTGGA
2651 AGCCTTGCCT TCCCGCTTCT ACATGCTTGA GCTTGAAAAG CAGTCACCTC
2701 CTCGGGGACC CCTCAGTGTA GTGACTAAGC CATCCACAGG CCAACTCGGC
2751 CAAGGGCAAC TTTAGCCACG CAAGGTAGCT GAGGTTTGTG AAACAGTAGG
2801 ATTCTCTTTT GGCAATGGAG AATTGCATCT GATGGTTCAA GTGTCCTGAG
2851 ATTGTTTGCT ACCTACCCCC AGTCAGGTTC TAGGTTGGCT TACAGGTATG
2901 TATATGTGCA GAAGAAACAC TTAAGATACA AGTTCTTTTG AATTCAACAG
2951 CAGATGCTTG CGATGCAGTG CGTCAGGTGA TTCTCACTCC TGTGGATGGC
3001 TTCATCCCTG CCTTCCTTCC TTTCTTTTTC CTTTTTTTTT TTTTTTTTTT
3051 TTTTTACAAA GAGCCTTCAT GTTTTTATAT ATTTCATAGA AATTTTTATA
3101 GCAGTTGCAG GTAAACTGTC AGGATTGGTT TTAAAATATT TTTGTAACTT
3151 TAAAATATTC TATAATTATG CATGTGATTT TAACATTTAA TATTCAAAAA
3201 TAAATCTCTT GCTGGATTTG AGAGTATTGC ATTTTTAAAG TCTCTCTTCT
3251 GTAACTGGAT GTTTTGGCAA CTTTGTGGGG AGAGACTGCT GGATTTCTTA
3301 AAGCAACGTA TTCCTGACAC TGGCCACAGA ATGCCTTTGG AAATCGGATG
3351 TACTGTTCTC TTGTTCACGT TTAGTGGTGT TTTGCTGTTT TGTTTTTTAA
3401 ACAAATGATG CTGAGAATAA GGAGAGAAAT GAATGTAGAG AGAGGTAGAG
3451 AGAGAAATAT GAACTCTAAC AAAGGACTGA GGAGTGCAGT CTGCTGGTTC
3501 AGGCTCTTCA AAAGATGTAG AAAAAGAGAT AGAAGGAACC ACCTATGCTT
3551 AAAATACTGT AAATATGCAG TGAGGTTTGG CAAAATCTAT TCCATGTGTG
3601 ATTTGCTTGT AGAAACAATT TTGAAAGCCC CTTGAGGAAA ATAAAAATCA
3651 AGAAGAACAC TTTTCTCCCT TTTCCATACA AATTAAAACT TAACAGCATC
3701 AAATTATTGG GACCAGAAAC CAAGTAATGT ATAATGTGGC TTTTGTTGAG
3751 TTAAATAAGA TGCTATATAA TGGAGAAGAA TTTGAAAATG CACAAAAAAA
3801 TCAATCTACA TTATCAGAAC CTGCAGTGAA ATTAAACTTA TGTTAAATAA
3851 AACCAGTTTG CAGGTGCACA AACTATGAGG GTCTTGTATC CACGTAACAC
3901 AGGTAGTTAC AAAAACATGT TATTGTACTG TGTAAAGATG CATAGTCATC
3951 TCATTTGGTT GGCTTTGTAC CTTGTACCTT TTTTAGCCTT GGCTTTTGTT
4001 GAACTAGAAC CCTCAGCACA TACTGTGTTG TACTTTTGTA AATGATTTTT
4051 TAAATGGAAT TTTGCACATA ATACATTGTA ATACTGTATG ATAATCATGT
4101 GTGAAAATAA TTTTTGAAAT AAAAAAAAAA AAAAAAA
```

BLAST Results

Entry I22483 from database EMBL:
Sequence 15 from patent US 5527896.
Length = 1829
Plus Strand HSPs:
Score = 9097 (1364.9 bits), Expect = 0.0, P = 0.0
Identities = 1821/1823 (99%), Positives = 1821/1823 (99%),

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 20 bp to 2602 bp; peptide length: 861
Category: known protein
Classification: Cell signaling/communication

```
  1 MVRTDVNLEN GLEPAETHSM VRHKDGGYSE EEDVKTCARD SGYDSLSNRL
 51 SILDRLLHTH PIWLQLSLSE EEAAEVLQAQ PPGIFLVHKS TKMQKKVLSL
101 RLPCEFGAPL KEFAIKESTY TFSLEGSGIS FADLFRLIAF YCISRDVLPF
151 TLKLPYAIST AKSEAQLEEL AQMGLNFWSS PADSKPPNLP PPHRPLSSDG
201 VCPASLRQLC LINGVHSIKT RTPSELECSQ TNGALCFINP LFLKVHSQDL
251 SGGLKRPSTR TPNANGTERT RSPPPRPPPP AINSLHTSPR LARTETQTSM
301 PETVNHNKHG NVALPGTKPT PIPPPRLKKQ ASFLEAEGGA KTLSGGRPGA
351 GPELELGTAG SPGGAPPEAA PGDCTRAPPP SSESRPPCHG GRQRLSDMSI
401 STSSSDSLEF DRSMPLFGYE ADTNSSLEDY EGESDQETMA PPIKSKKKRS
451 SSFVLPKLVK SQLQKVSGVF SSFMTPEKRM VRRIAELSRD KCTYFGCLVQ
501 DYVSFLQENK ECHVSSTDML QTIRQFMTQV KNYLSQSSEL DPPIESLIPE
551 DQIDVVLEKA MHKCILKPLK GHVEAMLKDF HMADGSWKQL KENLQLVRQR
601 NPQELGVFAP TPDFVDVEKI KVKFMTMQKM YSPEKKVMLL LRVCKLIYTV
651 MENNSGRMYG ADDFLPVLTY VIAQCDMLEL DTEIEYMMEL LDPSLLHGEG
701 GYYLTSAYGA LSLIKNFQEE QAARLLSSET RDTLRQWHKR RTTNRTIPSV
751 DDFQNYLRVA FQEVNSGCTG KTLLVRPYIT TEDVCQICAE KFKVGDPEEY
801 SLFLFVDETW QQLAEDTYPQ KIKAELHSRP QPHIFHFVYK RIKNDPYGII
851 FQNGEEDLTT S
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_20g21, frame 2

TREMBL:RNU80076_1 product: "RIN1"; Rattus norvegicus RIN1 mRNA, complete cds., N = 3, Score = 606, P = 6.8e-97

PIR:A38637 Ras interactor RIN1 - human, N = 3, Score = 587, P = 1.9e-92

TREMBL:HSRASINL_1 product: "ras inhibitor"; Human ras inhibitor mRNA, 3' end., N = 2, Score = 592, P = 9.8e-61

SWISSPROT:RIN1_HUMAN RAS INTERACTION/INTERFERENCE PROTEIN 1 (RAS INHIBITOR JC99) (FRAGMENT)., N = 2, Score = 587, P = 4.1e-60

PIR:B38637 Ras inhibitor (clone JC265) - human (fragment), N = 1, Score = 2446, P = 4.6e-254

```
>PIR:B38637 Ras inhibitor (clone JC265) - human (fragment)
           Length = 471

  HSPs:

 Score = 2446 (367.0 bits), Expect = 4.6e-254, P = 4.6e-254
 Identities = 471/471 (100%), Positives = 471/471 (100%)

Query:   391 GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS 450
             GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS
Sbjct:     1 GRQRLSDMSISTSSSDSLEFDRSMPLFGYEADTNSSLEDYEGESDQETMAPPIKSKKKRS 60

Query:   451 SSFVLPKLVKSQLQKVSGVFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK 510
             SSFVLPKLVKSQLQKVSGVFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK
Sbjct:    61 SSFVLPKLVKSQLQKVSGVFSSFMTPEKRMVRRIAELSRDKCTYFGCLVQDYVSFLQENK 120

Query:   511 ECHVSSTDMLQTIRQFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK 570
             ECHVSSTDMLQTIRQFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK
Sbjct:   121 ECHVSSTDMLQTIRQFMTQVKNYLSQSSELDPPIESLIPEDQIDVVLEKAMHKCILKPLK 180

Query:   571 GHVEAMLKDFHMADGSWKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM 630
             GHVEAMLKDFHMADGSWKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM
Sbjct:   181 GHVEAMLKDFHMADGSWKQLKENLQLVRQRNPQELGVFAPTPDFVDVEKIKVKFMTMQKM 240

Query:   631 YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYVIAQCDMLELDTEIEYMMEL 690
             YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYVIAQCDMLELDTEIEYMMEL
Sbjct:   241 YSPEKKVMLLLRVCKLIYTVMENNSGRMYGADDFLPVLTYVIAQCDMLELDTEIEYMMEL 300

Query:   691 LDPSLLHGEGGYYLTSAYGALSLIKNFQEEQAARLLSSETRDTLRQWHKRRTTNRTIPSV 750
             LDPSLLHGEGGYYLTSAYGALSLIKNFQEEQAARLLSSETRDTLRQWHKRRTTNRTIPSV
Sbjct:   301 LDPSLLHGEGGYYLTSAYGALSLIKNFQEEQAARLLSSETRDTLRQWHKRRTTNRTIPSV 360

Query:   751 DDFQNYLRVAFQEVNSGCTGKTLLVRPYITTEDVCQICAEKFKVGDPEEYSLFLFVDETW 810
             DDFQNYLRVAFQEVNSGCTGKTLLVRPYITTEDVCQICAEKFKVGDPEEYSLFLFVDETW
Sbjct:   361 DDFQNYLRVAFQEVNSGCTGKTLLVRPYITTEDVCQICAEKFKVGDPEEYSLFLFVDETW 420

Query:   811 QQLAEDTYPQKIKAELHSRPQPHIFHFVYKRIKNDPYGIIFQNGEEDLTTS 861
             QQLAEDTYPQKIKAELHSRPQPHIFHFVYKRIKNDPYGIIFQNGEEDLTTS
Sbjct:   421 QQLAEDTYPQKIKAELHSRPQPHIFHFVYKRIKNDPYGIIFQNGEEDLTTS 471
```

Pedant information for DKFZphutel_20g21, frame 2

Report for DKFZphutel_20g21.2

[LENGTH]	861
[MW]	96380.26
[pI]	6.15
[HOMOL]	PIR:B38637 Ras inhibitor (clone JC265) - human (fragment) 0.0
[FUNCAT]	08.13 vacuolar transport [S. cerevisiae, YML097c] 3e-10
[FUNCAT]	06.04 protein targeting, sorting and translocation [S. cerevisiae, YML097c] 3e-10
[FUNCAT]	30.03 organization of cytoplasm [S. cerevisiae, YML097c] 3e-10
[FUNCAT]	08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YML097c] 3e-10
[PIRKW]	alternative splicing 3e-59
[SUPFAM]	Ras interactor RIN1 3e-59

```
[KW]          All_Alpha
[KW]          LOW_COMPLEXITY    11.27 %

SEQ     MVRTDVNLENGLEPAETHSMVRHKDGGYSEEEDVKTCARDSGYDSLSNRLSILDRLLHTH
SEG     ............................................................
PRD     ccccceeeccccccccceeeeeeccccccccccceeeeeeccccccchhhhhhhhhhhhhh

SEQ     PIWLQLSLSEEEAAEVLQAQPPGIFLVHKSTKMQKKVLSLRLPCEFGAPLKEFAIKESTY
SEG     ...xxxxxxxxxxxxxxxxx........................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhhccccceeeeechhhhhhhhhhhccccccceeeeecc

SEQ     TFSLEGSGISFADLFRLIAFYCISRDVLPFTLKLPYAISTAKSEAQLEELAQMGLNFWSS
SEG     ............................................................
PRD     ceeecccccchhhhhhhhhhhhhhcceeeeeeecccchhhhhhhhhhhhhhhhhhcccccc

SEQ     PADSKPPNLPPPHRPLSSDGVCPASLRQLCLINGVHSIKTRTPSELECSQTNGALCFINP
SEG     .....xxxxxxxxxx.............................................
PRD     ccccccccccccccccccccccchhhhhcccccccccccccccccccccccccceeeecc

SEQ     LFLKVHSQDLSGGLKRPSTRTPNANGTERTRSPPPRPPPPAINSLHTSPRLARTETQTSM
SEG     ................................xxxxxxxx....................
PRD     cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc

SEQ     PETVNHNKHGNVALPGTKPTPIPPPRLKKQASFLEAEGGAKTLSGGRPGAGPELELGTAG
SEG     ..............xxxxxxxxxxx.................................xx
PRD     eeeecccccccccccccccccccccchhhhhhhhhhccccccccccccccccceeeeccc

SEQ     SPGGAPPEAAPGDCTRAPPPSSESRPPCHGGRQRLSDMSISTSSSDSLEFDRSMPLFGYE
SEG     xxxxxxxxxxxx....xxxxxxxxxxx........xxxxxxxxxxxxxxxxxx.......
PRD     ccccccccccccccccccccccccccccccccccccccccccccceeeccccccccccceee

SEQ     ADTNSSLEDYEGESDQETMAPPIKSKKKRSSSFVLPKLVKSQLQKVSGVFSSFMTPEKRM
SEG     .......................xxxxxxxxx............................
PRD     ccccccccccccccccccccccccccccccccccccchhhhhhhhhhhhhhhhhcchhhhh

SEQ     VRRIAELSRDKCTYFGCLVQDYVSFLQENKECHVSSTDMLQTIRQFMTQVKNYLSQSSEL
SEG     ............................................................
PRD     hhhhhhhhhchhhhhhhhhhhhhhhhhccccccccchhhhhhhhhhhhhhhhhhhhhhcc

SEQ     DPPIESLIPEDQIDVVLEKAMHKCILKPLKGHVEAMLKDFHMADGSWKQLKENLQLVRQR
SEG     ............................................................
PRD     ccccccccccchhhhhhhhhhhhcccccchhhhhhhhhhhhhcccccchhhhhhhhhhhhhh

SEQ     NPQELGVFAPTPDFVDVEKIKVKFMTMQKMYSPEKKVMLLLRVCKLIYTVMENNSGRMYG
SEG     ............................................................
PRD     ccccccccccccccchhhhhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhcccccc

SEQ     ADDFLPVLTYVIAQCDMLELDTEIEYMMELLDPSLLHGEGGYYLTSAYGALSLIKNFQEE
SEG     ............................................................
PRD     cccccccceeecccchhhhhhhhhhhhhhhcccccccccccceeeeehhhhhhhhhhhhhh

SEQ     QAARLLSSETRDTLRQWHKRRTTNRTIPSVDDFQNYLRVAFQEVNSGCTGKTLLVRPYIT
SEG     ............................................................
PRD     hhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhhhhhhhccccccccceeeeeccccccc

SEQ     TEDVCQICAEKFKVGDPEEYSLFLFVDETWQQLAEDTYPQKIKAELHSRPQPHIFHFVYK
SEG     ............................................................
PRD     chhhhhhhhheeecccccceeeeehhhhhcccccccchhhhhhhhhhhhccccceeeehhh

SEQ     RIKNDPYGIIFQNGEEDLTTS
SEG     .....................
PRD     hhccccceeeeeccccccccc
```

(No Prosite data available for DKFZphutel_20g21.2)

(No Pfam data available for DKFZphutel_20g21.2)

DKFZphutel_20h13
----

group: intracellular transport and trafficking

DKFZphutel_20h13 encodes a novel 955 amino acid protein with similarity to alpha-adaptins.

Adaptins are components of the adaptor complexes which link clathrin to receptors in coated vesicles. The alpha-adaptins, which are found exclusively in endocytic coated vesicles, separate into two bands on SDS gels, designated A and C. The novel protein is very similar to both alpha adaptin A and C. The novel protein is a new human alpha-adaptin.

The new protein can find application in modulating endocytosis and vesicle trafficking in cells.

strong similarity to alpha-adaptins

complete cDNA, complete cds start at Bp 78, EST hits

Sequenced by AGOWA

Locus: unknown

Insert length: 3352 bp
Poly A stretch at pos. 3297, polyadenylation signal at pos. 3279

```
   1 GCGCCCGGTC CCCGCTTGCC AGCCCCCGCT GCTCTGTGCC CTGTCCGGCC
  51 AGGCCTGGAG CCGACACCAC CGCCATCATG CCGGCCGTGT CCAAGGGCGA
 101 TGGGATGCGG GGGCTCGCGG TGTTCATCTC CGACATCCGG AACTGTAAGA
 151 GCAAAGAGGC GGAAATTAAG AGAATCAACA AGGAACTGGC CAACATCCGC
 201 TCCAAGTTCA AAGGAGACAA AGCCTTGGAT GGCTACAGTA AGAAAAAATA
 251 TGTGTGTAAA CTGCTTTTCA TCTTCCTGCT TGGCCATGAC ATTGACTTTG
 301 GGCACATGGA GGCTGTGAAT CTGTTGAGTT CCAATAAATA CACAGAGAAG
 351 CAAATAGGTT ACCTGTTCAT TTCTGTGCTG GTGAACTCGA ACTCGGAGCT
 401 GATCCGCCTC ATCAACAACG CCATCAAGAA TGACCTGGCC AGCCGCAACC
 451 CCACCTTCAT GTGCCTGGCC CTGCACTGCA TCGCCAACGT GGGCAGCCGG
 501 GAGATGGGCG AGGCCTTTGC CGCTGACATC CCCCGCATCC TGGTGGCCGG
 551 GGACAGCATG GACAGTGTCA AGCAGAGTGC GGCCCTGTGC CTCCTTCGAC
 601 TGTACAAGGC CTCGCCTGAC CTGGTGCCCA TGGGCGAGTG GACGGCGCGT
 651 GTGGTACACC TGCTCAATGA CCAGCACATG GGTGTGGTCA CGGCCGCCGT
 701 CAGCCTCATC ACCTGTCTCT GCAAGAAGAA CCCAGATGAC TTCAAGACGT
 751 GCGTCTCTCT GGCTGTGTCG CGCCTGAGCC GGATCGTCTC CTCTGCCTCC
 801 ACCGACCTCC AGGACTACAC CTACTACTTC GTCCCAGCAC CCTGGCTCTC
 851 GGTGAAGCTC CTGCGGCTGC TGCAGTGCTA CCCGCCTCCA GAGGATGCGG
 901 CTGTGAAGGG GCGGCTGGTG GAATGTCTGG AGACTGTGCT CAACAAGGCC
 951 CAGGAGCCCC CCAAATCCAA GAAGGTGCAG CATTCCAACG CCAAGAACGC
1001 CATCCTCTTC GAGACCATCA GCCTCATCAT CCACTATGAC AGTGAGCCCA
1051 ACCTCCTGGT TCGGGCCTGC AACCAGCTGG GCCAGTTCCT GCAGCACCGG
1101 GAGACCAACC TGCGCTACCT GGCCCTGGAG AGCATGTGCA CGCTGGCCAG
1151 CTCCGAGTTC TCCCATGAAG CCGTCAAGAC GCACATTGAC ACCGTCATCA
1201 ATGCCCTCAA GACGGAGCGG GACGTCAGCG TGCGGCAGCG GGCGGCTGAC
1251 CTCCTCTACG CCATGTGTGA CCGGAGCAAT GCCAAGCAGA TCGTGTCGGA
1301 GATGCTGCGG TACCTGGAGA CGGCAGACTA CGCCATCCGC GAGGAGATCG
1351 TCCTGAAGGT GGCCATCCTG GCCGAGAAGT ACGCCGTGGA CTACAGCTGG
1401 TACGTGGACA CCATCCTCAA CCTCATCCGC ATTGCGGGCG ACTACGTGAG
1451 TGAGGAGGTG TGGTACCGTG TGCTACAGAT CGTCACCAAC CGTGATGACG
1501 TCCAGGGCTA TGCCGCCAAG ACCGTCTTTG AGGCGCTCCA GGCCCCTGCC
1551 TGTCACGAGA ACATGGTGAA GGTTGGCGGC TACATCCTTG GGGAGTTTGG
1601 GAACCTGATT GCTGGGGACC CCCGCTCCAG CCCCCCAGTG CAGTTCTCCC
1651 TGCTCCACTC CAAGTTCCAT CTGTGCAGCG TGGCCACGCG GGCGCTGCTG
1701 CTGTCCACCT ACATCAAGTT CATCAACCTC TTCCCCGAGA CCAAGGCCAC
1751 CATCCAGGGC GTCCTGCGGG CCGGCTCCCA GCTGCGCAAT GCTGACGTGG
1801 AGCTGCAGCA GCGAGCCGTG GAGTACCTCA CCCTCAGCTC AGTGGCCAGC
1851 ACCGACGTCC TGGCCACGGT GCTGGAGGAG ATGCCGCCCT TCCCCGAGCG
1901 CGAGTCGTCC ATCCTGGCCA AGCTGAAACG CAAGAAGGGG CCAGGGGCCG
1951 GCAGCGCCCT GGACGATGGC CGGAGGGACC CCAGCAGCAA CGACATCAAC
2001 GGGGGCATGG AGCCCACCCC CAGCACTGTG TCGACGCCCT CGCCCTCCGC
2051 CGACCTCCTG GGGCTGCGGG CAGCCCCTCC CCCGGCAGCA CCCCCGGCTT
2101 CTGCAGGAGC AGGGAACCTT CTGGTGGACG TCTTCGATGG CCCGGCCGCC
2151 CAGCCCAGCC TGGGGCCCAC CCCCGAGGAG GCCTTCCTCA GCCCAGGTCC
2201 TGAGGACATC GGCCCTCCCA TTCCGGAAGC CGATGAGTTG CTGAATAAGT
2251 TTGTGTGTAA GAACAACGGG GTCCTGTTCG AGAACCAGCT GCTGCAGATC
2301 GGAGTCAAGT CAGAGTTCCG ACAGAACCTG GGCCGCATGT ATCTCTTCTA
2351 TGGCAACAAG ACCTCGGTGC AGTTCCAGAA TTTCTCACCC ACTGTGGTTC
2401 ACCCGGGAGA CCTCCAGACT CAGCTGGCTG TGCAGACCAA GCGCGTGGCG
2451 GCGCAGGTGG ACGGCGGCGC GCAGGTGCAG CAGGTGCTCA ATATCGAGTG
2501 CCTGCGGGAC TTCCTGACGC CCCCGCTGCT GTCCGTGCGC TTCCGGTACG
2551 GTGGCGCCCC CCAGGCCCTC ACCCTGAAGC TCCCAGTGAC CATCAACAAG
```

```
2601 TTCTTCCAGC CCACCGAGAT GGCGGCCCAG GATTTCTTCC AGCGCTGGAA
2651 GCAGCTGAGC CTCCCTCAAC AGGAGGCGCA GAAAATCTTC AAAGCCAACC
2701 ACCCCATGGA CGCAGAAGTT ACTAAGGCCA AGCTTCTGGG GTTTGGCTCT
2751 GCTCTCCTGG ACAATGTGGA CCCCAACCCT GAGAACTTCG TGGGGGCGGG
2801 GATCATCCAG ACTAAAGCCC TGCAGGTGGG CTGTCTGCTT CGGCTGGAGC
2851 CCAATGCCCA GGCCCAGATG TACCGGCTGA CCCTGCGCAC CAGCAAGGAG
2901 CCCGTCTCCC GTCACCTGTG TGAGCTGCTG GCACAGCAGT TCTGAGCCCT
2951 GGACTCTGCC CCGGGGGATG TGGCCGGCAC TGGGCAGCCC CTTGGACTGA
3001 GGCAGTTTTG GTGGATGGGG GACCTCCACT GGTGACAGAG AAGACACCAG
3051 GGTTTGGGGG ATGCCTGGGA CTTTCCTCCG GCCTTTTGTA TTTTTATTTT
3101 TGTTCATCTG CTGCTGTTTA CATTCTGGGG GGTTAGGGGG AGTCCCCCTC
3151 CCTCCCTTTC CCCCCCAAGC ACAGAGGGGA GAGGGGCCAG GGAAGTGGAT
3201 GTCTCCTCCC CTCCCACCCC ACCCTGTTGT AGCCCCTCCT ACCCCCTCCC
3251 CATCCAGGGG CTGTGTATTA TTGTGAGCGA ATAAACAGAG AGACGCTAAA
3301 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3351 AA
```

BLAST Results

No BLAST result

Medline entries

89155572:
Cloning of cDNAs encoding two related 100-kD coated vesicle proteins (alpha-adaptins).

97431776:
Alpha-adaptin, a marker for endocytosis, is expressed in complex patterns during Drosophila development.

Peptide information for frame 3

ORF from 78 bp to 2942 bp; peptide length: 955
Category: strong similarity to known protein

```
  1 MPAVSKGDGM RGLAVFISDI RNCKSKEAEI KRINKELANI RSKFKGDKAL
 51 DGYSKKKYVC KLLFIFLLGH DIDFGHMEAV NLLSSNKYTE KQIGYLFISV
101 LVNSNSELIR LINNAIKNDL ASRNPTFMCL ALHCIANVGS REMGEAFAAD
151 IPRILVAGDS MDSVKQSAAL CLLRLYKASP DLVPMGEWTA RVVHLLNDQH
201 MGVVTAAVSL ITCLCKKNPD DFKTCVSLAV SRLSRIVSSA STDLQDYTYY
251 FVPAPWLSVK LLRLLQCYPP PEDAAVKGRL VECLETVLNK AQEPPKSKKV
301 QHSNAKNAIL FETISLIIHY DSEPNLLVRA CNQLGQFLQH RETNLRYLAL
351 ESMCTLASSE FSHEAVKTHI DTVINALKTE RDVSVRQRAA DLLYAMCDRS
401 NAKQIVSEML RYLETADYAI REEIVLKVAI LAEKYAVDYS WYVDTILNLI
451 RIAGDYVSEE VWYRVLQIVT NRDDVQGYAA KTVFEALQAP ACHENMVKVG
501 GYILGEFGNL IAGDPRSSPP VQFSLLHSKF HLCSVATRAL LLSTYIKFIN
551 LFPETKATIQ GVLRAGSQLR NADVELQQRA VEYLTLSSVA STDVLATVLE
601 EMPPFPERES SILAKLKRKK GPGAGSALDD GRRDPSSNDI NGGMEPTPST
651 VSTPSPSADL LGLRAAPPPA APPASAGAGN LLVDVFDGPA AQPSLGPTPE
701 EAFLSPGPED IGPPIPEADE LLNKFVCKNN GVLFENQLLQ IGVKSEFRQN
751 LGRMYLFYGN KTSVQFQNFS PTVVHPGDLQ TQLAVQTKRV AAQVDGGAQV
801 QQVLNIECLR DFLTPPLLSV RFRYGGAPQA LTLKLPVTIN KFFQPTEMAA
851 QDFFQRWKQL SLPQQEAQKI FKANHPMDAE VTKAKLLGFG SALLDNVDPN
901 PENFVGAGII QTKALQVGCL LRLEPNAQAQ MYRLTLRTSK EPVSRHLCEL
951 LAQQF
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_20h13, frame 3

PIR:B30111 alpha-adaptin C - mouse, N = 1, Score = 3990, P = 0

PIR:S11276 alpha-adaptin c - rat, N = 1, Score = 3987, P = 0

SWISSPROT:ADAC_RAT ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)., N = 1, Score = 3982, P = 0

SWISSPROT:ADAC_MOUSE ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT)., N = 1, Score = 3976, P = 0

TREMBL:AB020706_1 gene: "KIAA0899"; product: "KIAA0899 protein"; Homo sapiens mRNA for KIAA0899 protein, partial cds., N = 1, Score = 3932, P = 0

```
>PIR:B30111 alpha-adaptin C - mouse
           Length = 938

  HSPs:

 Score = 3990 (598.6 bits), Expect = 0.0e+00, P = 0.0e+00
 Identities = 787/955 (82%), Positives = 858/955 (89%)

Query:     1 MPAVSKGDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC 60
             MPAVSKGDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC
Sbjct:     1 MPAVSKGDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC 60

Query:    61 KLLFIFLLGHDIDFGHMEAVNLLSSNKYTEKQIGYLFISVLVNSNSELIRLINNAIKNDL 120
             KLLFIFLLGHDIDFGHMEAVNLLSSN+YTEKQIGYLFISVLVNSNSELIRLINNAIKNDL
Sbjct:    61 KLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIGYLFISVLVNSNSELIRLINNAIKNDL 120

Query:   121 ASRNPTFMCLALHCIANVGSREMGEAFAADIPRILVAGDSMDSVKQSAALCLLRLYKASP 180
             ASRNPTFM LALHCIANVGSREM EAFA +IP+ILVAGD+MDSVKQSAALCLLRLY+ SP
Sbjct:   121 ASRNPTFMGLALHCIANVGSREMAEAFAGEIPKILVAGDTMDSVKQSAALCLLRLYRTSP 180

Query:   181 DLVPMGEWTARVVHLLNDQHMGVVTAAVSLITCLCKKNPDDFKTCVSLAVSRLSRIVSSA 240
             DLVPMG+WT+RVVHLLNDQH+GVVTAA SLIT L +KNP++FKT VSLAVSRLSRIV+SA
Sbjct:   181 DLVPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSVSLAVSRLSRIVTSA 240

Query:   241 STDLQDYTYYFVPAPWLSVKLLRLLQCYPPPEDAAVKGRLVECLETVLNKAQEPPKSKKV 300
             STDLQDYTYYFVPAPWLSVKLLRLLQCYPPP D AV+GRL ECLET+LNKAQEPPKSKKV
Sbjct:   241 STDLQDYTYYFVPAPWLSVKLLRLLQCYPPP-DPAVRGRLTECLETILNKAQEPPKSKKV 299

Query:   301 QHSNAKNAILFETISLIIHYDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLASSE 360
             QHSNAKNA+LFE ISLIIH+DSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLASSE
Sbjct:   300 QHSNAKNAVLFEAISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLASSE 359

Query:   361 FSHEAVKTHIDTVINALKTERDVSVRQRAADLLYAMCDRSNAKQIVSEMLRYLETADYAI 420
             FSHEAVKTHI+TVINALKTERDVSVRQRA DLLYAMCDRSNA+QIV+EML YLETADY+I
Sbjct:   360 FSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSNAQQIVAEMLSYLETADYSI 419

Query:   421 REEIVLKVAILAEKYAVDYSWYVDTILNLIRIAGDYVSEEVWYRVLQIVTNRDDVQGYAA 480
             REEIVLKVAILAEKYAVDY+WYVDTILNLIRIAGDYVSEEVWYRV+QIV NRDDVQGYAA
Sbjct:   420 REEIVLKVAILAEKYAVDYTWYVDTILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAA 479

Query:   481 KTVFEALQAPACHENMVKVGGYILGEFGNLIAGDPRSSPPVQFSLLHSKFHLCSVATRAL 540
             KTVFEALQAPACHEN+VKVGGYILGEFGNLIAGDPRSSP +QF+LLHSKFHLCSV TRAL
Sbjct:   480 KTVFEALQAPACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFNLLHSKFHLCSVPTRAL 539

Query:   541 LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYLTLSSVASTDVLATVLE 600
             LLSTYIKF+NLFPE KATIQ VLR+ SQL+NADVELQQRAVEYL LS+VASTD+LATVLE
Sbjct:   540 LLSTYIKFVNLFPEVKATIQDVLRSDSQLKNADVELQQRAVEYLRLSTVASTDILATVLE 599

Query:   601 EMPPFPERESSILAKLKRKKGPGAGSALDDGRRDPSSNDINGGMEPTP---STVSTPSPS 657
             EMPPFPERESSILAKLK+KKGP   + L++ +R+ S  D+NGG EP P   S  STPSPS
Sbjct:   600 EMPPFPERESSILAKLKKKKGPSTVTDLEETKRERSI-DVNGGPEPVPASTSAASTPSPS 658

Query:   658 ADLLGLRAAPP-PAAPPASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP 716
             ADLLGL A PP P  PP S+G G LLVDVF   A+  ++ P      L+PG ED
Sbjct:   659 ADLLGLGAVPPAPTGPPPSSGGG-LLVDVFSDSAS--AVAP------LAPGSEDN----- 704

Query:   717 EADELLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGNKTSVQFQNFSPTVVHP 776
                    +FVCKNNGVLFENQLLQIG+KSEFRQNLGRM++FYGNKTS QF NF+PT++
Sbjct:   705 -----FARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPTLICA 759

Query:   777 GDLQTQLAVQTKRVAAQVDGGAQVQQVLNIECLRDFLTPPLLSVRFRYGGAPQALTLKLP 836
              DLQT L +QTK V   VDGGAQVQQV+NIEC+ DF   P+L+++FRYGG  Q +++KLP
Sbjct:   760 DDLQTNLNLQTKPVDPTVDGGAQVQQVVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLP 819

Query:   837 VTINKFFQPTEMAAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSALLDN 896
             +T+NKFFQPTEMA+QDFFQRWKQLS PQQE Q IFKA HPMD E+TKAK++GFGSALL+
Sbjct:   820 ITLNKFFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEE 879

Query:   897 VDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRHLCELLAQQF 955
             VDPNP NFVGAGII TK  Q+GCLLRLEPN QAQMYRLTLRTSK+ VS+ LCELL++QF
```

```
Sbjct:   880 VDPNPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF 938
```

Pedant information for DKFZphutel_20h13, frame 3

Report for DKFZphutel_20h13.3

```
[LENGTH]        955
[MW]            105361.97
[pI]            7.75
[HOMOL]         PIR:A30111 alpha-adaptin A - mouse 0.0
[FUNCAT]        30.09 organization of intracellular transport vesicles      [S. cerevisiae,
YBL037w] 5e-67
[FUNCAT]        08.19 cellular import [S. cerevisiae, YBL037w] 5e-67
[FUNCAT]        06.10 assembly of protein complexes   [S. cerevisiae, YBL037w] 5e-67
[FUNCAT]        08.07 vesicular transport (golgi network, etc.)      [S. cerevisiae, YDR238c]
4e-04
[PIRKW]         heterodimer 0.0
[PIRKW]         transmembrane protein 1e-65
[PIRKW]         membrane trafficking 0.0
[PIRKW]         receptor 0.0
[SUPFAM]        beta-adaptin 5e-16
[PROSITE]       MYRISTYL        7
[PROSITE]       IG_MHC  1
[PROSITE]       AMIDATION       1
[PROSITE]       CK2_PHOSPHO_SITE        11
[PROSITE]       TYR_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        15
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY     6.81 %

SEQ    MPAVSKGDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKALDGYSKKKYVC
SEG    ............................................................
PRD    ccccccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhhh

SEQ    KLLFIFLLGHDIDFGHMEAVNLLSSNKYTEKQIGYLFISVLVNSNSELIRLINNAIKNDL
SEG    ............................................................
PRD    hhhhhhccccccchhhhhhhhhcccccchhhhhhhhhhhhhcchhhhhhhhhhhhhhhcc

SEQ    ASRNPTFMCLALHCIANVGSREMGEAFAADIPRILVAGDSMDSVKQSAALCLLRLYKASP
SEG    ............................................................
PRD    cccccchhhhhhhhhhcchhhhhhhhhhhhhheeecccccchhhhhhhhhhhhhhhhhcc

SEQ    DLVPMGEWTARVVHLLNDQHMGVVTAAVSLITCLCKKNPDDFKTCVSLAVSRLSRIVSSA
SEG    ............................................................
PRD    cccccccchhhhhhhhhcccceeeehhhhhhhhhhhcccchhhhhhhhhhhhhhhhhhcc

SEQ    STDLQDYTYYFVPAPWLSVKLLRLLQCYPPPEDAAVKGRLVECLETVLNKAQEPPKSKKV
SEG    ............................................................
PRD    ccccccceeeecccchhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhccccccc

SEQ    QHSNAKNAILFETISLIIHYDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLASSE
SEG    ............................................................
PRD    cccccchhhhhhhhhhhhhcccccceeeehhhhhhhhhhcccccceeeehhhhhhhhhcc

SEQ    FSHEAVKTHIDTVINALKTERDVSVRQRAADLLYAMCDRSNAKQIVSEMLRYLETADYAI
SEG    ............................................................
PRD    cchhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhhhhccchhhhhhhhhhhhhcccch

SEQ    REEIVLKVAILAEKYAVDYSWYVDTILNLIRIAGDYVSEEVWYRVLQIVTNRDDVQGYAA
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhcchhhhhhhhhhhhhhhcccccchhhhhhhhheeecccccchhhhh

SEQ    KTVFEALQAPACHENMVKVGGYILGEFGNLIAGDPRSSPPVQFSLLHSKFHLCSVATRAL
SEG    ............................................................
PRD    hhhhhhhhhhcccccceeeeeeeeccccccccccccccchhhhhhhhhhhhcccchhhhh

SEQ    LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYLTLSSVASTDVLATVLE
SEG    ............................................................
PRD    hhhhhhhhhhcccccchhhhhhhhhhhhccccchhhhhhhhhhhhhhhhhhhcchhhhhhhhhh

SEQ    EMPPFPERESSILAKLKRKKGPGAGSALDDGRRDPSSNDINGGMEPTPSTVSTPSPSADL
SEG    .............................................xxxxxxxxxxxxxxx
PRD    hccccccchhhhhhhhhhhccccccccccccccccccccccccccccccccccccccce

SEQ    LGLRAAPPPAAPPASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIPEADE
SEG    xxxxxxxxxxxxxxxxxxxxx........................xxxxxxxxxxxxxx.
```

```
PRD    eeccccccccccccccccccc eeeeeecccccccccccccceeeccccccccccccccccc
```

PRD	eecccccccccccccccccceeeeeecccccccccccccceeeccccccccccccccccc	
SEQ	LLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGNKTSVQFQNFSPTVVHPGDLQ	
SEG	....	
PRD	cceeeeecccccchhhhhhhcchhhhhcccccceeeccccccccccccceeeeeccchhh	
SEQ	TQLAVQTKRVAAQVDGGAQVQQVLNIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTIN	
SEG	.........xxxxxxxxxxxxxx.....................................	
PRD	hhhhhhhhccccccccccchhhhhhhhhhccccccceeeeeecccccccccccccccccc	
SEQ	KFFQPTEMAAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSALLDNVDPN	
SEG	....	
PRD	ccccchhhhhhhhhhhhhhhhchhhhhhhhhhhccchhhhhhhhhhhcccccceeeecccc	
SEQ	PENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTLRTSKEPVSRHLCELLAQQF	
SEG	....	
PRD	ccceeeceeeeeccccceeeeeecccchhhhhhhhhhhcccchhhhhhhhhhccc	

Prosite for DKFZphutel_20h13.3

PS00001	760->764	ASN_GLYCOSYLATION	PDOC00001
PS00005	54->57	PKC_PHOSPHO_SITE	PDOC00005
PS00005	85->88	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	163->166	PKC_PHOSPHO_SITE	PDOC00005
PS00005	189->192	PKC_PHOSPHO_SITE	PDOC00005
PS00005	258->261	PKC_PHOSPHO_SITE	PDOC00005
PS00005	297->300	PKC_PHOSPHO_SITE	PDOC00005
PS00005	379->382	PKC_PHOSPHO_SITE	PDOC00005
PS00005	384->387	PKC_PHOSPHO_SITE	PDOC00005
PS00005	470->473	PKC_PHOSPHO_SITE	PDOC00005
PS00005	787->790	PKC_PHOSPHO_SITE	PDOC00005
PS00005	819->822	PKC_PHOSPHO_SITE	PDOC00005
PS00005	832->835	PKC_PHOSPHO_SITE	PDOC00005
PS00005	935->938	PKC_PHOSPHO_SITE	PDOC00005
PS00005	938->941	PKC_PHOSPHO_SITE	PDOC00005
PS00006	5->9	CK2_PHOSPHO_SITE	PDOC00006
PS00006	104->108	CK2_PHOSPHO_SITE	PDOC00006
PS00006	368->372	CK2_PHOSPHO_SITE	PDOC00006
PS00006	379->383	CK2_PHOSPHO_SITE	PDOC00006
PS00006	470->474	CK2_PHOSPHO_SITE	PDOC00006
PS00006	482->486	CK2_PHOSPHO_SITE	PDOC00006
PS00006	597->601	CK2_PHOSPHO_SITE	PDOC00006
PS00006	626->630	CK2_PHOSPHO_SITE	PDOC00006
PS00006	636->640	CK2_PHOSPHO_SITE	PDOC00006
PS00006	698->702	CK2_PHOSPHO_SITE	PDOC00006
PS00006	938->942	CK2_PHOSPHO_SITE	PDOC00006
PS00007	388->395	TYR_PHOSPHO_SITE	PDOC00007
PS00007	411->419	TYR_PHOSPHO_SITE	PDOC00007
PS00007	434->443	TYR_PHOSPHO_SITE	PDOC00007
PS00008	202->208	MYRISTYL	PDOC00008
PS00008	508->514	MYRISTYL	PDOC00008
PS00008	561->567	MYRISTYL	PDOC00008
PS00008	623->629	MYRISTYL	PDOC00008
PS00008	759->765	MYRISTYL	PDOC00008
PS00008	826->832	MYRISTYL	PDOC00008
PS00008	908->914	MYRISTYL	PDOC00008
PS00009	630->634	AMIDATION	PDOC00009
PS00290	127->134	IG_MHC	PDOC00262

(No Pfam data available for DKFZphutel_20h13.3)

DKFZphute1_20m11
----

group: cell cycle

DKFZphute1_20m11 encodes a novel 225 amino acid protein with similarity to yeast sds22 and protein phosphatase-1 regulatory subunits.

sds22 is a regulatory polypeptide of protein phosphatase-1 that is required for the completion of mitosis in both fission and budding yeast. The novel protein seems to be a new regulator protein for protein phosphatase-1.

The new protein can find application in modulating/blocking the activity of protein phosphatase-1 and in modulating the cell cycle.

similarity to suppressor protein sds22

complete cDNA, complete cds, EST hits
localisation? only a part of the STS matches

Sequenced by AGOWA

Locus: /map="17"?

Insert length: 5822 bp
Poly A stretch at pos. 5803, polyadenylation signal at pos. 5786

```
   1 GGGCGCTTGG TTCCCCAGCA ACCGGGAGAC GCGTCTGCTG CGTGGAACCG
  51 CCGAGTTCCC AGCGCTTGAG AAGGAAAATT CTGGATCTGT TATCTGTGAG
 101 GAGGCCACTC CGTTGACAGT TGTGTAAAAC TCTGCTGCTT TCCCCAGCTC
 151 CAACCTCTCT GGTCTTCAAC AACACTATCA TCAGGGAAAA CGTGGGGGAA
 201 GATGAACCAG CCGTGCAACT CGATGGAGCC GAGGGTGATG GACGATGACA
 251 TGCTCAAGCT GGCCGTCGGG GACCAGGGCC CCCAGGAGGA GGCCGGGCAG
 301 CTGGCCAAGC AGGAGGGCAT CCTCTTCAAG GATGTCCTGT CCCTGCAGCT
 351 GGACTTTCGG AACATCCTCC GCATAGACAA CCTCTGGCAG TTTGAGAACT
 401 TGAGGAAGCT GCAGCTGGAC AATAACATCA TTGAGAAGAT CGAGGGCCTG
 451 GAGAACCTCG CACACCTGGT CTGGCTGGAT CTGTCTTTCA ACAACATTGA
 501 GACCATCGAG GGGCTGGACA CACTGGTGAA CCTGGAGGAC CTGAGCTTGT
 551 TCAACAACCG GATCTCCAAG ATCGACTCCC TGGACGCCCT CGTCAAGCTG
 601 CAGGTGTTGT CGCTGGGCAA CAACCGGATT GACAACATGA TGAACATCAT
 651 CTACCTCCGG CGGTTCAAGT GCCTGCGGAC GCTCAGCCTC TCTAGGAACC
 701 CTATCTCTGA GGCAGAGGAT TACAAGATGT TCATCTGTGC CTACCTTCCT
 751 GACCTCATGT ACCTGGACTA CCGGCGCATT GATGACCACA CAGCAAGTGT
 801 CTCCCTCTCA GTCTCCCAGC CCTGTGAGAC AGATTCCTCA AGCCCCCAGG
 851 TTTCTTGGAA AAGGGGCATT GAAGAGTAGC TTCCCCTGCC CACAACTAGG
 901 AGAGAAAGGG CAGCTCCCTC TTCCTAATCC CTTTACCTGA CTCTGTCAGA
 951 GTGATTCCAG CAGCACCCTT GTAAGTACTG TTTTGTGTGC GTTCCCAGGG
1001 GCCAGGCCTC TTCCACACAC TGTCCCAGGG CCACCTCACA GCCATCCTGC
1051 ACTGTCTAGT TTTCCAGATG AAGAAGCTGA GGAGGGCTGG GAGCAGTGGC
1101 TCACGCCTGT AATCCCAGCA CTTTGAGAGG CTGAGGCGGG AGGATCGCTT
1151 GAGCCAAGGA GTTCAAGACC AGCCTGGGCA ACATAGGGAG ACCCCATCTC
1201 TACAGAAACT ACCAAAATTA GCCAGGTGTG GTGGCACACA CCAGTAATCC
1251 TGGCTACTCA CAAGGCCGAG GTAGAAGAAT CGCTTGAGAC TAGGAGTTTG
1301 AGGCTGCAGT GAACTAAGAA GATGCCATTG CACTCCAGCC TGGGCAACAG
1351 AGTGAAAAAA TTAAAAAATT AGAAAAGAAA AGAAGTTGAG GAGGCCCAAG
1401 GAGGGCAAGC AGCCAGGATC ACTGGCTCAA GGCCAAGCCA GGATTCACCC
1451 TAAGTTGGTG TCATCCCAGG AGCAATATTA ACAGCTGAGC TCCAGAGGGA
1501 ACCAGGCCAT CAGAGGCTCA GGCCTGGCTC TCAGGGGCAG AGTCAGGGCT
1551 GGAGGTAGAG ACCTGAGTGT CATCTGAGGA TTGCCAATTG GCAGTAGTTG
1601 AAGCCATGGT ACAGGTGGGA TCACCTGGGG CACATGGAGT GAGCTGGGGG
1651 ACGGGGACTA AGTTCTAGAG GTGCCAGCAT TCCTGGCCAG GTACAGGGGG
1701 ATGAGCCAGT GCGGTGGAGA GAGCCAAGGG CCAGACCCTC GTGACCAGCC
1751 CTATGGCCTC ACTCTACCTC TGTCCTGTTG TCCTCCTTCC CTAAAAGAGG
1801 GCCAGAAGGC CTGCTGAGGG CTGTTGGGAG TGAGAGAGCA AGTCCTCTGT
1851 GGAGAACACC CAGTCTGGGG CGAGGGGAGC GCTCCATTGC TGTGGCTCCT
1901 GCCCTGGAGA TGGCCCCGGG AACCCCAGCC TGCCACGCTG CCTTCCGCTC
1951 CTCCTGGTCT TTCCCTGATT TCCCTGCGCT CACAAAAACC TGGTGAGGGT
2001 CATCAGGAGA TGGGCATTCT CATCCACGAG ACCTCATGGC TTTCACAGCC
2051 TTCATGCAGG CCCCTGTGCA ACACCCCTGC CCATGCGCGG GAGGCTGCAG
2101 CATGGCAGAG GCGGCATGGC AGAGGCGGTG TGGCTCGGAG GAACCTCTGG
2151 TAACAATGCC ACTCCCGTTC CCTGGTCAGA AAAAGCTTGC GGAGGCTAAG
2201 CACCAGTACA GCATCGACGA GCTGAAGCAC CAGGAGAACC TGATGCAGGC
2251 CCAGCTGGAG GACGAGCAGG CGCAGCGGGA GGAGCTAGAG AAGCACAAGA
2301 CTGCGTTTGT GGAACACCTG AATGGCTCCT TCCTGTTTGA CAGCATGTAC
2351 GCTGAGGACT CAGAGGGCAA CAATCTGTCC TACCTGCCTG GTGTCGGTGA
2401 GCTCCTTGAG ACCTACAAGG ACAAGTTTGT CATCATCTGC GTGAATATTT
2451 TTGAGTATGG CCTGAAACAG CAGGAGAAGC GGAAAACAGA GCTTGACACC
2501 TTCAGTGAAT GTGTCCGTGA GGCCATCCAG GAAAACCAGG AGCAGGGCAA
```

```
2551 ACGCAAGATT GCCAAATTCG AGGAGAAGCA CTTGTCGAGT TTAAGTGCCA
2601 TTCGAGAGGA GTTGGAACTG CCCAACATTG AGAAGATGAT CCTAGAATGC
2651 AGTGCTGACA TCAGTGAGTT GTTCGATGCG CTCATGACGC TGGAGATGCA
2701 GCTGGTGGAG CAGCTGGAGG TAAGGCTGGG CCCTGGGCAC AAGTGCCAGA
2751 ATCTGGCGAT GCAGCTGCAC ATCCATAGGT GAACTGTAGC CTTCATGGGC
2801 ACGCCTCTGC TGGAAACGTC CAGCACGACT CAGCGTGGCA GGCTGTAGCT
2851 TTCTTGCTCA TCAGTCCTGT TTGCTTTTAT TACATTTTAA TCATTTACAT
2901 TGGAAGTGAT TCTTGTGGAA AATGAGAGGT GAGCTCATTC TTCTGAAATG
2951 GTCCCCCTAT CCTGGAAGTC AGTGGGGAGA GGTTTTTGAT TAGACCCCTG
3001 GAGCTATCCG GGTACTCTAA AGGCAAAGCG CACCCCCACT TGGGGACCAA
3051 ACAAAGACCC CTCCGCATTG CAGCCTGCAG TTGCCGCTTC TCAGGTGACG
3101 TGAGGAGGCT GCAACTCAGC ACTAAGTAGT GAAAATGAAA AGCGCCGCTG
3151 TCTGAAATTC ATTAGCAGCC AGAGTATGTG TTACAAGGCA GCGGAGGCTG
3201 GGAGTCTGAA GTGGTGTGAT GAATTGAACC TCATCGGATG CTGCTGTGGC
3251 TGGGCCAAGT GATAGCACCT AATCAATTCC TCACACGTCA AGTGACACCT
3301 CAGACATGGG ATAGATTTCC CCATCACATC ACAGGGCAGG TGCTCCCTCC
3351 CTGCTGGAGA GCACAGGCAC TGCAGAAGCA GCGCACAGTG CCAGGGGCGA
3401 GTGAGGCAGC AGCTCCCAGC CTTTTCAGGC ACGGAGATTG CCTTTCAACA
3451 TCCAAACATT TCCCAGAACC CATGTGCCAT CCTACTTGTA TTACTGGTGG
3501 CCAGAAAGCC ACAAGCGCAA TCATGCTTTT CAATGACCCT ATTTTTATTC
3551 ACGAGAACAG CACATACATG TGTTTGAAAA TTATGTGAGG TGCTCACTCT
3601 GCAGACAGTA CTCACATTCC TATAGATTCC ACCCCTGCCC ACCTTGCAGC
3651 CCCTGGAGTC TATAGCAGAT GGGAGTGGGG CACTCCGAGA GTGGCAGGCC
3701 TGGAGATCAC ATCTTCCATT GTTCCTTCAA TCAACACTAA CTCCCATTTG
3751 GGCCTTAGGT GCCTTGCTAA GCACCACAAA ACAGCAACTA ACTGAAAGAG
3801 ATCTGGAGTG CCAGCCCGCT CCTACTGAGG GCCTCCTCTC TGTCAGGCAC
3851 CTTGCAAAGC ATTTTGTGTG AAGTGACTCA TTTAACCTCA CCACAACGCC
3901 ACAACGCAGG GATTATGCAG GTAACCTATT TCCCAGATGA GGAAGATAAG
3951 GCCCAAGGAG GTGAAATGCC TTTCCCAGAG TTACACAGAG TGCTGGAGCT
4001 GGGAATACTG ACCCAGGCAG TCTAGCTCTT AACAGCTCAC TCCACTGTTT
4051 CCCTGGAGGT GATGCACAGA TGTCACTGGG AAACCCAAAG GAGAGGGGGT
4101 TGGCTGTGTG TGTGTGTGTT GGGCAGGCAG GTAAGGGGAG TAAGACCAGG
4151 ACAAGTGTTC CTGGCAAAGT TCCGGTGACA GCATTAAACA TTCAGATGGT
4201 GAGGGAGTTA ATATGGTTGG AGAACAACAA CTTTAGAGAG AGCAGAGGGG
4251 TCAGTTCACA ACCATCTGCT CAGGAGGGTC AAGATGGGTG GTCTTTATGC
4301 TGAAGGTCTG TGATTAGAGG AGCTGGTTGC TAAATTTTGA GGAGTACCTT
4351 TTGCTCTGTG CTGGACATCT AAATATGCAT GTTAACTGTG TTCTTTAACA
4401 TTTCCAGGAG ACTATAAACA TGTTTGAAAG GAACATTGTT GACATGGTAG
4451 GACTGTTTAT CGAAAATGTC CAAAGCCTAT ATCCTTTCTG TGATGACCTT
4501 CCCCATGGGG AGGTGCTACA GAGCCCCTGG GCTTGTCCCG GCCTCTGGAC
4551 AAAAGAATGT TCCACAGGGT CTGAGGAGGT TTCCCGACCC TCAGAACAAT
4601 GATGGCCTGG TTAGAGCTGT GGTTTGGATG CCCAGAGGGA CAACATCCAA
4651 ACTGTTTGCA GTAGGCTCCC AGCATGATTG TTCTCATATG AGTGATGTTC
4701 ACTAGGAAAT GACGCCCCCT GTGTTGCAGG CAAGCACACT CTGGGGTTGA
4751 GGCAACCCCC ACGTGGAAGA CACTATAAGG AGTACATCAG GTGAAATGTT
4801 AGGGTGAGGA GCCAACATCG GAGCATGGCC AACCCTTCTT CCACCCGAAC
4851 TCAGGGCACT CCACATGGGG CAAACTGCTG TGCTCCAGCT AGCAGCAGCC
4901 CTGTGGTCCT GCCCTCCTGG GGCTCACAGT CCCTCAGGGA GACAAGTTGT
4951 AGAGGCAACA AGTGGTGCCA AATGCACAGG GTGAGAAGCA GTTAACCCAG
5001 AGGCCAGGAG CCTCCATGCA GGAGGGAGAG AAGAGTGTGA TGGCAGGGGC
5051 CGAGGGTCCG TCCGAGGTGT GGGGCAGGGG CAGGGAGTCG AGGAAGGCCC
5101 AGGGTTCGGA GCTTGTGAGT GGACGGTGCT GCCAGCCAGA ATTTCCGAGC
5151 TCGCCTTGGG CCCTTAAAGT CTGTCTCCCG CCGTCTGAGA GCATCAGGGA
5201 CGCGCCGGGC CTGCTCCTCC CGGGCCTTTG CTTAACTCGG GGCTGCACGA
5251 TGGCTCAGTG CCGGGACCTG GAGAATCACC ACCACGAGAA GCTCCTGGAG
5301 ATCTCTATCA GCACCCTGGA GAAGATTGTC GAGGGCGACC TGGACGAGGA
5351 CCTGCCTAAC GACCTGCGCG CGCTTTTTGT CGATAAAGAT ACGATTGTTA
5401 ATGCTGTCGG GGCATCGCAC GACATCCACC TCCTGAAGAT TGACAATCGA
5451 GAAGATGAGC TGGTGACCAG AATCAACTCT TGGTGTACAC GTTTAATAGA
5501 CAGGATTCAC AAGGATGAGA TCATGAGGAA CCGCAAGCGC GTGAAGGAGA
5551 TCAATCAGTA CATCGACCAC ATGCAGAGCG AACTGGACAA CCTGGAATGT
5601 GGCGACATCC TAGACTAGAT GAATGTCAGC CACAGGAGCT TCTTCAAAAC
5651 ATAGCACCAG CCCCAGCCAG GAGAAGGAAG TGCACACGCC TCACCCGCAC
5701 CTCTAGAGAG TTGCTGGGCA TCTCTCAACC GCGATCCCCA ACACCATTCT
5751 TCCCCCACCC CTGGAAAAAC TTCCAAAAGT AGAGAAAATA AAGGACTCAT
5801 TTCACAAAAA AAAAAAAAAA AA
```

BLAST Results

Entry HS1292248 from database EMBL:
human STS SHGC-53917.
Score = 874, P = 3.3e-33, identities = 180/185

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 202 bp to 876 bp; peptide length: 225
Category: similarity to known protein

```
  1 MNQPCNSMEP RVMDDDMLKL AVGDQGPQEE AGQLAKQEGI LFKDVLSLQL
 51 DFRNILRIDN LWQFENLRKL QLDNNIIEKI EGLENLAHLV WLDLSFNNIE
101 TIEGLDTLVN LEDLSLFNNR ISKIDSLDAL VKLQVLSLGN NRIDNMMNII
151 YLRRFKCLRT LSLSRNPISE AEDYKMFICA YLPDLMYLDY RRIDDHTASV
201 SLSVSQPCET DSSSPQVSWK RGIEE
```

BLASTP hits

Entry S68209 from database PIR:
sds22 protein homolog - human >TREMBL:HSSDS22MR_1 gene: "sds22"; product: "yeast sds22 homolog"; H.sapiens sds22-like mRNA
Score = 234, P = 1.2e-19, identities = 61/143, positives = 93/143

Entry A38439 from database PIR:
suppressor protein sds22(+) - fission yeast (Schizosaccharomyces pombe) >TREMBL:SPSDS22_1 gene: "sds22+"; S.pombe sds22+ gene, complete cds.
Score = 208, P = 5.6e-17, identities = 52/127, positives = 71/127

Entry S43988 from database PIR:
protein suppressor sds22 - fission yeast (Schizosaccharomyces pombe) >SWISSPROT:SD22_SCHPO PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22. >TREMBL:SPAC4A8_12 gene: "sds22"; product: "phosphatases ppl regulatory subunit"; S.pombe chromosome I cosmid c4A8.
Score = 208, P = 8.5e-17, identities = 52/127, positives = 71/127

Entry CEK10D2_5 from database TREMBL:
gene: "K10D2.1"; Caenorhabditis elegans cosmid K10D2.
Score = 214, P = 3.6e-16, identities = 50/125, positives = 75/125

Alert BLASTP hits for DKFZphutel_20m11, frame 1

No Alert BLASTP hits found

Pedant information for DKFZphutel_20m11, frame 1

Report for DKFZphutel_20m11.1

```
[LENGTH]        225
[MW]            25955.87
[pI]            4.63
[HOMOL]         PIR:S68209 sds22 protein homolog - human 1e-18
[FUNCAT]        03.22 cell cycle control and mitosis  [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]        30.10 nuclear organization     [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]        06.07 protein modification (glycolsylation, acylation, myristylation,
palmitylation, farnesylation and processing)        [S. cerevisiae, YKL193c] 2e-11
[FUNCAT]        30.05 organization of centrosome      [S. cerevisiae, YOR373w] 2e-06
[FUNCAT]        01.03.10 metabolism of cyclic and unusual nucleotides       [S. cerevisiae,
YJL005w] 3e-05
[FUNCAT]        03.10 sporulation and germination    [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]        30.02 organization of plasma membrane         [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]        10.04.03 second messenger formation  [S. cerevisiae, YJL005w] 3e-05
[FUNCAT]        04.07 rna transport    [S. cerevisiae, YPL169c] 9e-04
[FUNCAT]        04.05.01.04 transcriptional control  [S. cerevisiae, YCR065w] 9e-04
[EC]            4.6.1.1 Adenylate cyclase 2e-06
[PIRKW]         nucleus 5e-16
[PIRKW]         duplication 2e-06
[PIRKW]         tandem repeat 2e-06
[PIRKW]         cAMP biosynthesis 2e-06
[PIRKW]         glycoprotein 2e-06
[PIRKW]         phosphorus-oxygen lyase 2e-06
[SUPFAM]        leucine-rich alpha-2-glycoprotein repeat homology 5e-16
[SUPFAM]        fibromodulin 3e-07
[SUPFAM]        yeast adenylate cyclase catalytic domain homology 2e-06
[SUPFAM]        yeast adenylate cyclase 2e-06
[PROSITE]       CK2_PHOSPHO_SITE       2
[PROSITE]       PKC_PHOSPHO_SITE       1
```

```
[KW]          All_Alpha

SEQ    MNQPCNSMEPRVMDDDMLKLAVGDQGPQEEAGQLAKQEGILFKDVLSLQLDFRNILRIDN
PRD    ccccccccccccccchhhhhhcccccchhhhhhhhhhhchhhhhhhhhcccccccccccc

SEQ    LWQFENLRKLQLDNNIIEKIEGLENLAHLVWLDLSFNNIETIEGLDTLVNLEDLSLFNNR
PRD    hhhhhhhhhhhhccccccccccchhhhhhhhhccccccccccccchhhhhhhhhhccccc

SEQ    ISKIDSLDALVKLQVLSLGNNRIDNMMNIIYLRRFKCLRTLSLSRNPISEAEDYKMFICA
PRD    cccchhhhhhhhhhhhhccccccccccccccchhhhhhhhhcccccccccchhhhhhhhh

SEQ    YLPDLMYLDYRRIDDHTASVSLSVSQPCETDSSSPQVSWKRGIEE
PRD    hhcccccccccccccchhhhhhhhccccccccccccccccccccc
```

Prosite for DKFZphute1_20m11.1

PS00005	218->221	PKC_PHOSPHO_SITE	PDOC00005
PS00006	122->126	CK2_PHOSPHO_SITE	PDOC00006
PS00006	169->173	CK2_PHOSPHO_SITE	PDOC00006

(No Pfam data available for DKFZphute1_20m11.1)

DKFZphute1_20m24
----

group: metabolism

DKFZphute1_20m24 encodes a novel 611 amino acid protein with similarity to a hypothetical C.elegans protein and to yeast Alg9 protein.

This protein is a putative mannosyl transferase that is involved in the assembly of the core oligosaccharide Glc3Man9GlcNAc2.

The new protein can find application in modulation of glycosylation of proteins and as a new enzyme for biotechnologic production processes.

strong similarity to S.cerevisiae Alg9p

complete cDNA, complete cds, potential start at Bp 23, few EST hits
Alg9 is involved in the assembly of the core oligosaccharide
Glc3Man9GlcNAc2
HSAC381 corresponding genomic DNA (2 exons)
HSB8954 corresponding genomic DNA (1 exon)

Sequenced by AGOWA

Locus: /map="11"

Insert length: 1986 bp
Poly A stretch at pos. 1966, polyadenylation signal at pos. 1949

```
   1 TTCTTTTTTC CCCAGGCTTG CCATGGCTAG TCGAGGGGCT CGGCAGCGCC
  51 TGAAGGGCAG CGGGGCCAGC AGTGGGGATA CGGCCCCGGC TGCGGACAAG
 101 CTGCGGGAGC TGCTGGGCAG CCGAGAGGCG GGCGGCGCGG AGCACCGGAC
 151 CGAGTTATCT GGGAACAAAG CAGGACAAGT CTGGGCACCT GAAGGATCTA
 201 CTGCTTTCAA GTGTCTGCTT TCAGCAAGGT TATGTGCTGC TCTCCTGAGC
 251 AACATCTCTG ACTGTGATGA AACATTCAAC TACTGGGAGC CAACACACTA
 301 CCTCATCTAT GGGGAAGGGT TTCAGACTTG GGAATATTCC CCAGCATATG
 351 CCATTCGCTC CTATGCTTAC CTGTTGCTTC ATGCCTGGCC AGCTGCATTT
 401 CATGCAAGAA TTCTACAAAC TAATAAGATT CTTGTGTTTT ACTTTTTGCG
 451 ATGTCTTCTG GCTTTTGTGA GCTGTATTTG TGAACTTTAC TTTTACAAGG
 501 CTGTGTGCAA GAAGTTTGGG TTGCACGTGA GTCGAATGAT GCTAGCCTTC
 551 TTGGTTCTCA GCACTGGCAT GTTTTGCTCA TCATCAGCAT TCCTTCCTAG
 601 TAGCTTCTGT ATGTACACTA CGTTGATAGC CATGACTGGA TGGTATATGG
 651 ACAAGACTTC CATTGCTGTG CTGGGAGTAG CAGCTGGGGC TATCTTAGGC
 701 TGGCCATTCA GTGCAGCTCT TGGTTTACCC ATTGCCTTTG ATTTGCTGGT
 751 CATGAAACAC AGGTGGAAGA GTTTCTTTCA TTGGTCGCTG ATGGCCCTCA
 801 TACTATTTCT GGTGCCTGTG GTGGTCATTG ACAGCTACTA TTATGGGAAG
 851 TTGGTGATTG CACCACTCAA CATTGTTTTG TATAATGTCT TTACTCCTCA
 901 TGGACCTGAT CTTTATGGTA CAGAACCCTG GTATTTCTAT TTAATTAATG
 951 GATTTCTGAA TTTCAATGTA GCCTTTGCTT TGGCTCTCCT AGTCCTACCA
1001 CTGACTTCTC TTATGGAATA CCTGCTGCAG AGATTTCATG TTCAGAATTT
1051 AGGCCACCCG TATTGGCTTA CCTTGGCTCC AATGTATATT TGGTTTATAA
1101 TTTTCTTCAT CCAGCCTCAC AAAGAGGAGA GATTTCTTTT CCCTGTGTAT
1151 CCACTTATAT GTCTCTGTGG CGCTGTGGCT CTCTCTGCAC TTCAGAAATG
1201 TTACCACTTT GTGTTTCAAC GATATCGCCT GGAGCACTAT ACTGTGACAT
1251 CGAATTGGCT GGCATTAGGA ACTGTCTTCC TGTTTGGGCT CTTGTCATTT
1301 TCTCGCTCTG TGGCACTGTT CAGAGGATAT CACGGGCCCC TTGATTTGTA
1351 TCCAGAATTT TACCGAATTG CTACAGACCC AACCATCCAC ACTGTCCCAG
1401 AAGGCAGACC TGTGAATGTC TGTGTGGGAA AAGAGTGGTA TCGATTTCCC
1451 AGCAGCTTCC TTCTTCCTGA CAATTGGCAG CTTCAGTTCA TTCCATCAGA
1501 GTTCAGAGGT CAGTTACCAA AACCTTTTGC AGAAGGACCT CTGGCCACCC
1551 GGATTGTTCC TACTGACATG AATGACCAGA ATCTAGAAGA GCCATCCAGA
1601 TATATTGATA TCAGTAAATG CCATTATTTA GTGGATTTGG ACACCATGAG
1651 AGAAACACCC CGGGAGCCAA AATATTCATC CAATAAAGAA GAATGGATCA
1701 GCTTGGCCTA TAGACCATTC CTTGATGCTT CTAGATCTTC AAAGCTGCTG
1751 CGGGCATTCT ATGTCCCCTT CCTGTCAGAT CAGTATACAG TGTACGTAAA
1801 CTACACCATC CTCAAACCCC GGAAAGCAAA GCAAATCAGG AAGAAAAGTG
1851 GAGGTTAGCA ACACACCTGT GGCCCCAAAG GACAACCATC TTGTTAACTA
1901 TTGATTCCAG TGACCTGACT CCCTGCAAGT CATCGCCTGT AACATTTGTA
1951 ATAAAGGTCT TCTGACATGA AAAAAAAAAA AAAAAA
```

BLAST Results

Entry HSAC381 from database EMBL:
Homo sapiens chromosome 11 pac pDJ159o1, complete sequence.
Length = 42,771

Entry HSB8954 from database EMBL:

cSRL-50A3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-50A3.
Length = 601

Medline entries

96293493:
Stepwise assembly of the lipid-linked oligosaccharide in the endoplasmic reticulum of Saccharomyces cerevisiae: identification of the ALG9 gene encoding a putative mannosyl transferase.

Peptide information for frame 2

ORF from 23 bp to 1855 bp; peptide length: 611
Category: strong similarity to known protein

```
  1 MASRGARQRL KGSGASSGDT APAADKLREL LGSREAGGAE HRTELSGNKA
 51 GQVWAPEGST AFKCLLSARL CAALLSNISD CDETFNYWEP THYLIYGEGF
101 QTWEYSPAYA IRSYAYLLLH AWPAAFHARI LQTNKILVFY FLRCLLAFVS
151 CICELYFYKA VCKKFGLHVS RMMLAFLVLS TGMFCSSSAF LPSSFCMYTT
201 LIAMTGWYMD KTSIAVLGVA AGAILGWPFS AALGLPIAFD LLVMKHRWKS
251 FFHWSLMALI LFLVPVVVID SYYYGKLVIA PLNIVLYNVF TPHGPDLYGT
301 EPWYFYLING FLNFNVAFAL ALLVLPLTSL MEYLLQRFHV QNLGHPYWLT
351 LAPMYIWFII FFIQPHKEER FLFPVYPLIC LCGAVALSAL QKCYHFVFQR
401 YRLEHYTVTS NWLALGTVFL FGLLSFSRSV ALFRGYHGPL DLYPEFYRIA
451 TDPTIHTVPE GRPVNVCVGK EWYRFPSSFL LPDNWQLQFI PSEFRGQLPK
501 PFAEGPLATR IVPTDMNDQN LEEPSRYIDI SKCHYLVDLD TMRETPREPK
551 YSSNKEEWIS LAYRPFLDAS RSSKLLRAFY VPFLSDQYTV YVNYTILKPR
601 KAKQIRKKSG G
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_20m24, frame 2

SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II., N = 1, Score = 957, P = 2.7e-96

PIR:S63177 mannosyl transferase (EC 2.4.1.-) - yeast (Saccharomyces cerevisiae), N = 1, Score = 533, P = 2.3e-51

SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II., N = 1, Score = 957, P = 2.7e-96

PIR:S63177 mannosyl transferase (EC 2.4.1.-) - yeast (Saccharomyces cerevisiae), N = 1, Score = 533, P = 2.3e-51

>SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II.
Length = 653

HSPs:

Score = 957 (143.6 bits), Expect = 2.7e-96, P = 2.7e-96
Identities = 206/514 (40%), Positives = 296/514 (57%)

```
Query:     48 NKAGQVWAPEGSTAFKCLLSARLCAALLSNISDCDETFNYWEPTHYLIYGEGFQTWEYSP 107
              N     W     + FK LLS R+  A+   I+DCDE +NYWEP H  +YGEGFQTWEYSP
Sbjct:     43 NNPDNDWPFSFGSVFKMLLSIRISGAIWGIINDCDEVYNYWEPLHLFLYGEGFQTWEYSP 102

Query:    108 AYAIRSYAYLLLHAWPAAFHARILQTNKILVFYFLRCLLAFVSCICELYFYKAVCKKFGL 167
               YAIRSY Y+ LH  PA+  A +    KI+VF  +R  +     + E Y + A+CKK  +
Sbjct:    103 VYAIRSYFYIYLHYIPASLFANLFGDTKIVVFTLIRLTIGLFCLLGEYYAFDAICKKINI 162

Query:    168 HVSRMMLAFLVLSTGMFCSSSAFLPSSFCMYTTLIAMTGWYMDKTSIAVLGVAAGAILGW 227
                 R  + F + S+GMF +S+AF+PSSFCM  T   +  +  +  +  +  VA   ++GW
Sbjct:    163 ATGRFFILFSIFSSGMFLASTAFVPSSFCMAITFYILGAYLNENWTAGIFCVAFSTMVGW 222

Query:    228 PFSAALGLPIAFDLLVMKHRWKSFFHWSLMALILFLVPVVVIDSYYYGKLVIAPLNIVLY 287
```

```
              PFSA LGLPI  D+L++K      F   SL+  +       V+ DS+Y+GK V+APLNI LY
Sbjct:   223 PFSAVLGLPIVADMLLLKGLRIRFILTSLVIGLCIGGVQVITDSHYFGKTVLAPLNIFLY 282

Query:   288 NVFTPHGPDLYGTEPWYFYLINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPY 347
             NV +   GP LYG EP   FY+ N F N+N+     A     PL+   + Y   + +   Q+
Sbjct:   283 NVVSGPGPSLYGEEPLSFYIKNLFNNWNIVIFAAPFGFPLS--LAYFTKVWMSQDRNVAL 340

Query:   348 WLTLAPMYI-------WFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQKCYHFVFQR 400
             +   AP+ +          W +IF  Q HKEERFLFP+YP I     A+AL A  +      ++
Sbjct:   341 YQRFAPIILLAVTTAAWLLIFGSQAHKEERFLFPIYPFIAFFAALALDATNR---LCLKK 397

Query:   401 YRLEHYTVTSNWLALGTVFLFGLLSFSRSVALFRGYHGPLDLYPEFYRIATDPTIHTVPE 460
               ++       N L++  +  F +LS SR+ ++   Y   +++Y        T+ T +
Sbjct:   398 LGMD------NILSILFILCFAILSASRTYSIHNNYGSHVEIYRSLNAELTNRT-NFKNF 450

Query:   461 GRPVNVCVGKEWYRFPSSFLLPDNW------QLQFIPSEFRGQLPKPFAEGPL---ATRI 511
               P+ VCVGKEW+RFPSSF +P          +++FI SEFRG LPKPF +        TR
Sbjct:   451 HDPIRVCVGKEWHRFPSSFFIPQTVSDGKKVEMRFIQSEFRGLLPKPFLKSDKLVEVTRH 510

Query:   512 VPTDMNDQNLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEW 558
             +PT+MN+ N EE SRY+D+  C Y+VD+D M ++ REP +   ++ +
Sbjct:   511 IPTEMNNLNQEEISRYVDLDSCDYVVDVD-MPQSDREPDFRKMRQNY 556
```

Pedant information for DKFZphutel_20m24, frame 2

Report for DKFZphutel_20m24.2

```
[LENGTH]     611
[MW]         69863.78
[pI]         8.91
[HOMOL]      SWISSPROT:YTH3_CAEEL HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II. 2e-
93
[FUNCAT]     09.01 biogenesis of cell wall       [S. cerevisiae, YNL219c] 4e-69
[FUNCAT]     01.06.01 lipid, fatty-acid and sterol biosynthesis  [S. cerevisiae, YNL219c]
4e-69
[FUNCAT]     01.05.01 carbohydrate utilization    [S. cerevisiae, YNL219c] 4e-69
[PIRKW]      glycosyltransferase 9e-68
[PIRKW]      transmembrane protein 9e-68
[PIRKW]      hexosyltransferase 9e-68
[PROSITE]    MYRISTYL       9
[PROSITE]    CAMP_PHOSPHO_SITE      1
[PROSITE]    CK2_PHOSPHO_SITE       7
[PROSITE]    PKC_PHOSPHO_SITE       6
[PROSITE]    ASN_GLYCOSYLATION      2
[KW]         TRANSMEMBRANE  7
[KW]         LOW_COMPLEXITY     6.71 %

SEQ    MASRGARQRLKGSGASSGDTAPAADKLRELLGSREAGGAEHRTELSGNKAGQVWAPEGST
SEG    ............................................................
PRD    ccchhhhhhhcccccccccccchhhhhhhhcccccccccccceeeccccccccccccccch
MEM    ......................................................MMMMMM

SEQ    AFKCLLSARLCAALLSNISDCDETFNYWEPTHYLIYGEGFQTWEYSPAYAIRSYAYLLLH
SEG    ...xxxxxxxxxxxxx............................................
PRD    hhhhhhhhhhhhhhhhhhhccccceeecccccceeeeeccccceeeccccchhhhhhhhhc
MEM    MMMMMMMMMMMMMMMMM..........................................M

SEQ    AWPAAFHARILQTNKILVFYFLRCLLAFVSCICELYFYKAVCKKFGLHVSRMMLAFLVLS
SEG    ............................................................
PRD    cchhhhhhhhcchhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcc
MEM    MMMMMMMMMMMMMMMMMMMMMMMMMMMM................................

SEQ    TGMFCSSSAFLPSSFCMYTTLIAMTGWYMDKTSIAVLGVAAGAILGWPFSAALGLPIAFD
SEG    .................................xxxxxxxxxxxxx..............
PRD    cceeeecccccchhhhhhhhhhhhhhccccccceeeeeehhhhhccceeeeeeecchhhh
MEM    ..............................................MMMMMMMMMMMMMM

SEQ    LLVMKHRWKSFFHWSLMALILFLVPVVVIDSYYYGKLVIAPLNIVLYNVFTPHGPDLYGT
SEG    ............................................................
PRD    hhhhhhhhhhhhhhhhhhhhheeeeeeeecccccccccccceeeeeeeeccccccccccc
MEM    MMMMMMM.MMMMMMMMMMMMMMMMMMMMM...............................

SEQ    EPWYFYLINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLTLAPMYIWFII
SEG    ..........xxxxxxxxxxxxxxx...................................
PRD    cceeeeeecccccchhhhhhhhhhhchhhhhhhhhhhhhcccccceeeeeehhhhhhhhhh
MEM    ........MMMMMMMMMMMMMMMMMMMMMMMMMMMMM.......................
```

```
SEQ     FFIQPHKEERFLFPVYPLICLCGAVALSALQKCYHFVFQRYRLEHYTVTSNWLALGTVFL
SEG     ............................................................
PRD     hhcccchhhhhhccccceeehhhhhhhhhhhhhhhhhhhhhhhheeeeccchhhhhhhee
MEM     ............MMMMMMMMMMMMMMMMMMMMM.....MMMMMMMMMMMMMMMMMMMMM.

SEQ     FGLLSFSRSVALFRGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRFPSSFL
SEG     ............................................................
PRD     eehhhhhhheeeccccccccccccceeeecccccceeecccceeeeeecccccccccccc
MEM     ............................................................

SEQ     LPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQNLEEPSRYIDISKCHYLVDLD
SEG     ............................................................
PRD     ccccceeeecccccccccccccccceeeecccccccccccccccceeeeeeceeeeeecc
MEM     ............................................................

SEQ     TMRETPREPKYSSNKEEWISLAYRPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPR
SEG     ............................................................
PRD     ccccccccccccchhhhhhhhhhhhhhhhhhhhhhheeeeeeeeecceeeeeeeeeecccc
MEM     ............................................................

SEQ     KAKQIRKKSGG
SEG     ...........
PRD     hhhhhhccccc
MEM     ...........
```

Prosite for DKFZphutel_20m24.2

PS00001	77->81	ASN_GLYCOSYLATION	PDOC00001
PS00001	593->597	ASN_GLYCOSYLATION	PDOC00001
PS00004	606->610	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	67->70	PKC_PHOSPHO_SITE	PDOC00005
PS00005	133->136	PKC_PHOSPHO_SITE	PDOC00005
PS00005	541->544	PKC_PHOSPHO_SITE	PDOC00005
PS00005	545->548	PKC_PHOSPHO_SITE	PDOC00005
PS00005	553->556	PKC_PHOSPHO_SITE	PDOC00005
PS00005	572->575	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	79->83	CK2_PHOSPHO_SITE	PDOC00006
PS00006	329->333	CK2_PHOSPHO_SITE	PDOC00006
PS00006	457->461	CK2_PHOSPHO_SITE	PDOC00006
PS00006	541->545	CK2_PHOSPHO_SITE	PDOC00006
PS00006	545->549	CK2_PHOSPHO_SITE	PDOC00006
PS00006	553->557	CK2_PHOSPHO_SITE	PDOC00006
PS00008	12->18	MYRISTYL	PDOC00008
PS00008	14->20	MYRISTYL	PDOC00008
PS00008	32->38	MYRISTYL	PDOC00008
PS00008	47->53	MYRISTYL	PDOC00008
PS00008	166->172	MYRISTYL	PDOC00008
PS00008	182->188	MYRISTYL	PDOC00008
PS00008	218->224	MYRISTYL	PDOC00008
PS00008	222->228	MYRISTYL	PDOC00008
PS00008	234->240	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_20m24.2)

DKFZphutel_21d15
----

group: uterus derived

DKFZphutel_21d15 encodes a novel 191 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of testis-specific genes.

unknown

Sequenced by MediGenomix

Locus: /chromosome="3"

Insert length: 5292 bp
Poly A stretch at pos. 5273, polyadenylation signal at pos. 5252

```
   1 CTCCCACTAG TGTATGCCTT AATGGTGCCG CTCTTGTCCG CGTCTACGCT
  51 TGGGACCTTG GCTTCTGACT TGGAGAGTGT ACAGCTCTGC CCGACGGCAA
 101 CCCAGCTTGG GAAGAGAAGC CCCAGCGTGG GCTGGGGCTC AAGGCGCAGG
 151 AAGGCCGAGC CCGGCGCGGA CGCAGGCGGC TCCGGGCGGG CTCAGCACCC
 201 CCAGGCACCG TCTCCTAGTG ACCGCGGCGC TCGCGGGCCT GGCGGCCGTT
 251 GTCCGGGCGA CTGCGCAGCG CGGGCACCCC CGCGGCCCCT CCCCTGGGCG
 301 CGCGCGCGAC CTGGGTGCCA TGGCGGCAGC GGCGGTGACA GGCCAGCGGC
 351 CTGAGACCGC GGCGGCCGAG GAGGCCTCGA GGCCGCAGTG GGCGCCGCCA
 401 GACCACTGCC AGGCTCAGGC GGCGGCCGGG CTGGGCGACG GCGAGGACGC
 451 ACCGGTGCGT CCGCTGTGCA AGCCCCGCGG CATCTGCTCG CGCGCCTACT
 501 TCCTGGTGCT GATGGTGTTC GTGCACCTGT ACCTGGGTAA CGTGCTGGCG
 551 CTGCTGCTCT TCGTGCACTA CAGCAACGGC GACGAAAGCA GCGATCCCGG
 601 GCCCCAACAC CGTGCCCAGG GCCCCGGGCC CGAGCCCACC TTAGGTCCCC
 651 TCACCCGGCT GGAGGGCATC AAGGTGAGGA CCTCCCTGCC CCGCCGCGCT
 701 CCAGGCCCTG CACGGCTGAG CCCGAGAGGA CCGGCGCTCA GCCCGGGTCC
 751 CCACGCTGCC CCCGGCGCTG CTCTGCGTCG GTCCCGCGCG CTCCCACTCA
 801 CTCGCCTGCT GTCGCTCTCC GGGCCGGGGC GACTTGGCCC TTTTTGGGCA
 851 GCGCGGTCTG GCGCCCCAGC TGCCCGCTGT GCGCCTTTTC CTTAGGTGGG
 901 GCACGAGCGT AAGGTCCAGC TGGTCACCGA CAGGGATCAC TTCATCCGAA
 951 CCCTCAGCCT CAAGCCGCTG CTCTTCGAAA TCCCCGGCTT CCTGACTGAT
1001 GAAGAGTGTC GGCTCATCAT CCATCTGGCG CAGATGAAGG GGTTACAGCG
1051 CAGCCAGATC CTGCCTACTG AAGAGTATGA AGAGGCAATG AGCACTATGC
1101 AGGTCAGCCA GCTGGACCTC TTCCGGCTGC TGGACCAGAA CCGTGATGGG
1151 CACCTTCAGC TCCGTGAGGT TCTGGCCCAG ACTCGCCTGG GAAATGGATG
1201 GTGGATGACT CCAGAGAGCA TTCAGGAGAT GTACGCCGCG ATCAAGGCTG
1251 ACCCTGATGG TGACGGTGAG CTCACACCTC TGCACAGTCC TATCCCCGTG
1301 AGCCTCCTGC CCACTCCCAG GTGCACAATT TTGAAAACTT GGGCCCTTCC
1351 CCCACAGCCA GGCAGCCTCT CTGCACCCCT TTATAGTGGC CAGAGATGGG
1401 GAGGTGAAGA TCCAGCCTTG CTTTTTACCC CTGGGAAGTA GGCAGGCAGC
1451 CAGGCCCCCC GTTCCCCTTG GTGATGGTCT CGAGGGCAGT TCTTGGAGAC
1501 CCTTTTGATA ACATCAGGCA GAGTTGAGAG CCTGGGGACA GGAAGTAGGG
1551 CTGCTAGTTG GCAGAGAACA GAGTGGGTGG AGCAGGAGCA AGGCGACAGT
1601 GAGGCCAGCT AGAGCTTGGC TGTTTACCCT GCTCCATCCA TCTCTCCAGC
1651 CAGACACGAG GTCCACCCCA GCAGACAGCT TCCCTGGTCT AAGTGAGGTC
1701 TCCCTTGCCT TCCTCTTGTC CACCTGGAGT CATGCCGAAG CGCCTAAAAT
1751 GGTAGTGCTG CTACCTGTGC TAACTGCTGG GGAGGGGTGG GCAGGGAAGC
1801 TGTCATGCAA GTGGTGCCCC CTCTGGTAAT AACTCTCAGG AGGTTTCTGA
1851 GGTGTGGTCA TCACCCTCAT GCCCAAATTC TGGACCAAGA GAGGAAGATA
1901 CAGCAGTTAG AAAGGACTTG GAACAGTGGC TTTGCGGCTG GTGAACCAGA
1951 GTGAAGAATC TGGCCGTGAC CTGGCTGCCA CACTGCTATA GGCCCCAGAA
2001 CAGAGGTGGT GACAGTCTCA CAGCCCTTGA ATGTCCCCCA CCCTCAGAGG
2051 AATCTGGGCC AAAGAGTGGA AGGTGATGTC CTTGGGTCAG CCAGAATAAC
2101 ATGGAGCAAA GATACCAACT ACTCTTCCAG AACCCCAAGA GGGTAGAACC
2151 CCTGCTTAAT GGTTTGAGCA GGGACAGTGG AGAATGTTCT CATGAGAGGG
2201 GGTGGCCTGA CTTTCGTTGC TAAGTGGGCT GGTAACGCAG TAGGCAGGGC
2251 TGGCGAAGTA GGTTCCACCC AGGATGAAAC CTGGGGTCAT GAGGAACTCC
2301 CCGGGGGCTG GCCCTGCTTG CACCCTGGCG TATGTATGTA AGGCCCTGGA
2351 TGAGGCCCAG CACTGCCTGC TCTCTCCTCA CCCTCCACAG GCCGGAGAGT
2401 GGCCACCACT CTATATAGCC AGGCTGGAAG GCCAGGGTCC TGGCCATATG
2451 GCTCAAGCTT CCTTTGGAGA ACCTTCTCTG GCCACTCTAA TAGGGGGTGG
2501 GCCTCTTTCT TCTTAGGGCC AAATTAGGGC TTAAACTGAG AAAAGGAACT
2551 GCTCTGGGTC TTCCTGTAAG GCCTGATGTG ACAGAAACCA GGTTCATCTG
2601 ACCCAAAAGT CCAGGTGGGG GACAAGTGTA CAAGGCCCCT CAGTGCCTGA
2651 GGTCAGGGGC TGCTGCTGCC TTTGGGGTAG GTAGGGAAGT GCAGCCTGCC
2701 ACTGTTGCCT CCCAATATGG GCTTGGTGGG CATTGATGGT GGGTGCCCTG
2751 TGCAGGAGTG CTGAGTCTGC AGGAGTTCTC CAACATGGAC CTTCGGGACT
2801 TCCACAAGTA CATGAGGAGC CACAAGGCAG AGTCCAGTGA GCTGGTGCGG
```

```
2851 AACAGCCACC ATACCTGGCT CTACCAGGGT GAGGGTGCCC ACCACATCAT
2901 GCGTGCCATC CGCCAGAGGT GAGCACCTGA AGCTGTTCTC ACTGGAGCAG
2951 GGGGAGAAGA CTGGGCAGGG CCTCCACAGA AGTCCTTGTC TGGGGCCAAG
3001 AGGACAGAAT GGATTAACCC ATTTGGGATT AAGTTCCATT TGTTAGACCA
3051 GGATTGGGAC CCACTGAAAG ACAGGCAATT AACAAAGGCA AATTAGCCCT
3101 CCTTGCAGGC ACACAATGGG CAACTGGGGT TAGATAGAGA TTGAGCACTT
3151 CTTTCTGATT AGATAAATGA CCTCTTATCT TTGACCCCTT ATCTGACCCC
3201 GTCACAGCAG GAAAAGGGTT TTTAAATAAA CAACTTTCTT CCAGGGAGGA
3251 GGACCTCAGG ACTCCCCGCC CCCTTTATTT AGTGGAAATG TCAACATTTC
3301 CACATAGCAG GTGTCTCTGT CTTTGGCATC TGAGGGAGAA GGATCATCAT
3351 GAGTAACCCC CTCCTGCTCT TACAGGGCCA GTCTGAGATG GCTTAAGGGA
3401 CTTCCAGGGG AGGTGGGTAG GGGCAAAGCT TGTGGCAGGC CTAGGGTCCA
3451 CCTTGGCCAG CTCCTTCAGA TCACCACCTT GCCTGGGGCT GCCCAGCCAA
3501 ATGCCTGCTG CCCACCAGGG TGCTGCGCCT CACTCGCCTG TCGCCTGAGA
3551 TCGTGGAGCT CAGCGAGCCG CTGCAGGTTG TTCGATATGG TGAGGGGGGC
3601 CACTACCATG CCCACGTGGA CAGTGGGCCT GTGTACCCAG AGACCATCTG
3651 CTCCCATACC AAGCTGGTAG CCAACGAGTC TGTACCCTTC GAGACCTCCT
3701 GCCGGCAAGT ATCTCCCAAC TGGGGGCTGC CTTCAATCCT CAGACCAGGA
3751 ACACCCATGA CACAGGCACA GCCCTGCACT GTGGGCGTGC CCCTTGGCAT
3801 GGGGCCAGGA GATCACTGGG TTATCCCGGT TAGTGATGCC CTCACCTCTC
3851 CCCACAAGTT GTTTACCCAA TGGCTGGAAA GGGGTGGCTA CTGGTCATCG
3901 TGACCACTGG AGTCAACACA GACTGATGTA CCCACAGACA CCAAAACTTG
3951 CCCCCTGAGT TCTGAAGCAA GGGGCAAGGC TGGGCCCCTA GCTTGTCCTG
4001 CCCATTCCTC CAGGTGTTGA TCTTGATTCC ACTTAGAGAA GCTGAAGCTG
4051 TGCCTCCCTC CCCTGTCAAG CCAGTTCTTT CCTCTTCAGG TGGCTGTTCT
4101 GGCCCAGCCC CTTCCCATCC CCAAGGAGCC CTTCAGCGCG CCCTGTTGCT
4151 TCTGCTAGCC TACCTTTCCC TGCCAGGCCC TTGCTCAGGG CCATGGCATT
4201 TAACTAAGTG CACCTGTGAT CTTGGCCAAA AAACCATTGC AACTCACAGT
4251 AAGAGACTGG GTTTCGGGGA AGGAGGGGCT AGGGACATTT TGGCACTGGC
4301 CTGCCCTATT GTCTCCCATC CTAGTCTGTC CTGGTCCCTG GCAACAGGAA
4351 CCTGGGCAGC TTATCCTGCC CACAGGTAAG CCCCTGGGAG CATCCACAAC
4401 TGGGGACCTG CTCAGTGCCC CCCCTGCCTT ACAGCTACAT GACAGTGCTG
4451 TTTTATTTGA ACAACGTCAC TGGTGGGGGC GAGACTGTTT TCCCTGTAGC
4501 AGATAACAGA ACCTACGATG AAATGGTAAG GGTCAACTGG GCTATTACTC
4551 TTGTGGGCTG GCAGGGGCTT AGACAAGTGA AGTACACACC TCTCCAGGTC
4601 TAAGGATGTG GGCCCAAATT ATTCCTTGGG CATATCTGGT TGGTTTCCCT
4651 TTGGTCACCC TTGGCTGGCC TGGCCATAGA GTGGGGACAG GTTGAACACC
4701 CCACCACCCT GCTGCCCACA GAGTCTGATT CAGGATGACG TGGACCTCCG
4751 TGACACACGG AGGCACTGTG ACAAGGGAAA CCTGCGTGTC AAGCCCCAAC
4801 AGGGCACAGC AGTCTTCTGG TACAACTACC TGCCTGATGG GCAAGGTTGG
4851 GTGGGTGACG TAGACGACTA CTCGCTGCAC GGGGGCTGCC TGGTCACGCG
4901 CGGCACCAAG TGGATTGCCA ACAACTGGAT TAATGTGGAC CCCAGCCGAG
4951 CGCGGCAAGC GCTGTTCCAA CAGGAGATGG CCCGCCTTGC CCGAGAAGGG
5001 GGCACCGACT CACAGCCCGA GTGGGCTCTG GACCGGGCCT ACCGCGATGC
5051 GCGCGTGGAA CTCTGAGGGA AGAGTTAGCC CCGGTTCCCA GCCGCGGGTC
5101 GCCAGTTGCC CAAGATCAGG GGTCCGGCTG TCCTTCTGTC CTGCTGCAGA
5151 CTAAAGGTCT GGCCAATGTC TTGCCCCACC CCGCCAGCCG CGATACGGCG
5201 CAGTTCCTAT ATTCATGTTA TTTATTGTGT ACTGACTCCA TCTGCCCCGT
5251 CAAATAAAAA ACCACAAGGT TCGAAAAAAA AAAAAAAAAA GG
```

BLAST Results

Entry HSU64252 from database EMBL:
Human STS sequence NOTI-225.
Score = 959, P = 1.2e-36, identities = 195/199

Medline entries

No Medline entry

Peptide information for frame 1

ORF from the beginning to 351 bp; peptide length: 118
Category: questionable ORF
Classification: no clue

```
  1 LPLVYALMVP LLSASTLGTL ASDLESVQLC PTATQLGKRS PSVGWGSRRR
 51 KAEPGADAGG SGRAQHPQAP SPSDRGARGP GGRCPGDCAA RAPPRPLPWA
101 RARPGCHGGS GGDRPAA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_21d15, frame 1

No Alert BLASTP hits found

Peptide information for frame 2

ORF from 320 bp to 892 bp; peptide length: 191
Category: putative protein
Classification: no clue

```
    1 MAAAAVTGQR PETAAAEEAS RPQWAPPDHC QAQAAAGLGD GEDAPVRPLC
   51 KPRGICSRAY FLVLMVFVHL YLGNVLALLL FVHYSNGDES SDPGPQHRAQ
  101 GPGPEPTLGP LTRLEGIKVR TSLPRRAPGP ARLSPRGPAL SPGPHAAPGA
  151 ALRRSRALPL TRLLSLSGPG RLGPFWAARS GAPAARCAPF P
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_21d15, frame 2

PIR:EDBE75 immediate-early protein IE175 - human herpesvirus 1, N = 2,
Score = 106, P = 0.0067

>PIR:EDBE75 immediate-early protein IE175 - human herpesvirus 1
Length = 1,298

HSPs:

```
 Score = 106 (15.9 bits), Expect = 6.7e-03, Sum P(2) = 6.7e-03
 Identities = 36/103 (34%), Positives = 44/103 (42%)

Query:    87 GDESSDPGPQHRAQGPGPEPTLGPLTRLEGIKVRTSLPRRA-PGPARLS-PRGPALSPGP 144
             G +    PGP      G GP P    P T+  G       S  R    P PA  S P GP  +P
Sbjct:  726 GRKRKSPGPARPPGGGPRP---PKTKKSGADAPGSDARAPLPAPAPPSTPPGPEPAPAQ 782

Query:   145 HAAPGAALRRSRALPLT-RLLSLSGPGRLGPFWAARSGAPAARCAP 189
              AAP AA  ++R  P+         GP  LG  W  +    P+   AP
Sbjct:  783 PAAPRAAAAQARPRPVAVSRRPAEGPDPLGG-WRRQPPGPSHTAAP 827

 Score = 40 (6.0 bits), Expect = 6.7e-03, Sum P(2) = 6.7e-03
 Identities = 8/21 (38%), Positives = 9/21 (42%)

Query:    28 DHCQAQAAAGLGDGEDAPVRP 48
             DH +   A G G    AP  P
Sbjct:  212 DHAREARAVGRGPSSAAPAAP 232
```

Pedant information for DKFZphutel_21d15, frame 1

Report for DKFZphutel_21d15.1

```
[LENGTH]      117
[MW]          11797.32
[pI]          10.68
[KW]          Irregular
[KW]          SIGNAL_PEPTIDE 22
[KW]          LOW_COMPLEXITY     38.46 %

SEQ    LPLVYALMVPLLSASTLGTLASDLESVQLCPTATQLGKRSPSVGWGSRRRKAEPGADAGG
SEG    ..........xxxxxxxxxxxxxx....................................
PRD    cccccccccccccccccccchhhhhhhhcccccccccccccccccccccccccccccccc

SEQ    SGRAQHPQAPSPSDRGARGPGGRCPGDCAARAPPRPLPWARARPGCHGGSGGDRPAA
SEG    .............xxxxxxxxxxxxxxxxxxxxxxxxxxxxxx.............
PRD    ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
```

(No Prosite data available for DKFZphutel_21d15.1)

(No Pfam data available for DKFZphutel_21d15.1)

Pedant information for DKFZphutel_21d15, frame 2

Report for DKFZphutel_21d15.2

```
[LENGTH]        191
[MW]            19916.88
[pI]            10.43
[KW]            TRANSMEMBRANE  1
[KW]            LOW_COMPLEXITY     29.84 %

SEQ     MAAAAVTGQRPETAAAEEASRPQWAPPDHCQAQAAAGLGDGEDAPVRPLCKPRGICSRAY
SEG     ............................................................
PRD     ccceeeeccccchhhhhhhhhcccccchhhhhhhhccccccccccccccccccccchhhh
MEM     ............................................................

SEQ     FLVLMVFVHLYLGNVLALLLFVHYSNGDESSDPGPQHRAQGPGPEPTLGPLTRLEGIKVR
SEG     ........................................xxxxxxxxxxxxxxx.....
PRD     hhhhhhhhhhhhhhhhhhhhhccccccccccccccccccccccccccccccccceeeeee
MEM     .....MMMMMMMMMMMMMMMMM......................................

SEQ     TSLPRRAPGPARLSPRGPALSPGPHAAPGAALRRSRALPLTRLLSLSGPGRLGPFWAARS
SEG     .........................xxxxxxxxxxxxxxxxxxxxxxxxxxxxx..xxxx
PRD     eeccccccccccccccccccccccccccchhhhhhcccccceeeccccccccchhhhhhc
MEM     ............................................................

SEQ     GAPAARCAPFP
SEG     xxxxxxxxx..
PRD     ccccccccccc
MEM     ...........
```

(No Prosite data available for DKFZphutel_21d15.2)

(No Pfam data available for DKFZphutel_21d15.2)

DKFZphutel_22d2
----

group: signal transduction

DKFZphutel_22d2 encodes a novel 580 amino acid putative GTP-binding protein related to the ras protein. Additionally, the putative protein contains an EF-hand for calcium-binding.

G-proteins are involved in various signal transduction pathways, transferring the signal of a cellular receptor to an intracellular signal cascade.

The new protein can find clinical application in modulating/blocking the response to a cellular receptor.

similarity to GTP-binding proteins

complete cDNA, complete cds, potential start at Bp 64, EST hits
complete cds according to K08F11.5 and YAL048c

Sequenced by BMFZ

Locus: /map="17"

Insert length: 3247 bp
Poly A stretch at pos. 3230, no polyadenylation signal found

```
   1 CTCCTGGTGA GAGGAGTCCA CTCCGTGCGT GCGGGCGGAG GCCGGCCCCC
  51 GAGAGCCGCC GACATGAAGA AAGACGTGCG GATCCTGCTG GTGGGAGAAC
 101 CTAGAGTTGG GAAGACATCA CTGATTATGT CTCTGGTCAG TGAAGAATTT
 151 CCAGAAGAGG TTCCTCCCCG GGCAGAAGAA ATCACCATTC CAGCTGATGT
 201 CACCCCAGAG AGAGTTCCAA CACACATTGT AGATTACTCA GAAGCAGAAC
 251 AGAGTGATGA ACAACTTCAT CAAGAAATAT CTCAGGCTAA TGTCATCTGT
 301 ATAGTGTATG CCGTTAACAA CAAGCATTCT ATTGATAAGG TAACAAGTCG
 351 ATGGATTCCT CTCATAAATG AAAGAACAGA CAAAGACAGC AGGCTGCCTT
 401 TAATATTGGT TGGGAACAAA TCTGATCTGG TGGAATATAG TAGTATGGAG
 451 ACCATCCTTC CTATTATGAA CCAGTATACA GAAATAGAAA CCTGTGTGGA
 501 GTGTTCAGCG AAAAACCTGA AGAACATATC AGAGCTCTTT TATTACGCAC
 551 AGAAAGCTGT TCTTCATCCT ACAGGGCCCC TGTACTGCCC AGAGGAGAAG
 601 GAGATGAAAC CAGCTTGTAT AAAAGCCCTT ACTCGTATAT TTAAAATATC
 651 TGATCAAGAT AATGATGGTA CTCTCAATGA TGCTGAACTC AACTTCTTTC
 701 AGAGGATTTG TTTCAACACT CCATTAGCTC CTCAAGCTCT GGAGGATGTC
 751 AAGAATGTAG TCAGAAAACA TATAAGTGAT GGTGTGGCTG ACAGTGGGTT
 801 GACCCTGAAA GGTTTTCTCT TTTTACACAC ACTTTTTATC CAGAGAGGGA
 851 GACACGAAAC TACTTGGACT GTGCTTCGAC GATTTGGTTA TGATGATGAC
 901 CTGGATTTGA CACCTGAATA TTTGTTCCCC CTGCTGAAAA TACCTCCTGA
 951 TTGCACTACT GAATTAAATC ATCATGCATA TTTATTTCTC CAAAGCACCT
1001 TTGACAAGCA TGATTTGGAT AGAGACTGTG CTTTGTCACC TGATGAGCTT
1051 AAAGATTTAT TTAAAGTTTT CCCTTACATA CCTTGGGGGC CAGATGTGAA
1101 TAACACAGTT TGTACCAATG AAAGAGGCTG GATAACCTAC CAGGGATTCC
1151 TTTCCCAGTG GACGCTCACG ACTTATTTAG ATGTACAGCG GTGCCTGGAA
1201 TATTTGGGCT ATCTAGGCTA TTCAATATTG ACTGAGCAAG AGTCTCAAGC
1251 TTCAGCTGTT ACAGTGACAA GAGATAAAAA GATAGACCTG CAGAAAAAAC
1301 AAACTCAAAG AAATGTGTTC AGATGTAATG TAATTGGAGT GAAAAACTGT
1351 GGGAAAAGTG GAGTTCTTCA GGCTCTTCTT GGAAGAAACT TAATGAGGCA
1401 GAAGAAAATT CGTGAAGATC ATAAATCCTA CTATGCGATT AACACTGTTT
1451 ATGTATATGG ACAAGAGAAA TACTTGTTGT TGCATGATAT CTCAGAATCG
1501 GAATTTCTAA CTGAAGCTGA AATCATTTGT GATGTTGTAT GCCTGGTATA
1551 TGATGTCAGC AATCCCAAAT CCTTTGAATA CTGTGCCAGG ATTTTTAAGC
1601 AACACTTTAT GGACAGCAGA ATACCTTGCT TAATCGTAGC TGCAAAGTCA
1651 GACCTGCATG AAGTTAAACA AGAATACAGT ATTTCACCTA CTGATTTCTG
1701 CAGGAAACAC AAAATGCCTC CACCACAAGC CTTCACTTGC AATACTGCTG
1751 ATGCCCCCAG TAAGGATATC TTTGTTAAAT TGACAACAAT GGCCATGTAT
1801 CCGTAAGTAC TTGCTGTCTT CATTTTCATG TTGCATGGTT CATAACATTG
1851 CATGCCATTA TTAGCCATGA AGGGAATATC TTTGTCACAT AGGAATTGTT
1901 CAGCAACAGA AAGATACTTT GTAATGAGAA GGTACAAATT TGAGTAAATG
1951 CAAGTTTGGT TTGAATGCCA TAATAAAATG ATATAAACAG TGCTTCTGAC
2001 AATATCTGTA TATTTTTGAG CAGGCTGTAA CTATCTTAAT AGAATAGTAC
2051 AATAAAACAC AACCCCCCAC CCAGCATTAA AAAATAGTTT TACTGGAATA
2101 AAATGGGTTT GGCATCATGT TGTTTTATGC TTATAAAGCA TTTTCATATG
2151 AACAGAAAGT TTATATTTTT CTGTTTTTGA CCTTAGGTAT ATGAAGTTTT
2201 CTAAAATATT TTATTAATTT ATGTTGAAAT TGTGGGTATG CTTCAGTTAG
2251 GATATGTCTT TTTTAAGTGC TGTAAAGAGT AGTTGTAATT GGAATTTCTA
2301 CTGTATAAAT GTTTTACATT AAGTGTTACG AGCCACAAAT TTCATGTACA
2351 TTTATTATAT ATCTATACAT GCATATGCAC AAGCACATAA CTGTGGTCAT
2401 CTCTGTAGTT TACTAACTGC CTTAAAATTG CATGGTTCTT AATGGCATTC
2451 GCCTCAAGTA GTGTGTTTGT ATAAATTCTG TTTTGTAACA AAATAGTTTT
2501 TCAGGCAGTG CGTTTCTCAG GACTTTATAG CTTATTCTAC TTATTCTTAT
2551 GTTAGTCTCT AAATTATTTT TCTTCTTATG AAAACTACAG TGTAACACAG
```

```
2601 AGTAATAATC AAACATTGCT ATAAACCAAG AATGACATTT TTCAAAAAGG
2651 TGTTGATTTG TACAGATTTT TAAAGTCAGT TAACTTTACT GCTATTTTAT
2701 TACCTAATAC TTTTTTTAGA TGCAACAAAC CCTTGAATTT CTATTTGTAT
2751 TCGAAGACAA GTCATTCCTA TTATTATAGA ATAACCAAAA CCTTATTTAT
2801 GTTTTACCTT TGCTTTAAAA CTCTCATGTA TGTTATCTAC AGAGAGGATC
2851 ATTACAGAGA CAGACTCTCC CGAGACATGG GCCACACTGA TAGAATAGAG
2901 AATTTGAGAA AAATCTGGGT CTTTCTAAAA ACTGCTTTGT AAGTTACTTT
2951 TTCTTTATGA CTTCTGTGGG ATTTTGTTGA TATTTTCTTA GAGAATGACC
3001 AAATCTCCTT TCTTGCCATA ATTAACATTT AGTAATTATG TAGAAACGCA
3051 CTGCTTGGTC AGGCTTCCTG CCTAGCTATA TATTACGTTG TCTTCCTTAC
3101 TACATAAATG TACTTCTTTA ATCTTGTGAT TACAGTAACT GCAAGTGTGT
3151 TTTTACATCT GCATTTTTAA AACATTTTAC TGTAATTCTG TTGTGTGTGT
3201 GTGTGTTATA TGATAAATGT ACATACATGG AAAAAAAAAA AAAAAAA
```

BLAST Results

Entry AC004527 from database EMBL:
*** SEQUENCING IN PROGRESS *** NF1-related locus, Direct Submission;
HTGS phase 1, 10 unordered pieces.
Score = 1899, P = 1.1e-78, identities = 387/396

Entry HS148355 from database EMBL:
human STS SHGC-31220.
Score = 1826, P = 7.5e-78, identities = 388/406

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 64 bp to 1803 bp; peptide length: 580
Category: similarity to known protein

```
  1 MKKDVRILLV GEPRVGKTSL IMSLVSEEFP EEVPPRAEEI TIPADVTPER
 51 VPTHIVDYSE AEQSDEQLHQ EISQANVICI VYAVNNKHSI DKVTSRWIPL
101 INERTDKDSR LPLILVGNKS DLVEYSSMET ILPIMNQYTE IETCVECSAK
151 NLKNISELFY YAQKAVLHPT GPLYCPEEKE MKPACIKALT RIFKISDQDN
201 DGTLNDAELN FFQRICFNTP LAPQALEDVK NVVRKHISDG VADSGLTLKG
251 FLFLHTLFIQ RGRHETTWTV LRRFGYDDDL DLTPEYLFPL LKIPPDCTTE
301 LNHHAYLFLQ STFDKHDLDR DCALSPDELK DLFKVFPYIP WGPDVNNTVC
351 TNERGWITYQ GFLSQWTLTT YLDVQRCLEY LGYLGYSILT EQESQASAVT
401 VTRDKKIDLQ KKQTQRNVFR CNVIGVKNCG KSGVLQALLG RNLMRQKKIR
451 EDHKSYYAIN TVYVYGQEKY LLLHDISESE FLTEAEIICD VVCLVYDVSN
501 PKSFEYCARI FKQHFMDSRI PCLIVAAKSD LHEVKQEYSI SPTDFCRKHK
551 MPPPQAFTCN TADAPSKDIF VKLTTMAMYP
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphute1_22d2, frame 1

TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid
K08F11., N = 1, Score = 1357, P = 1.1e-138

TREMBL:SPCC320_4 gene: "SPCC320.04c"; product: "hypothetical protein";
S.pombe chromosome III cosmid c320., N = 1, Score = 889, P = 4.4e-89

TREMBL:CEUC47C12_3 gene: "C47C12.4"; Caenorhabditis elegans cosmid
C47C12., N = 2, Score = 408, P = 5.6e-74

PIR:S51971 probable membrane protein YAL048c - yeast (Saccharomyces
cerevisiae), N = 1, Score = 677, P = 1.3e-66

>TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid
K08F11.
Length = 625

HSPs:

```
 Score = 1357 (203.6 bits), Expect = 1.1e-138, P = 1.1e-138
 Identities = 263/582 (45%), Positives = 380/582 (65%)

Query:     4 DVRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTPERVPTHIVDYSEAEQ 63
             DVRI+L+G+   GKTSL+MSL+ +E+ + VP R + + IPADVTPE V T IVD S  E+
Sbjct:     9 DVRIVLIGDEGCGKTSLVMSLLEDEWVDAVPRRLDRVLIPADVTPENVTTSIVDLSIKEE 68

Query:    64 SDEQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLINERTDKDSRLPLILVGNKSDLV 123
              +  +  EI QANVIC+VY+V ++ ++D + ++W+PLI +    +      P+ILVGNKSD
Sbjct:    69 DENWIVSEIRQANVICVVYSVTDESTVDGIQTKWLPLIRQSFGEYHETPVILVGNKSDGT 128

Query:   124 EYSSMETILPIMNQYTEIETCVECSAKNLKNISELFYYAQKAVLHPTGPLYCPEEKEMKP 183
              ++ + ILPIM   TE+ETCVECSA+ +KN+SE+FYYAQKAV++PT PLY  + K++
Sbjct:   129 A-NNTDKILPIMEANTEVETCVECSARTMKNVSEIFYYAQKAVIYPTRPLYDADTKQLTD 187

Query:   184 ACIKALTRIFKISDQDNDGTLNDAELNFFQRICFNTPLAPQALEDVKNVVRKHISDGVAD 243
                KAL R+FKI D+DNDG L+D ELN FQ++CF  PL   ALEDVK  V      DGVA+
Sbjct:   188 RARKALIRVFKICDRDNDGYLSDTELNDFQKLCFGIPLTSTALEDVKRAVSDGCPDGVAN 247

Query:   244 SGLTLKGFLFLHTLFIQRGRHETTWTVLRRFGYDDDLDLTPEYLFPLLKIPPDCTTELNH 303
                L L GFL+LH LFI+RGRHETTW VLR+FGY+  L L+ +YL+P + IP  C+TEL+
Sbjct:   248 DSLMLAGFLYLHLLFIERGRHETTWAVLRKFGYETSLKLSEDYLYPRITIPVGCSTELSP 307

Query:   304 HAYLFLQSTFDKHDLDRDCALSPDELKDLFKVFPYIPWGPDVNNTVCTNERGWITYQGFL 363
                 F+ + F+K+D D+D  LSP EL++LF V P       D     + TN+RGW+TY G++
Sbjct:   308 EGVQFVSALFEKYDEDKDGCLSPSELQNLFSVCPVPVITKDNILALETNQRGWLTYNGYM 367

Query:   364 SQWTLTTYLDVQRCLEYLGYLGYSILTEQESQAS----AVTVTRDKKIDLQKKQTQRNVF 419
             + W +TT +++ +  E L YLG+ +        +A      ++ VTR++K DL+    T R VF
Sbjct:   368 AYWNMTTLINLTQTFEQLAYLGFPVGRSGPGRAGNTLDSIRVTRERKKDLENHGTDRKVF 427

Query:   420 RCNVIGVKNCGKSGVLQALLGRNLMRQKKIREDHKSYYAINTVYVYGQEKYLLLHDI--- 476
             +C V+G K+ GK+  +Q+L GR +     +I   H S + IN V V  + KYLLL ++
Sbjct:   428 QCLVVGAKDAGKTVFMQSLAGRGMADVAQIGRRH-SPFVINRVRVKEESKYLLLREVDVL 486

Query:   477 SESEFLTEAEIICDVVCLVYDVSNPKSFEYCARIFKQHFMDSRIPCLIVAAKSDLHEVKQ 536
             S  + L    E   DVV  +YD+SNP SF +CA +++++F  ++ PC+++A K +  EV Q
Sbjct:   487 SPQDALGSGETSADVVAFLYDISNPDSFAFCATVYQKYFYRTKTPCVMIATKVEREEVDQ 546

Query:   537 EYSISPTDFCRKHKMPPPQAFTCNTADAPSKDIFVKLTTMAMYP 580
              + + P +FCR+ ++P P  F+        S  IF +L  MA+YP
Sbjct:   547 RWEVPPEEFCRQFELPKPIKFSTGNIGQSSSPIFEQLAMMAVYP 590
```

Pedant information for DKFZphutel_22d2, frame 1

Report for DKFZphutel_22d2.1

[LENGTH] 580
[MW] 66541.61
[pI] 5.56
[HOMOL] TREMBL:CEUK08F11_3 gene: "K08F11.5"; Caenorhabditis elegans cosmid K08F11. 1e-149
[FUNCAT] 99 unclassified proteins [S. cerevisiae, YAL048c] 5e-81
[FUNCAT] 03.04 budding, cell polarity and filament formation [S. cerevisiae, YKR055w] 3e-11
[FUNCAT] 03.99 other cell growth, cell division and dna synthesis activities [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 10.04.07 g-proteins [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 03.10 sporulation and germination [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 11.01 stress response [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 03.22 cell cycle control and mitosis [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 01.03.13 regulation of nucleotide metabolism [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 01.05.04 regulation of carbohydrate utilization [S. cerevisiae, YNL098c] 8e-09
[FUNCAT] 30.03 organization of cytoplasm [S. cerevisiae, YOR101w] 4e-08
[FUNCAT] 11.10 cell death [S. cerevisiae, YOR101w] 4e-08
[FUNCAT] 10.02.07 g-proteins [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 30.04 organization of cytoskeleton [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 30.08 organization of golgi [S. cerevisiae, YPR165w] 7e-08
[FUNCAT] 08.07 vesicular transport (golgi network, etc.) [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 30.09 organization of intracellular transport vesicles [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 30.02 organization of plasma membrane [S. cerevisiae, YFL005w] 9e-08
[FUNCAT] 08.13 vacuolar transport [S. cerevisiae, YNL093w] 1e-07

```
[FUNCAT]        06.04 protein targeting, sorting and translocation  [S. cerevisiae, YNL093w]
1e-07
[FUNCAT]        08.19 cellular import  [S. cerevisiae, YNL093w] 1e-07
[FUNCAT]        10.05.07 g-proteins   [S. cerevisiae, YLR229c] 8e-07
[FUNCAT]        03.07 pheromone response, mating-type determination, sex-specific proteins
       [S. cerevisiae, YLR229c] 8e-07
[FUNCAT]        10.99 other signal-transduction activities   [S. cerevisiae, YCR027c] 3e-06
[FUNCAT]        09.09 biogenesis of intracellular transport vesicles      [S. cerevisiae,
YGL210w] 9e-04
[BLOCKS]        BL00410A Dynamin family proteins
[SCOP]          d1plk__ 3.25.1.3.1 cH-p21 Ras protein [human (Homo sapiens) 2e-42
[SCOP]          d1guaa_ 3.25.1.3.10 Rap1A [Human (Homo sapiens) 5e-59
[PIRKW]         transmembrane protein 1e-79
[PIRKW]         membrane trafficking 2e-06
[PIRKW]         acetylated amino end 3e-09
[PIRKW]         prenylated cysteine 3e-09
[PIRKW]         signal transduction 1e-07
[PIRKW]         transforming protein 3e-09
[PIRKW]         immediate-early protein 8e-06
[PIRKW]         alternative splicing 4e-08
[PIRKW]         P-loop 1e-10
[PIRKW]         lipoprotein 7e-10
[PIRKW]         proto-oncogene 3e-09
[PIRKW]         methylated carboxyl end 3e-09
[PIRKW]         membrane protein 3e-09
[PIRKW]         GTP binding 1e-10
[PIRKW]         thiolester bond 7e-10
[SUPFAM]        ras transforming protein 1e-10
[PROSITE]       ATP_GTP_A       2
[PROSITE]       MYRISTYL        3
[PROSITE]       EF_HAND 1
[PROSITE]       CAMP_PHOSPHO_SITE       1
[PROSITE]       CK2_PHOSPHO_SITE        14
[PROSITE]       TYR_PHOSPHO_SITE        4
[PROSITE]       PKC_PHOSPHO_SITE        5
[PROSITE]       ASN_GLYCOSYLATION       3
[PFAM]          Ras family (contains ATP/GTP binding P-loop)
[KW]            Irregular
[KW]            3D

SEQ     MKKDVRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITIPADVTPERVPTHIVDYSE
1jai-   ...EEEEEEEETTTTCHHHHHHHHHHCCCCCCCCCCCCEEEEEEEEETTEEEEEEEEECCC

SEQ     AEQSDEQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLINERTDKDSRLPLILVGNKS
1jai-   CGGGHHHHHHHHHHTTEEEEEEEETTTHHHHHHH-HHHHHHHHHHHCTTT-TCEEEEEETT

SEQ     DLVEYSSMETILPIMNQYTEIETCVECSAKNLKNISELFYYAQKAVLHPTGPLYCPEEKE
1jai-   TTTTTTTTHHHHHHHHHHHCCCE-EECTTTTTTTHHHHHH....................

SEQ     MKPACIKALTRIFKISDQDNDGTLNDAELNFFQRICFNTPLAPQALEDVKNVVRKHISDG
1jai-   ............................................................

SEQ     VADSGLTLKGFLFLHTLFIQRGRHETTWTVLRRFGYDDDLDLTPEYLFPLLKIPPDCTTE
1jai-   ............................................................

SEQ     LNHHAYLFLQSTFDKHDLDRDCALSPDELKDLFKVFPYIPWGPDVNNTVCTNERGWITYQ
1jai-   ............................................................

SEQ     GFLSQWTLTTYLDVQRCLEYLGYLGYSILTEQESQASAVTVTRDKKIDLQKKQTQRNVFR
1jai-   ............................................................

SEQ     CNVIGVKNCGKSGVLQALLGRNLMRQKKIREDHKSYYAINTVYVYGQEKYLLLHDISESE
1jai-   ............................................................

SEQ     FLTEAEIICDVVCLVYDVSNPKSFEYCARIFKQHFMDSRIPCLIVAAKSDLHEVKQEYSI
1jai-   ............................................................

SEQ     SPTDFCRKHKMPPPQAFTCNTADAPSKDIFVKLTTMAMYP
1jai-   ........................................
```

Prosite for DKFZphutel_22d2.1

PS00001	118->122	ASN_GLYCOSYLATION	PDOC00001
PS00001	154->158	ASN_GLYCOSYLATION	PDOC00001
PS00001	346->350	ASN_GLYCOSYLATION	PDOC00001
PS00004	411->415	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	94->97	PKC_PHOSPHO_SITE	PDOC00005
PS00005	105->108	PKC_PHOSPHO_SITE	PDOC00005

PS00005	148->151	PKC_PHOSPHO_SITE	PDOC00005
PS00005	247->250	PKC_PHOSPHO_SITE	PDOC00005
PS00005	414->417	PKC_PHOSPHO_SITE	PDOC00005
PS00006	59->63	CK2_PHOSPHO_SITE	PDOC00006
PS00006	105->109	CK2_PHOSPHO_SITE	PDOC00006
PS00006	126->130	CK2_PHOSPHO_SITE	PDOC00006
PS00006	139->143	CK2_PHOSPHO_SITE	PDOC00006
PS00006	143->147	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00006	203->207	CK2_PHOSPHO_SITE	PDOC00006
PS00006	311->315	CK2_PHOSPHO_SITE	PDOC00006
PS00006	325->329	CK2_PHOSPHO_SITE	PDOC00006
PS00006	370->374	CK2_PHOSPHO_SITE	PDOC00006
PS00006	390->394	CK2_PHOSPHO_SITE	PDOC00006
PS00006	477->481	CK2_PHOSPHO_SITE	PDOC00006
PS00006	483->487	CK2_PHOSPHO_SITE	PDOC00006
PS00006	541->545	CK2_PHOSPHO_SITE	PDOC00006
PS00007	153->161	TYR_PHOSPHO_SITE	PDOC00007
PS00007	376->384	TYR_PHOSPHO_SITE	PDOC00007
PS00007	153->162	TYR_PHOSPHO_SITE	PDOC00007
PS00007	448->457	TYR_PHOSPHO_SITE	PDOC00007
PS00008	240->246	MYRISTYL	PDOC00008
PS00008	425->431	MYRISTYL	PDOC00008
PS00008	433->439	MYRISTYL	PDOC00008
PS00017	11->19	ATP_GTP_A	PDOC00017
PS00017	425->433	ATP_GTP_A	PDOC00017
PS00018	197->210	EF_HAND	PDOC00018

Pfam for DKFZphutel_22d2.1

```
HMM_NAME       Ras family (contains ATP/GTP binding P-loop)

HMM                *KLVLIGDSGVGKSCLLIRFTQNeFnEeYIPTIGvDFYtKTIEIDGKtIK
                     ++L+G+  VGK++L   ++  EF+EE +P   ++  T   ++  +++
Query            6  RILLVGEPRVGKTSLIMSLVSEEFPEE-VPPR-AEEITIPADVTPERVP    52

HMM                LQIWDTAGQERYRsMRPMYYRGAMGFMLVYDITNRqSFENIr.NWweEIr
                     I D     E+ +     + + +A+++ +VY+++N+ S ++++ +W++ I+
Query           53 THIVDYSEAEQSDEQLHQEISQANVICIVYAVNNKHSIDKVTSRWIPLIN   102

HMM                RHCDrDENVPIMLVGNKCDLEDQRQVStEEGQeFAREWGAIPFMETSAKT
                   +  D+D+  P +LVGNK+DL +    ++T          +      +E+SAK+
Query          103 ERTDKDSRLPLILVGNKSDLVEYSSMETILPIMNQYTEI-ETCVECSAKN   151

HMM                NiNVEEAFMEIvReIlqrMqeqNqteNinidQpsrnrkrCCCIM*
                     N+ E F+ + +++L +      .  +++  +++++ +    C+
Query          152 LKNISELFYYAQKAVLHPT------GPLYCPEEKEMK-PACI--    186
```

DKFZphutel_22e12
----

group: signal transduction

DKFZphutel_22e12 encodes a novel 92 amino acid protein, with similarity to yeast, C.elegans, Drosophila and mammalian proteins.

The Drosophila cni and mammalian cornicon proteins are part of a signal transduction pathway involving hte EGF-receptor.

The new protein can find application in modulating the cornichon modulated signal transduction way and also the EGF receptor signaling processes.

strong similarity to S.cerevisiae YGL054c and cornichon

complete cDNA, complete cds, EST hits
cornicon is requiered for signal transduction in the EGF-receptor signal processing

Sequenced by BMFZ

Locus: unknown

Insert length: 519 bp
Poly A stretch at pos. 499, no polyadenylation signal found

```
  1 GTCGGGGCAT CCGAGCGGGT TTGACGGAAG GAGCGGCGGC GACGGAGGAG
 51 GAGGATGGAG GCGGTGGTGT TCGTCTTCTC TCTCCTCGAT TGTTGCGCGC
101 TCATCTTCCT CTCGGTCTAC TTCATAATTA CATTGTCTGA TTTAGAATGT
151 GATTACATTA ATGCTAGATC ATGTTGCTCA AAATTAAACA AGTGGGTAAT
201 TCCAGAATTG ATTGGCCATA CCATTGTCAC TGTATTACTG CTCATGTCAT
251 TGCACTGGTT CATCTTCCTT CTCAACTTAC CTGTTGCCAC TTGGAATATA
301 TATCGTATGA TCTTAGCTTT GATAAATGAC TGAAGCTGGA GAAGCCGTGG
351 TTGAAGTCAG CCTACACTAC AGTGCACAGT TGAGGAGCCA GAGACTTCTT
401 AAATCATCCT TAGAACCGTG ACCATAGCAG TATATATTTT CCTCTTGGAA
451 CAAAAAACTA TTTTTGCTGT ATTTTTACCA TATAAAGTAT TTAAAAAACA
501 TGAAAAAAAA AAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

95300228:
cornichon and the EGF receptor signaling process are necessary for both anterior-posterior
and dorsal-ventral pattern formation in Drosophila.

Peptide information for frame 1

ORF from 55 bp to 330 bp; peptide length: 92
Category: strong similarity to known protein

```
 1 MEAVVFVFSL LDCCALIFLS VYFIITLSDL ECDYINARSC CSKLNKWVIP
51 ELIGHTIVTV LLLMSLHWFI FLLNLPVATW NIYRMILALI ND
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_22e12, frame 1

PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae), N = 2, Score = 185, P = 5.7e-17

TREMBL:SPAC2C4_5 gene: "SPAC2C4.05"; product: "cornichon homolog";

```
S.pombe chromosome I cosmid c2C4., N = 1, Score = 163, P = 3.7e-12

PIR:S46084 probable membrane protein YBR210w - yeast (Saccharomyces
cerevisiae), N = 1, Score = 162, P = 4.8e-12

TREMBL:AF104398_1 product: "cornichon"; Homo sapiens cornichon mRNA,
complete cds., N = 1, Score = 141, P = 8e-10

SWISSPROT:CNI_DROVI CORNICHON PROTEIN., N = 1, Score = 139, P = 1.3e-09


>PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces
     cerevisiae)
            Length = 138

  HSPs:

 Score = 185 (27.8 bits), Expect = 5.7e-17, Sum P(2) = 5.7e-17
 Identities = 35/85 (41%), Positives = 56/85 (65%)

Query:     1 MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTV 60
             M A +F+ +++  C  +F  V+F I  +DLE DYIN    CSK+NK + PE   H  +++
Sbjct:     1 MGAWLFILAVVVNCINLFGQVHFTILYADLEADYINPIELCSKVNKLITPEAALHGALSL 60

Query:    61 LLLMSLHWFIFLLNLPVATWNIYRM 85
             L L++ +WF+FLLNLPV  +N+ ++
Sbjct:    61 LFLLNGYWFVFLLNLPVLAYNLNKI 85

 Score = 37 (5.6 bits), Expect = 5.7e-17, Sum P(2) = 5.7e-17
 Identities = 7/9 (77%), Positives = 9/9 (100%)

Query:    82 IYRMILALI 90
             +YRMI+ALI
Sbjct:   123 LYRMIMALI 131


            Pedant information for DKFZphutel_22e12, frame 1
            ----------------------------------------------

                     Report for DKFZphutel_22e12.1


[LENGTH]       92
[MW]           10614.98
[pI]           5.04
[HOMOL]        PIR:S64058 probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae)
5e-14
[FUNCAT]       03.04 budding, cell polarity and filament formation [S. cerevisiae, YGL054c]
2e-15
[PIRKW]        transmembrane protein 2e-11
[PROSITE]      CK2_PHOSPHO_SITE      3
[KW]           SIGNAL_PEPTIDE 33
[KW]           TRANSMEMBRANE  2


SEQ    MEAVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTV
PRD    ccchhhhhhhhhhhhhhhhhhhheeeccccccccccccccccccccceeehhhhhhhhhhh
MEM    ..................................................MMMMMMMMMM

SEQ    LLLMSLHWFIFLLNLPVATWNIYRMILALIND
PRD    hhhhhhhheeecccccchhhhhhhhhhhhccc
MEM    MMMMMMMMMMMMMMMMMMM..MMMMMM....


                     Prosite for DKFZphutel_22e12.1

PS00006        9->13   CK2_PHOSPHO_SITE       PDOC00006
PS00006       26->30   CK2_PHOSPHO_SITE       PDOC00006
PS00006       28->32   CK2_PHOSPHO_SITE       PDOC00006

(No Pfam data available for DKFZphutel_22e12.1)
```

DKFZphutel_22n2
----

group: uterus derived

DKFZphutel_22n2 encodes a novel 304 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

unknown

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: /map="553.3 cR from top of Chr11 linkage group"

Insert length: 1556 bp
Poly A stretch at pos. 1534, no polyadenylation signal found

```
   1 ACAACAGGCT GGTTGCTTGG CGTGGAATCC TAAAGTGGCC TGGCTTTGAG
  51 ACTGGAGTGA GACCCCAGCC CTAGGCTGGG GTTCTTTCCA TTATAGAGGA
 101 GACGGATTCA GAAGGGCTAC AGACCAAGGT TGTTGAAAAC CAGACATATG
 151 ATGAGCGTCT AGAGATTAAC GACTCCGAAG AGGTTGCAAG TATTTATACT
 201 CCAACCCCAA GACACCAAGG ACTTCCTCGT TCTGCCCATC TTCCTAACAA
 251 GGCTATGGCT GATAACAGCA GTGATGAGTG TGAAGAGGAA AATAACAAGG
 301 AGAAGAAGAA GACCTCACAG TTGACACCTC AACGGGGCTT TAGTGAAAAT
 351 GAGGATGACG ATGATGATGA TGATGATTCA TCTGAAACTG ATTCTGATTC
 401 TGATGATGAT GATGAAGAGC ATGGAGCCCC TCTGGAAGGG GCCTATGACC
 451 CTGCAGACTA TGAGCATTTG CCAGTTTCTG CTGAAATTAA GGAACTCTTC
 501 CAGTACATCA GTAGGTACAC ACCTCAGTTG ATTGACCTGG ACCACAAACT
 551 GAAGCCTTTC ATTCCTGATT TTATCCCAGC TGTCGGGGAT ATTGATGCAT
 601 TCTTAAAGGT CCCACGTCCT GATGGAAAGC CTGACAACCT TGGCCTATTG
 651 GTATTGGATG AACCTTCTAC AAAGCAGTCA GACCCTACGG TGCTCTCACT
 701 CTGGTTAACA GAGAATTCTA AGCAGCACAA CATCACACAA CATATGAAAG
 751 TAAAAAGCCT AGAAGATGCA GAAAAGAATC CCAAAGCCAT TGACACGTGG
 801 ATTGAGAGCA TCTCTGAATT ACACCGTTCT AAGCCCCCTG CGACTGTGCA
 851 CTACACCAGG CCCATGCCCG ACATTGACAC GCTGATGCAG GAATGGTCCC
 901 CGGAGTTTGA AGAGCTTTTG GGCAAGGTAA GCCTGCCCAC GGCAGAGATT
 951 GATTGCAGCC TGGCAGAGTA CATTGACATG ATCTGTGCCA TTCTAGACAT
1001 CCCTGTCTAC AAGAGTCGGA TCCAGTCCCT CCATCTGCTC TTTTCCCTCT
1051 ACTCAGAATT CAAGAACTCA CAGCATTTTA AAGCTCTCGC TGAAGGCAAG
1101 AAAGCATTCA CTCCTTCATC CAATTCCACC TCCCAAGCTG GAGACATGGA
1151 GACATTAACC TTCAGCTGAG ACACTTCCCA AGCTGCTGTT TCAAGGCTGA
1201 GCTGGCCCCT CTGCCCCAGC TGAGATGGAC AGATCGTTGT CAGCTACTTG
1251 ATGTCCTTGC CCATGCCACA GCTTGGCTCA GGGGCAGTGC ATGTCCTGCT
1301 GCCCTCTCTG CCAGAGGGCA CAGAACATGT TTGTTTAATG AACCTGCCTG
1351 CCTCAGATTG CTGTCCCCGG GGAGTTAATG CATCTACACC ACTGTGGGGA
1401 TTTGAGTTAT AAGAATTGGA ATTTCTGAGA TCCCATGGAG GTTAGATTGG
1451 GAGGAAAGCT TAAAAGATGT CCTTTTTGTG AGAGGGATGG AATTGTTTTC
1501 TTTCATTCGT AAAGTTAGTG AGTAAAGATT TTATAAATCA AAAAAAAAAA
1551 AAAAAA
```

BLAST Results

Entry HS188252 from database EMBL:
human STS WI-12265.
Score = 2554, P = 4.1e-109, identities = 556/587

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 255 bp to 1166 bp; peptide length: 304
Category: putative protein

```
  1 MADNSSDECE EENNKEKKKT SQLTPQRGFS ENEDDDDDDD DSSETDSDSD
 51 DDDEEHGAPL EGAYDPADYE HLPVSAEIKE LFQYISRYTP QLIDLDHKLK
101 PFIPDFIPAV GDIDAFLKVP RPDGKPDNLG LLVLDEPSTK QSDPTVLSLW
151 LTENSKQHNI TQHMKVKSLE DAEKNPKAID TWIESISELH RSKPPATVHY
201 TRPMPDIDTL MQEWSPEFEE LLGKVSLPTA EIDCSLAEYI DMICAILDIP
251 VYKSRIQSLH LLFSLYSEFK NSQHFKALAE GKKAFTPSSN STSQAGDMET
301 LTFS
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_22n2, frame 3

PIR:S38149 SIS2 protein - yeast (Saccharomyces cerevisiae), N = 1,
Score = 132, P = 1e-05

```
>PIR:S38149 SIS2 protein - yeast (Saccharomyces cerevisiae)
           Length = 562

  HSPs:

 Score = 132 (19.8 bits), Expect = 1.0e-05, P = 1.0e-05
 Identities = 24/63 (38%), Positives = 35/63 (55%)

Query:      3 DNSSDECEEENNKEKKKTSQLTPQRGFSENEDDDDDDDDSSETDSDSDDDDEEHGAPLEG 62
              +   DE EEE++ E++ T             +++DDDDDDD  + D D DDD++E  A   G
Sbjct:    497 EEDDDEDEEEDDDEEEDTEDKNENNNDDDDDDDDDDDDDDDDDDDDDDDEDEDEAETPG 556

Query:     63 AYD 65
                D
Sbjct:    557 IID 559

 Score = 122 (18.3 bits), Expect = 1.4e-04, P = 1.4e-04
 Identities = 20/52 (38%), Positives = 33/52 (63%)

Query:      4 NSSDECEEENNKEKKKTSQLTPQRGFSENEDDDDDDDDSSETDSDSDDDDEE 55
              N+ +E ++E+ +E      + T  +  + N+DDDDDDD  + D D DDDD++
Sbjct:    494 NNEEEDDDEDEEEDDDEEEDTEDKNENNNDDDDDDDDDDDDDDDDDDDDDDD 545
```

Pedant information for DKFZphutel_22n2, frame 3

Report for DKFZphutel_22n2.3

```
[LENGTH]        304
[MW]            34285.85
[pI]            4.37
[PROSITE]       AMIDATION       1
[PROSITE]       CAMP_PHOSPHO_SITE      2
[PROSITE]       CK2_PHOSPHO_SITE       10
[PROSITE]       PKC_PHOSPHO_SITE       1
[PROSITE]       ASN_GLYCOSYLATION      3
[KW]            All_Alpha
[KW]            LOW_COMPLEXITY    11.84 %

SEQ     MADNSSDECEEENNKEKKKTSQLTPQRGFSENEDDDDDDDDSSETDSDSDDDDEEHGAPL
SEG     .........xxxxxxxxxx..........xxxxxxxxxxxxxxxxxxxxxxxxxx.....
PRD     cccccchhhhhhchhhhhhccccccccccccccccccccccccccccccccccccccccc

SEQ     EGAYDPADYEHLPVSAEIKELFQYISRYTPQLIDLDHKLKPFIPDFIPAVGDIDAFLKVP
SEG     ............................................................
PRD     cccccccccccchhhhhhhhhhhhhhhccccccccccccccccccccccccccccceeecc

SEQ     RPDGKPDNLGLLVLDEPSTKQSDPTVLSLWLTENSKQHNITQHMKVKSLEDAEKNPKAID
SEG     ............................................................
PRD     cccccccccceeeeeccccccccccccchhhhhhccccccccccccchhhhhhhhcccccch

SEQ     TWIESISELHRSKPPATVHYTRPMPDIDTLMQEWSPEFEELLGKVSLPTAEIDCSLAEYI
SEG     ............................................................
PRD     hhhhhhhhhhccccccceeeeecccccchhhhhhccccchhhhhccccccccccccchhhhhhh

SEQ     DMICAILDIPVYKSRIQSLHLLFSLYSEFKNSQHFKALAEGKKAFTPSSNSTSQAGDMET
SEG     ............................................................
```

```
PRD     hhhhhhhccccchhhhhhhhhhhhhhhhhhhhhcchhhhhhhhcccccccccccccccccc

SEQ     LTFS
SEG     ....
PRD     cccc
```

Prosite for DKFZphutel_22n2.3

PS00001	4->8	ASN_GLYCOSYLATION	PDOC00001
PS00001	159->163	ASN_GLYCOSYLATION	PDOC00001
PS00001	290->294	ASN_GLYCOSYLATION	PDOC00001
PS00004	17->21	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	18->22	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	138->141	PKC_PHOSPHO_SITE	PDOC00005
PS00006	5->9	CK2_PHOSPHO_SITE	PDOC00006
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006
PS00006	43->47	CK2_PHOSPHO_SITE	PDOC00006
PS00006	45->49	CK2_PHOSPHO_SITE	PDOC00006
PS00006	47->51	CK2_PHOSPHO_SITE	PDOC00006
PS00006	49->53	CK2_PHOSPHO_SITE	PDOC00006
PS00006	168->172	CK2_PHOSPHO_SITE	PDOC00006
PS00006	181->185	CK2_PHOSPHO_SITE	PDOC00006
PS00006	185->189	CK2_PHOSPHO_SITE	PDOC00006
PS00006	235->239	CK2_PHOSPHO_SITE	PDOC00006
PS00009	280->284	AMIDATION	PDOC00009

(No Pfam data available for DKFZphutel_22n2.3)

DKFZphutel_22o2
----

group: uterus derived

DKFZphutel_22o2 encodes a novel 537 amino acid protein without similarity to known proteins.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to S.pombe SPBC3E7.03c

complete cDNA, complete cds, EST hits

Sequenced by BMFZ

Locus: map="11p15.5"

Insert length: 2714 bp
Poly A stretch at pos. 2695, polyadenylation signal at pos. 2677

```
   1 GCAGGGCACG GTGGGGGCTG AGATCGTTTC CTGTTGGAAC TTCTGGCCCA
  51 AGAAGCGCGG GTCACAAGGA GAGGGGTCAG TTCGGTTCAG AGCGACTCAG
 101 CCCCTCGACT CGGGTCTTAA AACCTCCGAG CCGCCAGTTC TGCCTCAGGC
 151 CGCGCCCCCT TAAAGCGCCA CCAGACGCTG CGCCCCGTTA AAGCGCCACC
 201 AGACGCCGCG CCCCGTCCCG GCCTCCCCCG CGCGCTGGCG CGGGGCTTTC
 251 TGGGCCAGGG CGGGGCCGGC GAACTGCGGC CCGGAACGGC TGAGGAAGGG
 301 CCCGTCCCGC CTTCCCCGGC GCGCCATGGA GCCCCGGGCG GTTGCAGAAG
 351 CCGTGGAGAC GGGTGAGGAG GATGTGATTA TGGAAGCTCT GCGGTCATAC
 401 AACCAGGAGC ACTCCCAGAG CTTCACGTTT GATGATGCCC AACAGGAGGA
 451 CCGGAAGAGA CTGGCGGAGC TGCTGGTCTC CGTCCTGGAA CAGGGCTTGC
 501 CACCCTCCCA CCGTGTCATC TGGCTGCAGA GTGTCCGAAT CCTGTCCCGG
 551 GACCGCAACT GCCTGGACCC GTTCACCAGC CGCCAGAGCC TGCAGGCACT
 601 AGCCTGCTAT GCTGACATCT CTGTCTCTGA GGGGTCCGTC CCAGAGTCCG
 651 CAGACATGGA TGTTGTACTG GAGTCCCTCA AGTGCCTGTG CAACCTCGTG
 701 CTCAGCAGCC CTGTGGCACA GATGCTGGCA GCAGAGGCCC GCCTAGTGGT
 751 GAAGCTCACA GAGCGTGTGG GGCTGTACCG TGAGAGGAGC TTCCCCCACG
 801 ATGTCCAGTT CTTTGACTTG CGGCTCCTCT TCCTGCTAAC GGCACTCCGC
 851 ACCGATGTGC GCCAGCAGCT GTTTCAGGAG CTGAAAGGAG TGCGCCTGCT
 901 AACTGACACA CTGGAGCTGA CGCTGGGGGT GACTCCTGAA GGGAACCCCC
 951 CACCCACGCT CCTTCCTTCC CAAGAGACTG AGCGGGCCAT GGAGATCCTC
1001 AAAGTGCTCT TCAACATCAC CCTGGACTCC ATCAAGGGGG AGGTGGACGA
1051 GGAAGACGCT GCCCTTTACC GACACCTGGG GACCCTTCTC CGGCACTGTG
1101 TGATGATCGC TACTGCTGGA GACCGCACAG AGGAGTTCCA CGGCCACGCA
1151 GTGAACCTCC TGGGGAACTT GCCCCTCAAG TGTCTGGATG TTCTCCTCAC
1201 CCTGGAGCCA CATGGAGACT CCACGGAGTT CATGGGAGTG AATATGGATG
1251 TGATTCGTGC CCTCCTCATC TTCCTAGAGA AGCGTTTGCA CAAGACACAC
1301 AGGCTGAAGG AGAGTGTAGC TCCCGTGCTG AGCGTGCTGA CTGAATGTGC
1351 CCGGATGCAC CGCCCAGCCA GGAAGTTCCT GAAGGCCCAG GGATGGCCAC
1401 CTCCCCAGGT GCTGCCCCCT CTGCGGGATG TGAGGACACG GCCTGAGGTT
1451 GGGGAGATGC TGCGGAACAA GCTTGTCCGC CTCATGACAC ACCTGGACAC
1501 AGATGTGAAG AGGGTGGCTG CCGAGTTCTT GTTTGTCCTG TGCTCTGAGA
1551 GTGTGCCCCG ATTCATCAAG TACACAGGCT ATGGGAATGC TGCTGGCCTT
1601 CTGGCTGCCA GGGGCCTCAT GGCAGGAGGC CGGCCCGAGG GCCAGTACTC
1651 AGAGGATGAG GACACAGACA CAGATGAGTA CAAGGAAGCC AAAGCCAGCA
1701 TAAACCCTGT GACCGGGAGG GTGGAGGAGA AGCCGCCTAA CCCTATGGAG
1751 GGCATGACAG AGGAGCAGAA GGAGCACGAG GCCATGAAGC TGGTGACCAT
1801 GTTTGACAAG CTCTCCAGGA ACAGAGTCAT CCAGCCAATG GGGATGAGTC
1851 CCCGGGGTCA TCTTACGTCC CTGCAGGATG CCATGTGCGA GACTATGGAG
1901 CAGCAGCTCT CCTCGGACCC TGACTCGGAC CCTGACTGAG GATGGCAGCT
1951 CTTCTGCTCC CCCATCAGGA CTGGTGCTGC TTCCAGAGAC TTCCTTGGGG
2001 TTGCAACCTG GGGAAGCCAC ATCCCACTGG ATCCACACCC GCCCCCACTT
2051 CTCCATCTTA GAAACCCCTT CTCTTGACTC CCGTTCTGTT CATGATTTGC
2101 CTCTGGTCCA GTTTCTCATC TCTGGACTGC AACGGTCTTC TTGTGCTAGA
2151 ACTCAGGCTC AGCCTCGAAT TCCACAGACG AAGTACTTTC TTTTGTCTGC
2201 GCCAAGAGGA ATGTGTTCAG AAGCTGCTGC CTGAGGGCAG GGCCTACCTG
2251 GGCACACAGA AGAGCATATG GGAGGGCAGG GGTTTGGGTG TGGGTGCACA
2301 CAAAGCAAGC ACCATCTGGG ATTGGCACAC TGGCAGAGCC AGTGTGTTGG
2351 GGTATGTGCT GCACTTCCCA GGGAGAAAAC CTGTCAGAAC TTTCCATACG
2401 AGTATATCAG AACACACCCT TCCAAGGTAT GTATGCTCTG TTGTTCCTGT
2451 CCTGTCTTCA CTGAGCGCAG GGCTGGAGGC CTCTTAGACA TTCTCCTTGG
2501 TCCTCGTTCA GCTGCCCACT GTAGTATCCA CAGTGCCCGA GTTCTCGCTG
2551 GTTTTGGCAA TTAAACCTCC TTCCTACTGG TTTAGACTAC ACTTACAACA
2601 AGGAAAATGC CCCTCGTGTG ACCATAGATT GAGATTTATA CCACATACCA
2651 CACATAGCCA CAGAAACATC ATCTTGAAAT AAAGAAGAGT TTTGGACAAA
2701 AAAAAAAAAA AAAA
```

BLAST Results

Entry AF015416 from database EMBL:
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
Score = 3356, P = 2.0e-144, identities = 672/673

Entry HS263253 from database EMBL:
human STS SHGC-15914.
Score = 1143, P = 9.0e-46, identities = 245/255

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 326 bp to 1936 bp; peptide length: 537
Category: similarity to unknown protein

```
  1 MEPRAVAEAV ETGEEDVIME ALRSYNQEHS QSFTFDDAQQ EDRKRLAELL
 51 VSVLEQGLPP SHRVIWLQSV RILSRDRNCL DPFTSRQSLQ ALACYADISV
101 SEGSVPESAD MDVVLESLKC LCNLVLSSPV AQMLAAEARL VVKLTERVGL
151 YRERSFPHDV QFFDLRLLFL LTALRTDVRQ QLFQELKGVR LLTDTLELTL
201 GVTPEGNPPP TLLPSQETER AMEILKVLFN ITLDSIKGEV DEEDAALYRH
251 LGTLLRHCVM IATAGDRTEE FHGHAVNLLG NLPLKCLDVL LTLEPHGDST
301 EFMGVNMDVI RALLIFLEKR LHKTHRLKES VAPVLSVLTE CARMHRPARK
351 FLKAQGWPPP QVLPPLRDVR TRPEVGEMLR NKLVRLMTHL DTDVKRVAAE
401 FLFVLCSESV PRFIKYTGYG NAAGLLAARG LMAGGRPEGQ YSEDEDTDTD
451 EYKEAKASIN PVTGRVEEKP PNPMEGMTEE QKEHEAMKLV TMFDKLSRNR
501 VIQPMGMSPR GHLTSLQDAM CETMEQQLSS DPDSDPD
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_22o2, frame 2

TREMBL:SPBC3E7_3 gene: "SPBC3E7.03c"; product: "hypothetical protein";
S.pombe chromosome II cosmid c3E7., N = 1, Score = 112, P = 0.0023

```
>TREMBL:SPBC3E7_3 gene: "SPBC3E7.03c"; product: "hypothetical protein";
     S.pombe chromosome II cosmid c3E7.
            Length = 362

  HSPs:

 Score = 112 (16.8 bits), Expect = 2.3e-03, P = 2.3e-03
 Identities = 71/289 (24%), Positives = 124/289 (42%)

Query:   215 SQETERAM-EILKVLFNITLDSIKGEVDEEDAALYRHLGTLLRHCVMIATAGDRTEEFHG 273
             SQ+ E  + EIL++LF I+  S   E DE+   L       L+       +   +
Sbjct:    12 SQDNEMVLTEILRLLFPISKRSYLKEEDEQKILL------LVIEIWASSLNNNPNSPLRW 65

Query:   274 HAVN-LLG-NLPLKCLDVLLTLEPHGDSTEFMGVNMDVIRALLIFLEKRLHKTH----RL 327
             HA N LL  NL L  LD + +        T    +   +I   + +LEK L+        +
Sbjct:    66 HATNALLSFNLQLLSLDQAIYVSEIACQT----LQSILISREVEYLEKGLNLCFDIAAKY 121

Query:   328 KESVAPVLSVLTECARMHRPARKFLKAQGWPPPQVLPPLRDVRTRP-EVGEMLRNKLVRL 386
             + ++ P+L++L              +          +L P  D R +  + G+  R  L+RL
Sbjct:   122 QNTLPPILAILLSLLSFFNIKQNL--------SMLLFPTNDDRKQSLQKGKSFRCLLLRL 173

Query:   387 MT-HLDTDVKRVAAEFLFVLCSESVPRFIKYTGYGNAAGLLAARGLMAGGRPEGQYS--- 442
             +T  +   +    A  L  LC       +  + G G A G+          M     P  + +
Sbjct:   174 LTIPIVEPIGTYYASLLNELCDGDSQQIARIFGAGYAMGISQHSETMPFPSPLSKAASPV 233

Query:   443 -EDEDTDTDEYKEAKASINPVTGRV--EEKPPNPMEGMTEEQKEHEAMKLVTMFDKLSRN 499
              +        + +E   +I+P+TG +          +E +++E+KE EA +L  +F +L +N
Sbjct:   234 FQKNSRGQENTEENNLAIDPITGSMCTNRNKSQRLE-LSQEEKEREAERLFYLFQRLEKN 292
```

```
Query:    500 RVIQ 503
                IQ
Sbjct:    293 STIQ 296
```

Pedant information for DKFZphutel_22o2, frame 2

Report for DKFZphutel_22o2.2

```
[LENGTH]      537
[MW]          60372.53
[pI]          5.20
[BLOCKS]      BL00415L Synapsins proteins
[PROSITE]     MYRISTYL         4
[PROSITE]     CK2_PHOSPHO_SITE        13
[PROSITE]     PKC_PHOSPHO_SITE        10
[PROSITE]     ASN_GLYCOSYLATION       1
[KW]          All_Alpha
[KW]          LOW_COMPLEXITY      9.50 %
```

```
SEQ   MEPRAVAEAVETGEEDVIMEALRSYNQEHSQSFTFDDAQQEDRKRLAELLVSVLEQGLPP
SEG   ............................................................
PRD   ccchhhhhhhhhcccchhhhhhhhhhcccccceeecccchhhhhhhhhhhhhhhhhhccccc

SEQ   SHRVIWLQSVRILSRDRNCLDPFTSRQSLQALACYADISVSEGSVPESADMDVVLESLKC
SEG   ............................................................
PRD   cceeeeecccccccccccccccccchhhhhhhhhhhceeeeccccccccchhhhhhhhh

SEQ   LCNLVLSSPVAQMLAAEARLVVKLTERVGLYRERSFPHDVQFFDLRLLFLLTALRTDVRQ
SEG   .........................................xxxxxxxxxxxxxx...
PRD   hhhhccccchhhhhhhhhhhhhhhhhcccccccccccccchhhhhhhhhhhhhhhhhh

SEQ   QLFQELKGVRLLTDTLELTLGVTPEGNPPPTLLPSQETERAMEILKVLFNITLDSIKGEV
SEG   ............................................................
PRD   hhhhhhchhhhhhhhhhhhcccccccccccccchhhhhhhhhhhhhhhhhhccccchhh

SEQ   DEEDAALYRHLGTLLRHCVMIATAGDRTEEFHGHAVNLLGNLPLKCLDVLLTLEPHGDST
SEG   ............................................................
PRD   hhhhhhhhhhhhhhhhhhhhccccccccccccceeeeeccccccccceeeeeeeccccccc

SEQ   EFMGVNMDVIRALLIFLEKRLHKTHRLKESVAPVLSVLTECARMHRPARKFLKAQGWPPP
SEG   ............................................................
PRD   eeeehhhhhhhhhhhhhhhhhhhhhhhhcccceeeehhhhhhhhchhhhhhhhcccccccc

SEQ   QVLPPLRDVRTRPEVGEMLRNKLVRLMTHLDTDVKRVAAEFLFVLCSESVPRFIKYTGYG
SEG   .........................................................xxx
PRD   cccccccccccchhhhhhhhhhhhhhhhhcccchhhhhhhhhhhhhhcccccceeeecccc

SEQ   NAAGLLAARGLMAGGRPEGQYSEDEDTDTDEYKEAKASINPVTGRVEEKPPNPMEGMTEE
SEG   xxxxxxxxxxxxxxx.......xxxxxxxxx.............................
PRD   chhhhhhhhhccccccccccccccccccchhhhhhhhhcccccceeeccccccccchhhh

SEQ   QKEHEAMKLVTMFDKLSRNRVIQPMGMSPRGHLTSLQDAMCETMEQQLSSDPDSDPD
SEG   ................................................xxxxxxxxx
PRD   hhhhhhhhhhhhhhhhcccccccccccccccccchhhhhhhhhhhhhhhhhcccccccc
```

Prosite for DKFZphutel_22o2.2

PS00001	230->234	ASN_GLYCOSYLATION	PDOC00001
PS00005	61->64	PKC_PHOSPHO_SITE	PDOC00005
PS00005	69->72	PKC_PHOSPHO_SITE	PDOC00005
PS00005	84->87	PKC_PHOSPHO_SITE	PDOC00005
PS00005	117->120	PKC_PHOSPHO_SITE	PDOC00005
PS00005	145->148	PKC_PHOSPHO_SITE	PDOC00005
PS00005	218->221	PKC_PHOSPHO_SITE	PDOC00005
PS00005	235->238	PKC_PHOSPHO_SITE	PDOC00005
PS00005	324->327	PKC_PHOSPHO_SITE	PDOC00005
PS00005	463->466	PKC_PHOSPHO_SITE	PDOC00005
PS00005	508->511	PKC_PHOSPHO_SITE	PDOC00005
PS00006	12->16	CK2_PHOSPHO_SITE	PDOC00006
PS00006	34->38	CK2_PHOSPHO_SITE	PDOC00006
PS00006	52->56	CK2_PHOSPHO_SITE	PDOC00006
PS00006	99->103	CK2_PHOSPHO_SITE	PDOC00006
PS00006	104->108	CK2_PHOSPHO_SITE	PDOC00006
PS00006	263->267	CK2_PHOSPHO_SITE	PDOC00006
PS00006	371->375	CK2_PHOSPHO_SITE	PDOC00006

PS00006	388->392	CK2_PHOSPHO_SITE	PDOC00006
PS00006	442->446	CK2_PHOSPHO_SITE	PDOC00006
PS00006	447->451	CK2_PHOSPHO_SITE	PDOC00006
PS00006	491->495	CK2_PHOSPHO_SITE	PDOC00006
PS00006	515->519	CK2_PHOSPHO_SITE	PDOC00006
PS00006	530->534	CK2_PHOSPHO_SITE	PDOC00006
PS00008	57->63	MYRISTYL	PDOC00008
PS00008	420->426	MYRISTYL	PDOC00008
PS00008	424->430	MYRISTYL	PDOC00008
PS00008	430->436	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_22o2.2)

DKFZphutel_23e13
----

group: metabolism

DKFZphtes3_15j18 encodes a novel 148 amino acid protein with similarity to 27K heat shock proteins.

The novel protein contains a serine protease of the subtilase family with an aspartic acid-containing active site. Subtilases are an extensive family of serine proteases whose catalytic activity is provided by a charge relay system similar to that of the trypsin family of serine proteases but which evolved by independent convergent evolution. The sequence around the residues involved in the catalytic triad (aspartic acid, serine and histidine) are completely different from that of the analogous residues in the trypsin serine proteases. Thus the novel protein is a new member of this family.

The new protein can find application in modulation of proteinase activity in cells and as a new enzyme for proteomics and biotechnologic production processes.

heat shock protein HSP27

strong similarity to heat shock 27K proteins

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: /map="578.9 cR from top of Chr12 linkage group"

Insert length: 1854 bp
Poly A stretch at pos. 1831, polyadenylation signal at pos. 1810

```
   1 GGTTTATTAA GCTCCTGGCT CCGCTCTAGA CCTCAGCGGT TCTGGCTGCC
  51 AGCCTGGGCA GCCTGGGAAG CCTGGGAGGA CGGTGGCTTG CCGGTCTGTC
 101 GTGAGGCAGT GCGGACGGGG ACCCTCTGGG ATTCTGCTGG ATCTGCCCCG
 151 GGGGTTACCT TTGGGGGCTG GGACCCCAGT CGAGGGGACA CAACCGTCCC
 201 TGGCAGTGGT TGGTTCTGCT TCTCCCTGCA GAAAAGCAGC ATTTTCGGAA
 251 GCTGAAGAAT AAGCTAGCCC AGCCACACCA CCTTGTTGTG TGACCTTGGG
 301 CAGGTGGTTC TGTCTCTCTG AGCCTCTGTT TCTCTCTGAG CTGAGCAGCC
 351 ACCATGGCTG ACGGTCAGAT GCCCTTCTCC TGCCACTACC CAAGCCGCCT
 401 GCGCCGAGAC CCCTTCCGGG ACTCTCCCCT CTCCTCTCGC CTGCTGGATG
 451 ATGGCTTTGG CATGGACCCC TTCCCAGACG ACTTGACAGC CTCTTGGCCC
 501 GACTGGGCTC TGCCTCGTCT CTCCTCCGCC TGGCCAGGCA CCCTAAGGTC
 551 GGGCATGGTG CCCCGGGGCC CCACTGCCAC CGCCAGGTTT GGGGTGCCTG
 601 CCGAGGGCAG GACCCCCCCA CCCTTCCCTG GGGAGCCCTG GAAAGTGTGT
 651 GTGAATGTGC ACAGCTTCAA GCCAGAGGAG TTGATGGTGA AGACCAAAGA
 701 TGGATACGTG GAGGTGTCTG GCAAACATGA AGAGAAACAG CAAGAAGGTG
 751 GCATTGTTTC TAAGAACTTC ACAAAGAAAA TCCAGCTTCC TGCAGAGGTG
 801 GATCCTGTGA CAGTATTTGC CTCACTTTCC CCAGAGGGTC TGCTGATCAT
 851 CGAAGCTCCC CAGGTCCCTC CTTACTCAAC ATTTGGAGAG AGCAGTTTCA
 901 ACAACGAGCT TCCCCAGGAC AGCCAGGAAG TCACCTGTAC CTGAGATGCC
 951 AGTACTGGCC CATCCTTGTT TTGTCCCCAA CCCTAGGGCT TCTCTGATTC
1001 CAGGATACAT TACTTTAGCT GAACTCAGAT TTAGTGCAAG TAAAATGTTA
1051 GAGGGTGCGG GGGTGAGGAC TGACCACAGA TTCCCTGGAT AGTGTAGTGG
1101 TAGATTTCTC CACAGGATAG CGCAATTGGC AAATCATGCT TGGTTGTGTT
1151 AGGCCAAAAT ACTAGTTTTG CTTTCTTTAC CTTTTCTATC TTGATGAAAA
1201 TGTTGCACAT TCTATAGTTG CAAAACACAT AAAAGGGGAC TTAACATTTC
1251 ACGTTGTATC TTACTTGCAG TGAATGCAAG GGTTACTTTT CTCTGGGGAC
1301 CTCCCCCATC ACCCAGGTTC CTACTCTGGG CTCCCGATTC CCATGGCTCC
1351 CAAACCATGC CGCATGGTTT GGTTAATGAA ACCCAGTAGC TAACCCCACT
1401 GTGCTTCCAC ATGCCTGGCC TAAAATGGGT GATATACAGG TCTTATATCC
1451 CCATATGGAA TTTATCCATC AACCACATAA AAACAAACAG TGCCTTCTGC
1501 CCTCTGCCCA GATGTGTCCA GCACGTTCTC AAAGTTTCCA CATTAGCACT
1551 CCCTAAGGAC GCTGGGAGCC TGTCAGTTTA TGATCTGACC TAGGTCCCCC
1601 CTTTCTTCTG TCCCCTGTGT TTAAGTCGGG ATTTTTACAG AGGGAGCTGT
1651 CTCCAGACAG CTCCATCAGG AACCAAGCAA AGGCCAGATA GCCTGACAGA
1701 TAGGCTAGTG GTATTGTGTA TATGGGCGGG ACGTGTGTGT CATTATTATT
1751 TGAGTTATGC TGTTGTTTAG GGGTAAATAA CAGTAAATAA TTAATAATAA
1801 TAATAATAAT AATAAAGGAG CTGACGTTCT TAAAAAAGAA AAAAAAAAAA
1851 AAAA
```

BLAST Results

Entry HS286348 from database EMBL:
human STS TIGR-A002J47.
Score = 510, P = 1.2e-16, identities = 102/102

Medline entries

95394379:
Cloning and sequencing of a cDNA encoding the canine HSP27 protein.

94110260:
Physiological and pathological changes in levels of the two small stress proteins, HSP27 and alpha B crystallin, in rat hindlimb muscles

Peptide information for frame 3

ORF from 354 bp to 941 bp; peptide length: 196
Category: strong similarity to known protein
Prosite motifs: SUBTILASE_ASP (28-39)

```
  1 MADGQMPFSC HYPSRLRRDP FRDSPLSSRL LDDGFGMDPF PDDLTASWPD
 51 WALPRLSSAW PGTLRSGMVP RGPTATARFG VPAEGRTPPP FPGEPWKVCV
101 NVHSFKPEEL MVKTKDGYVE VSGKHEEKQQ EGGIVSKNFT KKIQLPAEVD
151 PVTVFASLSP EGLLIIEAPQ VPPYSTFGES SFNNELPQDS QEVTCT
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_23e13, frame 3

PIR:JC4244 heat-shock 27K protein - dog, N = 1, Score = 304, P = 4.3e-27

PIR:JN0924 heat shock 27 protein - rat, N = 1, Score = 301, P = 8.9e-27

TREMBL:MM03561_1 product: "heat shock protein HSP27"; Mus musculus heat shock protein HSP27 internal deletion variant b mRNA, complete cds., N = 1, Score = 301, P = 8.9e-27

```
>PIR:JC4244 heat-shock 27K protein - dog
          Length = 209

  HSPs:

 Score = 304 (45.6 bits), Expect = 4.3e-27, P = 4.3e-27
 Identities = 80/182 (43%), Positives = 102/182 (56%)

Query:    1 MADGQMPFSC-HYPSRLRRDPFRD-SPLSSRLLDDGFGMDPFPDDLTASWPDWALPRLSS 58
            M + ++PFS     PS    DPFRD  P  SRL D  FG+   P++    W  W      S
Sbjct:    1 MTERRVPFSLLRSPSW---DPFRDWYPAHSRLFDQAFGLPRLPEE----WAQWFG---HS 50

Query:   59 AWPGTLRSGMVP---RGPTATARFGVPAEGR--TPPPFPG--------EPWKVCVNVHSF 105
             WPG +R   +P    GP A A   PA  R  +    G          + W+V ++V+ F
Sbjct:   51 GWPGYVRP--IPPAVEGPAAAAAAAAPAYSRALSRQLSSGVSEIRQTADRWRVSLDVNHF 108

Query:  106 KPEELMVKTKDGYVEVSGKHEEKQQEGGIVSKNFTKKIQLPAEVDPVTVFASLSPEGLLI 165
             PEEL VKTKDG VE++GKHEE+Q E G +S+  T K  LP  VDP  V +SLSPEG L
Sbjct:  109 APEELTVKTKDGVVEITGKHEERQDEHGYISRRLTPKYTLPPGVDPTLVSSSLSPEGTLT 168

Query:  166 IEAPQVPPYSTFGE 179
            +EAP  P +   E
Sbjct:  169 VEAPMPKPATQSAE 182
```

Pedant information for DKFZphutel_23e13, frame 3

Report for DKFZphutel_23e13.3

[LENGTH] 196
[MW] 21604.37

```
[pI]            5.00
[HOMOL]         PIR:JC4244 heat-shock 27K protein - dog 3e-22
[BLOCKS]        BL01031C
[PIRKW]         blocked amino end 1e-13
[PIRKW]         acetylated amino end 4e-13
[PIRKW]         phosphoprotein 7e-21
[PIRKW]         glycoprotein 2e-11
[PIRKW]         heat shock 7e-21
[PIRKW]         molecular chaperone 4e-13
[PIRKW]         alternative splicing 1e-19
[PIRKW]         eye lens 6e-14
[PIRKW]         stress-induced protein 7e-21
[SUPFAM]        alpha-crystallin 7e-21
[PROSITE]       SUBTILASE_ASP  1
[PROSITE]       MYRISTYL       2
[PROSITE]       CK2_PHOSPHO_SITE       2
[PROSITE]       PKC_PHOSPHO_SITE       6
[PROSITE]       ASN_GLYCOSYLATION      1
[PFAM]          Heat shock hsp20 proteins
[KW]            All_Beta
[KW]            LOW_COMPLEXITY     7.14 %

SEQ   MADGQMPFSCHYPSRLRRDPFRDSPLSSRLLDDGFGMDPFPDDLTASWPDWALPRLSSAW
SEG   .............................xxxxxxxxxxxxxx................
PRD   ccccccccccccccccccccccccccchhhhhcccccccccccccccccccccccccccc

SEQ   PGTLRSGMVPRGPTATARFGVPAEGRTPPPFPGEPWKVCVNVHSFKPEELMVKTKDGYVE
SEG   ............................................................
PRD   cccccccccccccchhhhhhhcccccchhhhhheeeeeeccccceeeeeccccceee

SEQ   VSGKHEEKQQEGGIVSKNFTKKIQLPAEVDPVTVFASLSPEGLLIIEAPQVPPYSTFGES
SEG   ............................................................
PRD   ecchhhhhcccceeeeccccccccccccccceeeeccccceeeeeccccccccccccc

SEQ   SFNNELPQDSQEVTCT
SEG   ................
PRD   cccccccccceeeccc
```

Prosite for DKFZphute1_23e13.3

```
PS00001    138->142   ASN_GLYCOSYLATION    PDOC00001
PS00005     27->30    PKC_PHOSPHO_SITE     PDOC00005
PS00005     63->66    PKC_PHOSPHO_SITE     PDOC00005
PS00005     76->79    PKC_PHOSPHO_SITE     PDOC00005
PS00005    104->107   PKC_PHOSPHO_SITE     PDOC00005
PS00005    122->125   PKC_PHOSPHO_SITE     PDOC00005
PS00005    140->143   PKC_PHOSPHO_SITE     PDOC00005
PS00006     47->51    CK2_PHOSPHO_SITE     PDOC00006
PS00006    176->180   CK2_PHOSPHO_SITE     PDOC00006
PS00008     62->68    MYRISTYL             PDOC00008
PS00008    132->138   MYRISTYL             PDOC00008
PS00136     28->39    SUBTILASE_ASP        PDOC00125
```

Pfam for DKFZphute1_23e13.3

```
HMM_NAME      Heat shock hsp20 proteins

HMM               *AMMrpPWDWRE.....DpDHFeVrMDMPGFKPEEIKVkVEDNNVLvIeG
                   A    P++ R         + ++V++++  FKPEE+ VK+ D+ +++++G
Query          77  ARFGVPAEGR-TPPPFPGEPWKVCVNVHSFKPEELMVKTKDG-YVEVSG     123

HMM               EHEREEEREDDkWWWHERIYRHFMRRFrLPENVDpDqIkAsMSdNGVLTI
                  +HE    E++        + + ++  F  +++LP +VDP  + AS+S++G+L I
Query         124 KHE---EKQQ----EGGIVSKNFTKKIQLPAEVDPVTVFASLSPEGLLII     166

HMM               TVPKpEP*
                  ++P ++P
Query         167 EAPQVPP    173
```

DKFZphutel_23g11

group: uterus derived

DKFZphutel_23g11 encodes a novel 256 amino acid protein with similarity to S.pombe SPAC31G5.12c and S. cerevisiae Maf1p.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes.

similarity to SPAC31G5.12c and Maf1p

complete cDNA, complete cds, EST hits

Sequenced by EMBL

Locus: unknown

Insert length: 1674 bp
Poly A stretch at pos. 1664, polyadenylation signal at pos. 1644

```
   1 GGGGGAGGCG GAGGTCGCTC GCTCGCTCGC TCGGCTCGCT GACTCGCCGG
  51 AGCGCTCTGT GGCGGTCGGC GGCAGGTCGG TCGCGAGAGC GGGCTCTGTG
 101 GAAGGGGGCG AGGCTATGTC GCGGTGGCAG CCCGGATGGG CCGGCAGGGC
 151 CGGGAGTAAC GGGACGTCGC CGCGGAGCTT CTTCCCCCGG ATACAGTGCG
 201 GCCCGAGCGG AGGCCGCGGC GCCGCCCTCC GATCTTGAAG AGCCCGCGCT
 251 GCGCGGAGCC CGCCCCCGCC TGCGCACCGG CACCGACGCG GAGCGACCAG
 301 CCCAGCCAGA CCCGGCCCGG CGCGGCCTGA TCTAACCCAG CCAGGCAGGC
 351 AATACTAGCC CCTCTGGAGC ACGGAGCTCC TTCCCCAAAG ACATGAAGCT
 401 ATTGGAGAAC TCGAGCTTTG AAGCCATCAA CTCACAGCTG ACTGTGGAGA
 451 CCGGAGATGC CCACATCATT GGCAGGATTG AGAGCTACTC ATGTAAGATG
 501 GCAGGAGACG ACAAACACAT GTTCAAGCAG TTCTGCCAGG AGGGCCAGCC
 551 CCACGTGCTG GAGGCACTTT CTCCACCCCA GACTTCAGGA CTGAGCCCCA
 601 GCAGACTCAG CAAAAGCCAA GGCGGTGAGG AGGAGGGCCC CCTCAGTGAC
 651 AAGTGCAGCC GCAAGACCCT CTTCTACCTG ATTGCCACGC TCAATGAGTC
 701 CTTCAGGCCT GACTATGACT TCAGCACAGC CCGCAGCCAT GAGTTCAGCC
 751 GGGAGCCCAG CCTTAGCTGG GTGGTGAATG CAGTCAACTG CAGTCTGTTC
 801 TCAGCTGTGC GGGAGGACTT CAAGGATCTG AAACCACAGC TGTGGAACGC
 851 GGTGGACGAG GAGATCTGCC TGGCTGAATG TGACATCTAC AGCTATAACC
 901 CAGACTTGGA CTCAGATCCC TTCGGGGAGG ATGGTAGCCT CTGGTCCTTC
 951 AACTACTTCT TCTACAACAA GCGGCTCAAG CGAATCGTCT TCTTTAGCTG
1001 CCGTTCCATC AGTGGCTCCA CCTACACACC CTCAGAGGCA GGCAACGAGC
1051 TGGACATGGA GCTGGGGGAG GAGGAGGTGG AGGAAGAAAG CAGAAGCAGG
1101 GGCAGTGGGG CCGAGGAGAC CAGCACCATG GAGGAGGACA GGGTCCCAGT
1151 GATCTGTATT TGATGAGGAG GAGCCGAGGC CCCAGCTTCA TCCAGCTTCA
1201 ACCAATGCCT GGACCTGTCC ACCTGAGAGG CCCCTGGGGC CTCCCCAGCT
1251 GCTGGCCAGA CCCTGGCGCT GCCACAGTCC TGGCACTGCC CAAGGCCATA
1301 CCTGCCTAGC CCTTTGGCTC CATCCTGTGG ATGCCCACTC ACCCCTCAGA
1351 CTCCTGCTGC CCATGCTGTG GCCGGACTTG TCAGCAGGGG GCCTGGTGGG
1401 AGGAGCGACT GCCCTGCCCA AATGAACTGC CACAGCAGGG ACAGCTGGAC
1451 CGCAGAGTTT ATTTTTGTAT TTCTACTGGG CCTGCACACT CCAGCCCAAA
1501 GGGTCTGTGG CCGGAGGCCC CACGAGCAGG CCCCAGCAGT CACCGGCTCT
1551 GGTCTTGGGC CGGCCCCGGT GCCCACCTGT ACCCCCACCT CGCCCATTTG
1601 GCCGCGTGCA CTGAGTGTCA CTTTGCTGCA GCTCGTTTCT TTCCAATAAA
1651 AGTTTCTGTG ACTTAAAAAA AAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 393 bp to 1160 bp; peptide length: 256
Category: similarity to known protein

```
  1 MKLLENSSFE AINSQLTVET GDAHIIGRIE SYSCKMAGDD KHMFKQFCQE
 51 GQPHVLEALS PPQTSGLSPS RLSKSQGGEE EGPLSDKCSR KTLFYLIATL
101 NESFRPDYDF STARSHEFSR EPSLSWVVNA VNCSLFSAVR EDFKDLKPQL
151 WNAVDEEICL AECDIYSYNP DLDSDPFGED GSLWSFNYFF YNKRLKRIVF
201 FSCRSISGST YTPSEAGNEL DMELGEEEVE EESRSRGSGA EETSTMEEDR
251 VPVICI
```

BLASTP hits

Entry SPAC31G5_12 from database TREMBL:
gene: "SPAC31G5.12c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c31G5.
Score = 272, P = 9.3e-24, identities = 51/127, positives = 80/127

Entry SPD656_1 from database TREMBL:
product: "ORF N150"; Yeast DNA for bfr2+ protein/pad1+ protein/sks1+ protein, ORF N313, ORF N150, complete cds, and for ORF N118, partial cds.
Score = 263, P = 8.4e-23, identities = 50/127, positives = 79/127

Entry S50986 from database PIR:
MAF1 protein - yeast (Saccharomyces cerevisiae) >SWISSPROT:MAF1_YEAST MAF1 PROTEIN. >TREMBL:SC19492_1 gene: "MAF1"; product: "Maf1p"; Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds. >TREMBL:SC8119_11 gene: "MAF1p"; product: "Maf1p"; S.cerevisiae chromosome IV cosmid 8119.
Score = 180, P = 2.3e-17, identities = 43/133, positives = 75/133

Entry AF098499_2 from database TREMBL:
gene: "C43H8.2"; Caenorhabditis elegans cosmid C43H8.
Score = 263, P = 9.2e-23, identities = 78/252, positives = 118/252

Alert BLASTP hits for DKFZphute1_23g11, frame 3

No Alert BLASTP hits found

Pedant information for DKFZphute1_23g11, frame 3

Report for DKFZphute1_23g11.3

```
[LENGTH]     256
[MW]         28869.95
[pI]         4.51
[HOMOL]      TREMBL:SPAC31G5_12 gene: "SPAC31G5.12c"; product: "hypothetical protein"; S.pombe chromosome I cosmid c31G5. 4e-23
[FUNCAT]     06.04 protein targeting, sorting and translocation  [S. cerevisiae, YDR005c] 6e-13
[PROSITE]    MYRISTYL           3
[PROSITE]    CK2_PHOSPHO_SITE     5
[PROSITE]    PKC_PHOSPHO_SITE     6
[PROSITE]    ASN_GLYCOSYLATION    3
[KW]         All_Alpha
[KW]         LOW_COMPLEXITY     7.81 %

SEQ   MKLLENSSFEAINSQLTVETGDAHIIGRIESYSCKMAGDDKHMFKQFCQEGQPHVLEALS
SEG   ............................................................
PRD   ccccchhhhhhhhhhhhcccccceeeeeccccchhhhhcchhhhhhhhhccccceeeeccc

SEQ   PPQTSGLSPSRLSKSQGGEEEGPLSDKCSRKTLFYLIATLNESFRPDYDFSTARSHEFSR
SEG   ............................................................
PRD   cccccccccccccccccccccccccccchhhhhhhhhhhcccccccccccccccccccc

SEQ   EPSLSWVVNAVNCSLFSAVREDFKDLKPQLWNAVDEEICLAECDIYSYNPDLDSDPFGED
SEG   ............................................................
PRD   cccccchhhhhhhhhhhhchhhhhhhhhhhhhhhhcccccceeecccccccccccccc

SEQ   GSLWSFNYFFYNKRLKRIVFFSCRSISGSTYTPSEAGNELDMELGEEEVEEESRSRGSGA
SEG   ..........................................xxxxxxxxxxxxxxxxxx
PRD   ccceeeceeechhhhhhhhhhhccccccccccccccccchhhhhhhhhhhhhcccccc

SEQ   EETSTMEEDRVPVICI
SEG   xx..............
PRD   cccccccccceeeccc
```

Prosite for DKFZphutel_23g11.3

PS00001	6->10	ASN_GLYCOSYLATION	PDOC00001
PS00001	101->105	ASN_GLYCOSYLATION	PDOC00001
PS00001	132->136	ASN_GLYCOSYLATION	PDOC00001
PS00005	33->36	PKC_PHOSPHO_SITE	PDOC00005
PS00005	85->88	PKC_PHOSPHO_SITE	PDOC00005
PS00005	89->92	PKC_PHOSPHO_SITE	PDOC00005
PS00005	103->106	PKC_PHOSPHO_SITE	PDOC00005
PS00005	112->115	PKC_PHOSPHO_SITE	PDOC00005
PS00005	202->205	PKC_PHOSPHO_SITE	PDOC00005
PS00006	7->11	CK2_PHOSPHO_SITE	PDOC00006
PS00006	99->103	CK2_PHOSPHO_SITE	PDOC00006
PS00006	212->216	CK2_PHOSPHO_SITE	PDOC00006
PS00006	238->242	CK2_PHOSPHO_SITE	PDOC00006
PS00006	244->248	CK2_PHOSPHO_SITE	PDOC00006
PS00008	66->72	MYRISTYL	PDOC00008
PS00008	181->187	MYRISTYL	PDOC00008
PS00008	239->245	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_23g11.3)

DKFZphutel_24c19
----

group: transmembrane protein

DKFZphutel_24c19 encodes a novel 195 amino acid protein without similarity to known proteins.

The novel protein contains 1 transmembrane region.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of uterus-specific genes and as a new marker for uterine cells.

unknown
membrane regions: 1
Summary DKFZphutel_24c19 encodes a novel 195 amino acid protein, with no similarity to known proteins.

unknown

complete cDNA, complete cds, EST hits
TRANSMEMBRANE 1

Sequenced by Qiagen

Locus: unknown

Insert length: 769 bp
Poly A stretch at pos. 746, polyadenylation signal at pos. 735

```
  1 ACGAGTCAGC CAAAGATGGC TGCGCCCAGG TAATTTGAGC AAAGGCCACA
 51 GTGAACTCCG GCGTGGCTGA GGAAGACCGG AGGAGGCACC CACAGGCTGC
101 TGGGAGGAGA GCATAAGGCT CAAAATGGAA AATCATAAAT CCAATAATAA
151 GGAAAACATA ACAATTGTTG ATATATCCAG AAAAATTAAC CAGCTTCCAG
201 AAGCAGAAAG GAATCTACTT GAAAATGGAT CGGTTTATGT TGGATTAAAT
251 GCTGCTCTTT GTGGCCTCAT AGCAAACAGT CTTTTTCGAC GCATCTTGAA
301 TGTGACAAAG GCTCGCATAG CTGCTGGCTT ACCAATGGCA GGGATACCTT
351 TTCTTACAAC AGACTTAACT TACAGATGTT TTGTAAGTTT TCCTTTGAAT
401 ACAGGTGATT TGGATTGTGA AACCTGTACC ATAACACGGA GTGGACTGAC
451 TGGTCTTGTT ATTGGTGGTC TATACCCTGT TTTCTTGGCT ATACCTGTAA
501 ATGGTGGTCT AGCAGCCAGG TATCAATCAG CTCTGTTACC ACACAAAGGG
551 AACATCTTAA GTTACTGGAT TAGAACTTCT AAGCCTGTCT TTAGAAAGAT
601 GTTATTTCCT ATTTTGCTCC AGACTATGTT TTCAGCATAC CTTGGGTCTG
651 AACAATATAA ACTACTTATA AAGGCCCTTC AGTTATCTGA ACCTGGCAAA
701 GAAATTCACT GATTTTAAAC AAATATGTAA ACAAAAATAA AATGGTAAAA
751 ACAAAAAAAA AAAAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 125 bp to 709 bp; peptide length: 195
Category: putative protein

```
  1 MENHKSNNKE NITIVDISRK INQLPEAERN LLENGSVYVG LNAALCGLIA
 51 NSLFRRILNV TKARIAAGLP MAGIPFLTTD LTYRCFVSFP LNTGDLDCET
101 CTITRSGLTG LVIGGLYPVF LAIPVNGGLA ARYQSALLPH KGNILSYWIR
151 TSKPVFRKML FPILLQTMFS AYLGSEQYKL LIKALQLSEP GKEIH
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_24c19, frame 2

No Alert BLASTP hits found

Pedant information for DKFZphutel_24c19, frame 2

Report for DKFZphutel_24c19.2

```
[LENGTH]      195
[MW]          21527.45
[pI]          9.36
[PROSITE]     MYRISTYL        6
[PROSITE]     CK2_PHOSPHO_SITE        1
[PROSITE]     PKC_PHOSPHO_SITE        3
[PROSITE]     ASN_GLYCOSYLATION       3
[KW]          TRANSMEMBRANE   1

SEQ    MENHKSNNKENITIVDISRKINQLPEAERNLLENGSVYVGLNAALCGLIANSLFRRILNV
PRD    cccccccccceeeeeehhhhhhccchhhhhhhcccccceeeecchhhhhhhhhhhhhhhh
MEM    ............................................................

SEQ    TKARIAAGLPMAGIPFLTTDLTYRCFVSFPLNTGDLDCETCTITRSGLTGLVIGGLYPVF
PRD    hhhhhhhcccccccceeeeecccccccccccccccccccccccccccccceeeeccccceee
MEM    .............................................MMMMMMMMMMMMMMM

SEQ    LAIPVNGGLAARYQSALLPHKGNILSYWIRTSKPVFRKMLFPILLQTMFSAYLGSEQYKL
PRD    eeeccccccchhhhhhcccccccceeeeeeeccccchhhhhchhhhhhhhhhhhhhcchhhhh
MEM    MMM.........................................................

SEQ    LIKALQLSEPGKEIH
PRD    hhhhhhhcccccccc
MEM    ...............
```

Prosite for DKFZphutel_24c19.2

PS00001	11->15	ASN_GLYCOSYLATION	PDOC00001
PS00001	34->38	ASN_GLYCOSYLATION	PDOC00001
PS00001	59->63	ASN_GLYCOSYLATION	PDOC00001
PS00005	18->21	PKC_PHOSPHO_SITE	PDOC00005
PS00005	82->85	PKC_PHOSPHO_SITE	PDOC00005
PS00005	151->154	PKC_PHOSPHO_SITE	PDOC00005
PS00006	13->17	CK2_PHOSPHO_SITE	PDOC00006
PS00008	40->46	MYRISTYL	PDOC00008
PS00008	47->53	MYRISTYL	PDOC00008
PS00008	68->74	MYRISTYL	PDOC00008
PS00008	110->116	MYRISTYL	PDOC00008
PS00008	127->133	MYRISTYL	PDOC00008
PS00008	142->148	MYRISTYL	PDOC00008

(No Pfam data available for DKFZphutel_24c19.2)

DKFZphutel_24e11
----

group: intracellular transport and trafficking

DKFZphutel_24e11 encodes a novel 226 amino acid protein, with similarity to human/mouse golgi 4-transmembrane spanning transporter MTP. MTP may function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment. Thus, the novel protein also seems to be involved in nucleotide sugar transport.

The new protein can find application in modulating the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartments.

similarity to 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP

complete cDNA, complete cds, EST hits
potential start at 184,
TRANSMEMBRANE 4
function in the transport of nucleosides and/or nucleoside derivatives
between the cytosol and
the lumen of an intracellular membrane-bound compartment?

Sequenced by Qiagen

Locus: /map="8"

Insert length: 2005 bp
Poly A stretch at pos. 1988, polyadenylation signal at pos. 1963

```
   1 ACGCGTCCGG CAGAAGCTCG GAGCTCTCGG GGTATCGAGG AGGCAGGCCC
  51 GCGGGCGCAC GGGCGAGCGG GCCGGGAGCC GGAGCGGCGG AGGAGCCGGC
 101 AGCAGCGGCG CGGCGGGCTC CAGGCGAGGC GGTCGACGCT CCTGAAAACT
 151 TGCGCGCGCG CTCGCGCCAC TGCGCCCGGA GCGATGAAGA TGGTCGCGCC
 201 CTGGACGCGG TTCTACTCCA ACAGCTGCTG CTTGTGCTGC CATGTCCGCA
 251 CCGGCACCAT CCTGCTCGGC GTCTGGTATC TGATCATCAA TGCTGTGGTA
 301 CTGTTGATTT TATTGAGTGC CCTGGCTGAT CCGGATCAGT ATAACTTTTC
 351 AAGTTCTGAA CTGGGAGGTG ACTTTGAGTT CATGGATGAT GCCAACATGT
 401 GCATTGCCAT TGCGATTTCT CTTCTCATGA TCCTGATATG TGCTATGGCT
 451 ACTTACGGAG CGTACAAGCA ACGCGCAGCC TGGATCATCC CATTCTTCTG
 501 TTACCAGATC TTTGACTTTG CCCTGAACAT GTTGGTTGCA ATCACTGTGC
 551 TTATTTATCC AAACTCCATT CAGGAATACA TACGGCAACT GCCTCCTAAT
 601 TTTCCCTACA GAGATGATGT CATGTCAGTG AATCCTACCT GTTTGGTCCT
 651 TATTATTCTT CTGTTTATTA GCATTATCTT GACTTTTAAG GGTTACTTGA
 701 TTAGCTGTGT TTGGAACTGC TACCGATACA TCAATGGTAG GAACTCCTCT
 751 GATGTCCTGG TTTATGTTAC CAGCAATGAC ACTACGGTGC TGCTACCCCC
 801 GTATGATGAT GCCACTGTGA ATGGTGCTGC CAAGGAGCCA CCGCCACCTT
 851 ACGTGTCTGC CTAAGCCTTC AAGTGGGCGG AGCTGAGGGC AGCAGCTTGA
 901 CTTTGCAGAC ATCTGAGCAA TAGTTCTGTT ATTTCACTTT TGCCATGAGC
 951 CTCTCTGAGC TTGTTTGTTG CTGAAATGCT ACTTTTTAAA ATTTAGATGT
1001 TAGATTGAAA ACTGTAGTTT TCAACATATG CTTTGCTAGA ACACTGTGAT
1051 AGATTAACTG TAGAATTCTT CCTGTACGAT TGGGGATATA ACGGGCTTCA
1101 CTAACCTTCC CTAGGCATTG AAACTTCCCC CAAATCTGAT GGACCTAGAA
1151 GTCTGCTTTT GTACCTGCTG GGCCCCAAAG TTGGGCATTT TTCTCTCTGT
1201 TCCCTCTCTT TTGAAAATGT AAAATAAAAC CAAAAATAGA CAACTTTTTC
1251 TTCAGCCATT CCAGCATAGA GAACAAAACC TTATGGAAAC AGGAATGTCA
1301 ATTGTGTAAT CATTGTTCTA ATTAGGTAAA TAGAAGTCCT TATGTATGTG
1351 TTACAAGAAT TTCCCCCACA ACATCCTTTA TGACTGAAGT TCAATGACAG
1401 TTTGTGTTTG GTGGTAAAGG ATTTTCTCCA TGGCCTGAAT TAAGACCATT
1451 AGAAAGCACC AGGCCGTGGG AGCAGTGACC ATCTACTGAC TGTTCTTGTG
1501 GATCTTGTGT CCAGGGACAT GGGGTGACAT GCCTCGTATG TGTTAGAGGG
1551 TGGAATGGAT GTGTTTGGCG CTGCATGGGA TCTGGTGCCC CTCTTCTCCT
1601 GGATTCACAT CCCCACCCAG GGCCCGCTTT TACTAAGTGT TCTGCCCTAG
1651 ATTGGTTCAA GGAGGTCATC CAACTGACTT TATCAAGTGG AATTGGGATA
1701 TATTTGATAT ACTTCTGCCT AACAACATGG AAAAGGGTTT TCTTTTCCCT
1751 GCAAGCTACA TCCTACTGCT TTGAACTTCC AAGTATGTCT AGTCACCTTT
1801 TAAAATGTAA ACATTTTCAG AAAAATGAGG ATTGCCTTCC TTGTATGCGC
1851 TTTTTACCTT GACTACCTGA ATTGCAAGGG ATTTTTATAT ATTCATATGT
1901 TACAAAGTCA GCAACTCTCC TGTTGGTTCA TTATTGAATG TGCTGTAAAT
1951 TAAGTCGTTT GCAATTAAAA CAAGGTTTGC CCACATCCAA AAAAAAAAAA
2001 AAAAA
```

BLAST Results

Entry HS012351 from database EMBL:

human STS SHGC-31823.
Score = 1629, P = 3.1e-67, identities = 343/354

Medline entries

96199248:
Identification of a novel membrane transporter associated with intracellular membranes by phenotypic complementation in the yeast Saccharomyces cerevisiae.

Peptide information for frame 1

ORF from 184 bp to 861 bp; peptide length: 226
Category: strong similarity to known protein

```
  1 MKMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP
 51 DQYNFSSSEL GGDFEFMDDA NMCIAIAISL LMILICAMAT YGAYKQRAAW
101 IIPFFCYQIF DFALNMLVAI TVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN
151 PTCLVLIILL FISIILTFKG YLISCVWNCY RYINGRNSSD VLVYVTSNDT
201 TVLLPPYDDA TVNGAAKEPP PPYVSA
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_24e11, frame 1

SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108)., N = 1, Score = 551, P = 2.9e-53

SWISSPROT:MTRP_MOUSE GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP., N = 1, Score = 539, P = 5.3e-52

TREMBL:HS304981_1 product: "E3 protein"; Human retinoic acid-inducible E3 protein mRNA, complete cds., N = 1, Score = 127, P = 3.4e-06

```
>SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP
     (KIAA0108).
          Length = 233

  HSPs:

 Score = 551 (82.7 bits), Expect = 2.9e-53, P = 2.9e-53
 Identities = 102/221 (46%), Positives = 148/221 (66%)

Query:     9 RFYSNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQY---NFSSSELGGDF- 64
             RFYS  CC CCHVRTGTI+LG WY+++N ++ ++L   +  P+     N     +G  +
Sbjct:    13 RFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAVNIQYEVIGNYYS 72

Query:    65 -EFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVL 123
              E M D N C+  A+S+LM +I +M  YGA    +  W+IPFFCY++FDF L+ LVAI+ L
Sbjct:    73 SERMAD-NACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDFVLSCLVAISSL 131

Query:   124 IYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYLISCVWNCYRYI 183
              Y   I+EY+ QLP +FPY+DD+++++ +CL+ I+L+F ++ + FK YLI+CVWNCY+YI
Sbjct:   132 TYLPRIKEYLDQLP-DFPYKDDLLALDSSCLLFIVLVFFALFIIFKAYLINCVWNCYKYI 190

Query:   184 NGRNSSDVLVYVTSN-DTTVLLPPYDDATVNGAAKEPPPPYVSA 226
             N RN  ++ VY         +LP Y+ A V    KEPPPPY+ A
Sbjct:   191 NNRNVPEIAVYPAFEAPPQYVLPTYEMA-VKMPEKEPPPPYLPA 233
```

Pedant information for DKFZphutel_24e11, frame 1

Report for DKFZphutel_24e11.1

```
[LENGTH]      226
[MW]          25419.11
```

```
[pI]            4.65
[HOMOL]         SWISSPROT:MTRP_HUMAN GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108).
5e-40
[PROSITE]       CK2_PHOSPHO_SITE      3
[PROSITE]       TYR_PHOSPHO_SITE      1
[PROSITE]       PKC_PHOSPHO_SITE      1
[PROSITE]       ASN_GLYCOSYLATION     3
[KW]            SIGNAL_PEPTIDE 49
[KW]            TRANSMEMBRANE  2
[KW]            LOW_COMPLEXITY    20.80 %

SEQ     MKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPDQYNFSSSEL
SEG     ................................xxxxxxxxxxxxxxxx............
PRD     ccceeeeeeecccceeeeeeeeccceeecceeehhhhhhhhhhhhhccccccceeecccc
MEM     ............................................................

SEQ     GGDFEFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAI
SEG     ...........xxxxxxxxxxxxxxxxxx...............................
PRD     ccccccccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhhhhhhhhh
MEM     .........MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ     TVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYLISCVWNCY
SEG     .................................xxxxxxxxxxxxx..............
PRD     hhhcccchhhhhhhccccccccccceeeecccccceeehhhhhhhhhhhhheeeeeeeee
MEM     MMMMMM.....................MMMMMMMMMMMMMMMMMMMMMMMMMMMMM....

SEQ     RYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGAAKEPPPPYVSA
SEG     ..............................................
PRD     eecccccccccceeeeeecccccccccccccccccccccccccccc
MEM     ..............................................
```

Prosite for DKFZphutel_24e11.1

PS00001	54->58	ASN_GLYCOSYLATION	PDOC00001
PS00001	187->191	ASN_GLYCOSYLATION	PDOC00001
PS00001	198->202	ASN_GLYCOSYLATION	PDOC00001
PS00005	167->170	PKC_PHOSPHO_SITE	PDOC00005
PS00006	56->60	CK2_PHOSPHO_SITE	PDOC00006
PS00006	128->132	CK2_PHOSPHO_SITE	PDOC00006
PS00006	196->200	CK2_PHOSPHO_SITE	PDOC00006
PS00007	186->195	TYR_PHOSPHO_SITE	PDOC00007

(No Pfam data available for DKFZphutel_24e11.1)

DKFZphutel_24j6
----

group: cell structure and motility

DKFZphutesl_24j6 encodes a novel 571 amino acid protein with strong similarity to rat cell adhesion regulator (CAR1).

The novel protein is very similar to Carl and thus seems to be involved in regulation cell-cell adhesion. It contains a RGD cell attachment site.

The new protein can find application in modulation of cell-cell-adhesion.

strong similarity to rat CAR1 A.thaliana T19C21.5

complete cDNA, complete cds, EST hits
potential frame shift at Bp 1241 according to CAR1
but frame shift might be in CAR1 sequence!
ESTs T73366 AA362984 confirm this sequence

Sequenced by Qiagen

Locus: /map="939.9 cR from top of Chr2 linkage group"

Insert length: 3333 bp
Poly A stretch at pos. 3316, no polyadenylation signal found

```
   1 ACGCGTCCGA GCTGGCTCAG GGCGTCCGCT AGGCTCGGAC GACCTGCTGA
  51 GCCTCCCAAA CCGCTTCCAT AAGGCTTTGC CTTTCCAACT TCAGCTACAG
 101 TGTTAGCTAA GTTTGGAAAG AAGGAAAAAA GAAAATCCCT GGGCCCCTTT
 151 TCTTTTGTTC TTTGCCAAAG TCGTCGTTGT AGTCTTTTTG CCCAAGGCTG
 201 TTGTGTTTTT AGAGGTGCTA TCTCCAGTTC CTTGCACTCC TGTTAACAAG
 251 CACCTCAGCG AGAGCAGCAG CAGCGATAGC AGCCGCAGAA GAGCCAGCGG
 301 GGTCGCCTAG TGTCATGACC AGGGCGGGAG ATCACAACCG CCAGAGAGGA
 351 TGCTGTGGAT CCTTGGCCGA CTACCTGACC TCTGCAAAAT TCCTTCTCTA
 401 CCTTGGTCAT TCTCTCTCTA CTTGGGGAGA TCGGATGTGG CACTTTGCGG
 451 TGTCTGTGTT TCTGGTAGAG CTCTATGGAA ACAGCCTCCT TTTGACAGCA
 501 GTCTACGGGC TGGTGGTGGC AGGGTCTGTT CTGGTCCTGG GAGCCATCAT
 551 CGGTGACTGG GTGGACAAGA ATGCTAGACT TAAAGTGGCC CAGACCTCGC
 601 TGGTGGTACA GAATGTTTCA GTCATCCTGT GTGGAATCAT CCTGATGATG
 651 GTTTTCTTAC ATAAACATGA GCTTCTGACC ATGTACCATG GATGGGTTCT
 701 CACTTCCTGC TATATCCTGA TCATCACTAT TGCAAATATT GCAAATTTGG
 751 CCAGTACTGC TACTGCAATC ACAATCCAAA GGGATTGGAT TGTTGTTGTT
 801 GCAGGAGAAG ACAGAAGCAA ACTAGCAAAT ATGAATGCCA CAATACGAAG
 851 GATTGACCAG TTAACCAACA TCTTAGCCCC CATGGCTGTT GGCCAGATTA
 901 TGACATTTGG CTCCCCAGTC ATCGGCTGTG GCTTTATTTC GGGATGGAAC
 951 TTGGTATCCA TGTGCGTGGA GTACGTCCTG CTCTGGAAGG TTTACCAGAA
1001 AACCCCAGCT CTAGCTGTGA AAGCTGGTCT TAAAGAAGAG GAAACTGAAT
1051 TGAAACAGCT GAATTTACAC AAAGATACTG AGCCAAAACC CCTGGAGGGA
1101 ACTCATCTAA TGGGTGTGAA AGACTCTAAC ATCCATGAGC TTGAACATGA
1151 GCAAGAGCCT ACTTGTGCCT CCCAGATGGC TGAGCCCTTC CGTACCTTCC
1201 GAGATGGATG GGTCTCCTAC TACAACCAGC CTGTGTTTCT GGCTGGCATG
1251 GGTCTTGCTT TCCTTTATAT GACTGTCCTG GGCTTTGACT GCATCACCAC
1301 AGGGTACGCC TACACTCAGG GACTGAGTGG TTCCATCCTC AGTATTTTGA
1351 TGGGAGCATC AGCTATAACT GGAATAATGG GAACTGTAGC TTTTACTTGG
1401 CTACGTCGAA AATGTGGTTT GGTTCGGACA GGTCTGATCT CAGGATTGGC
1451 ACAGCTTTCC TGTTTGATCT TGTGTGTGAT CTCTGTATTC ATGCCTGGAA
1501 GCCCCCTGGA CTTGTCCGTT TCTCCTTTTG AAGATATCCG ATCAAGGTTC
1551 ATTCAAGGAG AGTCAATTAC ACCTACCAAG ATACCTGAAA TTACAACTGA
1601 AATATACATG TCTAATGGGT CTAATTCTGC TAATATTGTC CCGGAGACAA
1651 GTCCTGAATC TGTGCCCATA ATCTCTGTCA GTCTGCTGTT TGCAGGCGTC
1701 ATTGCTGCTA GAATCGGTCT TTGGTCCTTT GATTTAACTG TGACACAGTT
1751 GCTGCAAGAA AATGTAATTG AATCTGAAAG AGGCATTATA AATGGTGTAC
1801 AGAACTCCAT GAACTATCTT CTTGATCTTC TGCATTTCAT CATGGTCATC
1851 CTGGCTCCAA ATCCTGAAGC TTTTGGCTTG CTCGTATTGA TTTCAGTCTC
1901 CTTTGTGGCA ATGGGCCACA TTATGTATTT CCGATTTGCC CAAAATACTC
1951 TGGGAAACAA GCTCTTTGCT TGCGGTCCTG ATGCAAAAGA AGTTAGGAAG
2001 GAAAATCAAG CAAATACATC TGTTGTTTGA GACAGTTTAA CTGTTGCTAT
2051 CCTGTTACTA GATTATATAG AGCACATGTG CTTATTTTGT ACTGCAGAAT
2101 TCCAATAAAT GGCTGGGTGT TTTGCTCTGT TTTTACCACA GCTGTGCCTT
2151 GAGAACTAAA AGCTGTTTAG GAAACCTAAG TCAGCAGAAA TTAACTGATT
2201 AATTTCCCTT ATGTTGAGGC ATGGAAAAAA AATTGGAAAA GAAAAACTCA
2251 GTTTAAATAC GGAGACTATA ATGATAACAC TGAATTCCCC TATTTCTCAT
2301 GAGTAGATAC AATCTTACGT AAAAGAGTGG TTAGTCACGT GAATTCAGTT
2351 ATCATTTGAC AGATTCTTAT CTGTACTAGA ATTCAGATAT GTCAGTTTTC
2401 TGCAAAACTC ACTCTTGTTC AAGACTAGCT AATTTATTTT TTTGCATCTT
2451 AGTTATTTTT AAAAACAAAT TCTTCAAGTA TGAAGACTAA ATTTTGATAA
2501 CTAATATTAT CCTTATTGAT CCTATTGATC TTAAGGTATT TACATGTATG
```

```
2551 TGGAAAAACA AAACACTTAA CTAGAATTCT CTAATAAGGT TTATGGTTTA
2601 GCTTAAAGAG CACCTTTGTA TTTTTATTAT CAGATGGGGC AACATATTGT
2651 ATGAAGCATA TGTAGCACTT CACAGCATGG TTATCATGTA AGCTGCAGGT
2701 AGAAGCAAAG CTGTAAAGTA GATTTATCAC ACAATGACTG CATACAGACT
2751 TCAAATATGT CAATAGTTTG GTCATAGAAC CTAGAAGCCA AAAGCCACAC
2801 AGAAGGGCAA GAATCCCAAT TTAACTCATG TTATCATCAT TAGTGATCTG
2851 TGTTGTAGAA CATGAGGGTG TAAGCCTTCA GCCTGGCAAG TTACATGTAG
2901 AAAGCCCACA CTTGTGAAGG TTTTGTTTTA CAAATCACTT GATTTAACAC
2951 ACTCAGGTAG AATATTTTTA TTTTTACTGT TTTATACCCA GAAGTTATTT
3001 CTACATTGTT CTACAGCAAG AATATTCATA AAAGTATCCC TTTCAAATGC
3051 CTTTGAGAAG AATAGAAGAA AAAAAGTTTG TATATATTTT AAAAAATTGT
3101 TTTAAAAGTC AGTTTGCAAC ATGTCTGTAC CAAGATGGTA CTTTGCCTTA
3151 ACCGTTTATA TGCACTTTCA TGGAGACTGC AATACGTTGC TATGAGCACT
3201 TTCTTTATCC TTGGAGTTTA ATCCTTTGCT TCATCTTTCT ACAGTATGAC
3251 ATAATGATTT GCTATGTTGT AAAATCTTTG TAAAAAATTT CTATATAAAA
3301 ATATTTTGAA AATCTTAAAA AAAAAAAAAA AAA
```

BLAST Results

Entry HS389210 from database EMBL:
human STS SHGC-10164.
Score = 1592, P = 1.5e-64, identities = 346/364

Entry HS933343 from database EMBL:
human STS WI-16551.
Score = 1193, P = 5.7e-46, identities = 241/244

Medline entries

No Medline entry

Peptide information for frame 3

ORF from 315 bp to 2027 bp; peptide length: 571
Category: strong similarity to known protein

```
  1 MTRAGDHNRQ RGCCGSLADY LTSAKFLLYL GHSLSTWGDR MWHFAVSVFL
 51 VELYGNSLLL TAVYGLVVAG SVLVLGAIIG DWVDKNARLK VAQTSLVVQN
101 VSVILCGIIL MMVFLHKHEL LTMYHGWVLT SCYILIITIA NIANLASTAT
151 AITIQRDWIV VVAGEDRSKL ANMNATIRRI DQLTNILAPM AVGQIMTFGS
201 PVIGCGFISG WNLVSMCVEY VLLWKVYQKT PALAVKAGLK EEETELKQLN
251 LHKDTEPKPL EGTHLMGVKD SNIHELEHEQ EPTCASQMAE PFRTFRDGWV
301 SYYNQPVFLA GMGLAFLYMT VLGFDCITTG YAYTQGLSGS ILSILMGASA
351 ITGIMGTVAF TWLRRKCGLV RTGLISGLAQ LSCLILCVIS VFMPGSPLDL
401 SVSPFEDIRS RFIQGESITP TKIPEITTEI YMSNGSNSAN IVPETSPESV
451 PIISVSLLFA GVIAARIGLW SFDLTVTQLL QENVIESERG IINGVQNSMN
501 YLLDLLHFIM VILAPNPEAF GLLVLISVSF VAMGHIMYFR FAQNTLGNKL
551 FACGPDAKEV RKENQANTSV V
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphute1_24j6, frame 3

TREMBLNEW:U76714_1 gene: "CAR1"; product: "cell adhesion regulator"; Rattus norvegicus cell adhesion regulator (CAR1) mRNA, complete cds., N = 1, Score = 1472, P = 7.2e-151

TREMBL:AC004683_5 gene: "T19C21.5"; Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence., N = 2, Score = 437, P = 2.8e-60

TREMBL:AF039046_2 gene: "R09B5.4"; Caenorhabditis elegans cosmid R09B5., N = 2, Score = 323, P = 1.5e-43

```
>TREMBLNEW:U76714_1 gene: "CAR1"; product: "cell adhesion regulator";
     Rattus norvegicus cell adhesion regulator (CAR1) mRNA, complete cds.
            Length = 405
```

```
HSPs:

Score = 1472 (220.9 bits), Expect = 7.2e-151, P = 7.2e-151
Identities = 288/319 (90%), Positives = 297/319 (93%)

Query:    1 MTRAGDHNRQRGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNSLLL 60
            MT++ D   Q GCCGSLA+YLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNSLLL
Sbjct:    1 MTKSRDQTHQEGCCGSLANYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNSLLL 60

Query:   61 TAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL 120
            TAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHK+EL
Sbjct:   61 TAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKNEL 120

Query:  121 LTMYHGWVLTSCYILIITIANIANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRI 180
            L MYHGWVLT CYILIITIANIANLASTATAITIQRDWIVVVAGE+RS+LA+MNATIRRI
Sbjct:  121 LNMYHGWVLTVCYILIITIANIANLASTATAITIQRDWIVVVAGENRSRLADMNATIRRI 180

Query:  181 DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKTPALAVKAGLK 240
            DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEY LLWKVYQKTPALAVKA LK
Sbjct:  181 DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYFLLWKVYQKTPALAVKAALK 240

Query:  241 EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTFRDGWV 300
             EE+ELKQL   KDTEPKPLEGTHLMG KDSNI ELE EQEPTCASQ+AEPFRTFRDGWV
Sbjct:  241 VEESELKQLTSPKDTEPKPLEGTHLMGEKDSNIRELECEQEPTCASQIAEPFRTFRDGWV 300

Query:  301 SYYNQPVFLAGMGLAF-LY 318
            SYYNQPVFL   G  F LY
Sbjct:  301 SYYNQPVFLGWHGPGFPLY 319
```

Pedant information for DKFZphutel_24j6, frame 3

Report for DKFZphutel_24j6.3

```
[LENGTH]        571
[MW]            62542.72
[pI]            6.08
[HOMOL]         TREMBL:U76714_1 gene: "CAR1"; product: "cell adhesion regulator"; Rattus
norvegicus cell adhesion regulator (CAR1) mRNA, complete cds. 1e-141
[BLOCKS]        BL00341D
[PROSITE]       MYRISTYL          15
[PROSITE]       MITOCH_CARRIER 1
[PROSITE]       CK2_PHOSPHO_SITE      6
[PROSITE]       PROKAR_LIPOPROTEIN    1
[PROSITE]       PKC_PHOSPHO_SITE      4
[PROSITE]       ASN_GLYCOSYLATION     4
[PFAM]          Laminin B (Domain IV)
[KW]            TRANSMEMBRANE  4
[KW]            LOW_COMPLEXITY     8.76 %

SEQ  MTRAGDHNRQRGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELYGNSLLL
SEG  ............................................................
PRD  cccccccccccccccchhhhhhhheeeeccceeeccchhhhhhhhhheeeeeccccee
MEM  ...............................................MMMMMMMMMMMMM

SEQ  TAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVVQNVSVILCGIILMMVFLHKHEL
SEG  .xxxxxxxxxxxxxxx............................................
PRD  ehhhhhhhccceeeeccccccchhhhhhhhhhhhheeecccchhhhhhhhhhhhhhhhhh
MEM  MMMMMMMMMMMMMMMM...........MMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMMM

SEQ  LTMYHGWVLTSCYILIITIANIANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRI
SEG  ............xxxxxxxxxxxxxxxxxxxxx...........................
PRD  hhccccchhhhhhhhhhhhhhhhhhhhhhheeeecccceeeeeeeccccchhhhhhhhhhh
MEM  MMMMMMM.....................................................

SEQ  DQLTNILAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKTPALAVKAGLK
SEG  ............................................................
PRD  hhhhhhccceeeeceeeeeecceeeeeeeecccchhhhhhhhhhhhhhccccchhhhhhhh
MEM  ............................................................

SEQ  EEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIHELEHEQEPTCASQMAEPFRTFRDGWV
SEG  ............................................................
PRD  hhhhhhhhhhccccccccccceeeeeecccccccccccccccccccccccccccccccee
MEM  ............................................................

SEQ  SYYNQPVFLAGMGLAFLYMTVLGFDCITTGYAYTQGLSGSILSILMGASAITGIMGTVAF
SEG  ............................................................
PRD  eeecceeeecccchhhhhhcccccceeeeeeeeeccccceeeeeeeeccccceeeeehhhhhh
```

```
MEM   ............................................................

SEQ   TWLRRKCGLVRTGLISGLAQLSCLILCVISVFMPGSPLDLSVSPFEDIRSRFIQGESITP
SEG   .........................................................xxx
PRD   hhhhhhccccccccchhhhhhhhhhhhhhhhcccccccccccccchhhhhhcccccccccc
MEM   ............................................................

SEQ   TKIPEITTEIYMSNGSNSANIVPETSPESVPIISVSLLFAGVIAARIGLWSFDLTVTQLL
SEG   xxxxxxxxxx..................................................
PRD   ccccccceeeeeccccccccccccccccccceeeeeehhhhhhhhhhccccchhhhhhhhhh
MEM   ..............................MMMMMMMMMMMMMMMMMMMMMMMM......

SEQ   QENVIESERGIINGVQNSMNYLLDLLHFIMVILAPNPEAFGLLVLISVSFVAMGHIMYFR
SEG   ............................................................
PRD   hhhhhcccccceeeeccccchhhhhhhhhhheeeeeccccccceeeeeeeeccccccceeee
MEM   ..............................MMMMMMMMMMMMMMMMMMMMMMMMMMMM...

SEQ   FAQNTLGNKLFACGPDAKEVRKENQANTSVV
SEG   ...............................
PRD   eecccccceeeecccchhhhhhhhcccccc
MEM   ...............................
```

Prosite for DKFZphutel_24j6.3

PS00001	100->104	ASN_GLYCOSYLATION	PDOC00001
PS00001	174->178	ASN_GLYCOSYLATION	PDOC00001
PS00001	434->438	ASN_GLYCOSYLATION	PDOC00001
PS00001	567->571	ASN_GLYCOSYLATION	PDOC00001
PS00005	23->26	PKC_PHOSPHO_SITE	PDOC00005
PS00005	176->179	PKC_PHOSPHO_SITE	PDOC00005
PS00005	294->297	PKC_PHOSPHO_SITE	PDOC00005
PS00005	487->490	PKC_PHOSPHO_SITE	PDOC00005
PS00006	16->20	CK2_PHOSPHO_SITE	PDOC00006
PS00006	36->40	CK2_PHOSPHO_SITE	PDOC00006
PS00006	294->298	CK2_PHOSPHO_SITE	PDOC00006
PS00006	396->400	CK2_PHOSPHO_SITE	PDOC00006
PS00006	403->407	CK2_PHOSPHO_SITE	PDOC00006
PS00006	445->449	CK2_PHOSPHO_SITE	PDOC00006
PS00008	12->18	MYRISTYL	PDOC00008
PS00008	65->71	MYRISTYL	PDOC00008
PS00008	76->82	MYRISTYL	PDOC00008
PS00008	193->199	MYRISTYL	PDOC00008
PS00008	267->273	MYRISTYL	PDOC00008
PS00008	311->317	MYRISTYL	PDOC00008
PS00008	336->342	MYRISTYL	PDOC00008
PS00008	339->345	MYRISTYL	PDOC00008
PS00008	353->359	MYRISTYL	PDOC00008
PS00008	368->374	MYRISTYL	PDOC00008
PS00008	373->379	MYRISTYL	PDOC00008
PS00008	435->441	MYRISTYL	PDOC00008
PS00008	461->467	MYRISTYL	PDOC00008
PS00008	490->496	MYRISTYL	PDOC00008
PS00008	494->500	MYRISTYL	PDOC00008
PS00013	122->133	PROKAR_LIPOPROTEIN	PDOC00013
PS00215	404->414	MITOCH_CARRIER	PDOC00189

Pfam for DKFZphutel_24j6.3

```
HMM_NAME      Laminin B (Domain IV)

HMM               *YWRlPERFLGDQvTsYGGkLe*
                   Y+R  +  LG+++ + G + +
Query         538  YFRFAQNTLGNKLFACGPDAK     558
```

DKFZphutel_2h3
----

group: differentiation/development

DKFZphutel_2h3 encodes a novel 267 amino acid protein, with similarity to ITM2 (integral membrane protein 2) of chicken and mouse.

The novel protein contains a prenyl group binding site (CAAX box) and seems to be post-translationally modified by the attachment of either a farnesyl or a geranyl-geranyl group. The similar gallus G. protein E25 a marker for chondro-osteogenic differentiation.

The new protein can find application as a useful marker for chondro-osteogenic cell differentiation and for the modulation of chondro-osteogenic cell differentiation.

strong similarity to mouse E25 and gallus E3-16

complete cDNA, EST hits
complete cds according to E25 start at Bp 56
putative transmembrane protein (1 TM)

Sequenced by AGOWA

Locus: unknown

Insert length: 2033 bp
Poly A stretch at pos. 2007, polyadenylation signal at pos. 1986

```
   1 GGACCGAGGC TGCACCGGCA GAGGCTGCGG GGCGGACGCG CGGGCCGGCG
  51 CAGCCATGGT GAAGATTAGC TTCCAGCCCG CCGTGGCTGG CATCAAGGGC
 101 GACAAGGCTG ACAAGGCGTC GGCGTCGGCC CCTGCGCCGG CCTCGGCCAC
 151 CGAGATCCTG CTGACGCCGG CTAGGGAGGA GCAGCCCCCA CAACATCGAT
 201 CCAAGAGGGG GAGCTCAGTG GGCGGCGTGT GCTACCTGTC GATGGGCATG
 251 GTCGTGCTGC TCATGGGCCT CGTGTTCGCC TCTGTCTACA TCTACAGATA
 301 CTTCTTTCTT GCACAGCTGG CCCGAGATAA CTTCTTCCGC TGTGGTGTGC
 351 TGTATGAGGA CTCCCTGTCC TCCCAGGTCC GGACTCAGAT GGAGCTGGAA
 401 GAGGATGTGA AAATCTACCT CGACGAGAAC TACGAGCGCA TCAACGTGCC
 451 TGTGCCCCAG TTTGGCGGCG GTGACCCTGC AGACATCATC CATGACTTCC
 501 AGCGGGGTCT GACTGCGTAC CATGATATCT CCCTGGACAA GTGCTATGTC
 551 ATCGAACTCA ACACCACCAT TGTGCTGCCC CCTCGCAACT TCTGGGAGCT
 601 CCTCATGAAC GTGAAGAGGG GGACCTACCT GCCGCAGACG TACATCATCC
 651 AGGAGGAGAT GGTGGTCACG GAGCATGTCA GTGACAAGGA GGCCCTGGGG
 701 TCCTTCATCT ACCACCTGTG CAACGGGAAA GACACCTACC GGCTCCGGCG
 751 CCGGGCAACG CGGAGGCGGA TCAACAAGCG TGGGGCCAAG AACTGCAATG
 801 CCATCCGCCA CTTCGAGAAC ACCTTCGTGG TGGAGACGCT CATCTGCGGG
 851 GTGGTGTGAG GCCCTCCTCC CCCAGAACCC CCTGCCGTGT TCCTCTTTTC
 901 TTCTTTCCAG CTGCTCTCTG GCCCTCCTCC TTCCCCCTGC TTAGCTTGTA
 951 CTTTGGACGC GTTTCTATAG AGGTGACATG TCTCTCCATT CCTCTCCAAC
1001 CCTGCCCACC TCCCTGTACC AGAGCTGTGA TCTCTCGGTG GGGGGCCCAT
1051 CTCTGCTGAC CTGGGTGTGG CGGAGGGAGA GGCGATGCTG CAAAGTGTTT
1101 TCTGTGTCCC ACTGTCTTGA AGCTGGGCCT GCCAAAGCCT GGGCCCACAG
1151 CTGCACCGGC AGCCCAAGGG GAAGGACCGG TTGGGGGAGC CGGGCATGTG
1201 AGGCCCTGGG CAAGGGGATG GGGCTGTGGG GGCGGGGCGG CATGGGCTTC
1251 AGAAGTATCT GCACAATTAG AAAAGTCCTC AGAAGCTTTT TCTTGGAGGG
1301 TACACTTTCT TCACTGTCCC TATTCCTAGA CCTGGGGCTT GAGCTGAGGA
1351 TGGGACGATG TGCCCAGGGA GGGACCCACC AGAGCACAAG AGAAGGTGGC
1401 TACCTGGGGG TGTCCCAGGG ACTCTGTCAG TGCCTTCAGC CCACCAGCAG
1451 GAGCTTGGAG TTTGGGGAGT GGGGATGAGT CCGTCAAGCA CAACTGTTCT
1501 CTGAGTGGAA CCAAAGAAGC AAGGAGCTAG GACCCCCAGT CCTGCCCCCC
1551 AGGAGCACAA GCAGGGTCCC CTCAGTCAAG GCAGTGGGAT GGGCGGCTGA
1601 GGAACGGGGC AGGCAAGGTC ACTGCTCAGT CACGTCCACG GGGGACGAGC
1651 CGTGGGTTCT GCTGAGTAGG TGGAGCTCAT TGCTTTCTCC AAGCTTGGAA
1701 CTGTTTTGAA AGATAACACA GAGGGAAAGG GAGAGCCACC TGGTACTTGT
1751 CCACCCTGCC TCCTCTGTTC TGAAATTCCA TCCCCCTCAG CTTAGGGGAA
1801 TGCACCTTTT TCCCTTTCCT TCTCACTTTT GCATGTTTTT ACTGATCATT
1851 CGATATGCTA ACCGTTCTCA GCCCTGAGCC TTGGAGAGGA GGGCTGTAAC
1901 GCCTTCAGTC AGTCTCTGGG GATGAAACTC TTAAATGCTT TGTATATTTT
1951 CTCAATTAGA TCTCTTTTCA GAAGTGTCTA TAGAACAATA AAAATCTTTT
2001 ACTTCTGAAA AAAAAAAAAA AAAAGGGCGG CCG
```

BLAST Results

Entry B64417 from database EMBL:
CIT-HSP-2023A7.TR CIT-HSP Homo sapiens genomic clone 2023A7.
Length = 715
Plus Strand HSPs:

```
Score = 1546 (232.0 bits), Expect = 7.8e-64, P = 7.8e-64
Identities = 310/311 (99%)
```

Medline entries

96325063:
Isolation of markers for chondro-osteogenic differentiation using cDNA library subtraction.
Molecular cloning and characterization of a gene belonging to a novel multigene family of
integral membrane proteins.

Peptide information for frame 2

ORF from 56 bp to 856 bp; peptide length: 267
Category: strong similarity to known protein

```
   1 MVKISFQPAV AGIKGDKADK ASASAPAPAS ATEILLTPAR EEQPPQHRSK
  51 RGSSVGGVCY LSMGMVVLLM GLVFASVYIY RYFFLAQLAR DNFFRCGVLY
 101 EDSLSSQVRT QMELEEDVKI YLDENYERIN VPVPQFGGGD PADIIHDFQR
 151 GLTAYHDISL DKCYVIELNT TIVLPPRNFW ELLMNVKRGT YLPQTYIIQE
 201 EMVVTEHVSD KEALGSFIYH LCNGKDTYRL RRRATRRRIN KRGAKNCNAI
 251 RHFENTFVVE TLICGVV
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphutel_2h3, frame 2

SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16)., N = 1, Score = 573, P = 1.3e-55

SWISSNEW:ITMB_MOUSE INTEGRAL MEMBRANE PROTEIN 2B (E25B PROTEIN)., N = 1, Score = 560, P = 3.2e-54

SWISSNEW:ITMA_HUMAN INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN)., N = 1, Score = 456, P = 3.3e-43

```
>SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN
     E3-16).
          Length = 262

  HSPs:

 Score = 573 (86.0 bits), Expect = 1.3e-55, P = 1.3e-55
 Identities = 117/264 (44%), Positives = 172/264 (65%)

Query:    1 MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY 60
            MVK+SF  A+A    + A+K   ++         ++L+ P   ++P        G
Sbjct:    1 MVKVSFNSALA--HKEAANKEEENS-------QVLILPPDAKEPEDVVVPAGHKRAWCWC 51

Query:   61 LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSLS-----SQVRTQM-- 112
            +  G+  +L G++    Y+Y+YF   Q       + CG+ Y ED LS       +Q+++
Sbjct:   52 MCFGLAFMLAGVILGGAYLYKYFAFQQ---GGVYFCGIKYIEDGLSLPESGAQLKSARYH 108

Query:  113 ELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTI 172
             +E++++I  +E+ E I+VPVP+F   DPADI+HDF R LTAY D+SLDKCYVI LNT++
Sbjct:  109 TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV 168

Query:  173 VLPPRNFWELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRR 232
            V+PP+NF ELL+N+K GTYLPQ+Y+I E+M+VT+ + + + LG FIY LC GK+TY+L+R
Sbjct:  169 VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVDQLGFFIYRLCRGKETYKLQR 228

Query:  233 RATRRRINKRGAKNCNAIRHFENTFVVETLIC 264
            +   + I KR A NC  IRHFEN F +ETLIC
Sbjct:  229 KEAMKGIQKREAVNCRKIRHFENRFAMETLIC 260
```

Pedant information for DKFZphutel_2h3, frame 2

Report for DKFZphutel_2h3.2

```
[LENGTH]        267
[MW]            30253.96
[pI]            8.16
[HOMOL]         SWISSNEW:ITMB_CHICK INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16).
1e-49
[PROSITE]       MYRISTYL        4
[PROSITE]       PRENYLATION     1
[PROSITE]       CAMP_PHOSPHO_SITE       3
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       TYR_PHOSPHO_SITE        1
[PROSITE]       PKC_PHOSPHO_SITE        4
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            TRANSMEMBRANE   1
[KW]            LOW_COMPLEXITY     15.36 %

SEQ     MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY
SEG     ...............xxxxxxxxxxxxxxxx.............................
PRD     ccccccccchhhhhhhhhhhhhhhhhcccccccceeecccccccccccccccccccccchh
MEM     ........................................................MMMM

SEQ     LSMGMVVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLYEDSLSSQVRTQMELEEDVKI
SEG     ..xxxxxxxxxxx...............................................
PRD     hhhhhhhhhhhhhhhhhhhcchhhhhhhhhhccceeeeeeeccccccccchhhhhhhhhhhh
MEM     MMMMMMMMMMMMMMMMMMMMMMMM....................................

SEQ     YLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTIVLPPRNFW
SEG     ............................................................
PRD     hhccccceeeeccccccccccccccchhhhhhhhhhhhhhhccccceeeeeccceeeccccchhh
MEM     ............................................................

SEQ     ELLMNVKRGTYLPQTYIIQEEMVVTEHVSDKEALGSFIYHLCNGKDTYRLRRRATRRRIN
SEG     ................................................xxxxxxxxxxxx
PRD     hhhhhhccccccceeeeehhhhhhhccccchhhhhheeeccccchhhhhhhhhhhhhhh
MEM     ............................................................

SEQ     KRGAKNCNAIRHFENTFVVETLICGVV
SEG     xx.........................
PRD     hhhhccceeeeccccchhhhhheeeccc
MEM     ...........................
```

Prosite for DKFZphutel_2h3.2

PS00001	169->173	ASN_GLYCOSYLATION	PDOC00001
PS00004	50->54	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	187->191	CAMP_PHOSPHO_SITE	PDOC00004
PS00004	232->236	CAMP_PHOSPHO_SITE	PDOC00004
PS00005	49->52	PKC_PHOSPHO_SITE	PDOC00005
PS00005	209->212	PKC_PHOSPHO_SITE	PDOC00005
PS00005	227->230	PKC_PHOSPHO_SITE	PDOC00005
PS00005	235->238	PKC_PHOSPHO_SITE	PDOC00005
PS00006	30->34	CK2_PHOSPHO_SITE	PDOC00006
PS00006	110->114	CK2_PHOSPHO_SITE	PDOC00006
PS00006	209->213	CK2_PHOSPHO_SITE	PDOC00006
PS00007	119->127	TYR_PHOSPHO_SITE	PDOC00007
PS00008	52->58	MYRISTYL	PDOC00008
PS00008	71->77	MYRISTYL	PDOC00008
PS00008	138->144	MYRISTYL	PDOC00008
PS00008	243->249	MYRISTYL	PDOC00008
PS00294	264->268	PRENYLATION	PDOC00266

(No Pfam data available for DKFZphutel_2h3.2)

DKFZphmcf1_1a11
----

group: transmembrane protein

DKFZphmcf1_1a11 encodes a novel 393 amino acid protein with weak similarity to S.pombe SPBC29A3_3 protein and S. cerevisiae putative membrane protein YDR255c.

The novel protein contains 1 transmembrane region.
No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of mammary carcinoma-specific genes and as a new marker for mammary carcinoma cells.

similarity to YDR255c and SPBC29A3.03c
membrane regions: 1
Summary DKFZphmcf1_1a11 encodes a novel 393 amino acid protein, with similarity to YDR255c and SPBC29A3.03c.

similarity to YDR255c and SPBC29A3.03c

complete cDNA, complete cds, EST hits
potential start at Bp 110 matches kozak consensus

Sequenced by DKFZ

Locus: /map="542.7 cR from top of Chr5 linkage group"

Insert length: 1819 bp
Poly A stretch at pos. 1808, no polyadenylation signal found

```
   1 CCCGGCCCAG CCCCCGAAGA GCCGCCTCAG CCGGGGGGAG TTGCTCGGAC
  51 TCAAACGTCC AGTCCTCGTG CGACCGCGCT GGGTCGGAAG TGAGCAGGCT
 101 GAGGCCACCA TGGAGCAGTG TGCGTGCGTG GAGAGAGAGC TGGACAAGGT
 151 CCTGCAGAAG TTCCTGACCT ACGGGCAGCA CTGTGAGCGG AGCCTGGAGG
 201 AGCTGCTGCA CTACGTGGGC CAGCTGCGGG CTGAGCTGGC CAGCGCAGCC
 251 CTCCAGGGGA CCCCTCTCTC AGCCACCCTC TCTCTGGTGA TGTCACAGTG
 301 CTGCCGGAAG ATCAAAGATA CGGTGCAGAA ACTGGCTTCG GACCATAAGG
 351 ACATTCACAG CAGTGTATCC CGAGTGGGCA AAGCCATTGA CAGGAACTTC
 401 GACTCTGAGA TCTGTGGTGT TGTGTCAGAT GCGGTGTGGG ACGCGCGGGA
 451 ACAGCAGCAG CAGATCCTGC AGATGGCCAT CGTGGAACAC CTGTATCAGC
 501 AGGGCATGCT CAGCGTGGCC GAGGAGCTGT GCCAGGAATC AACGCTGAAT
 551 GTGGACTTGG ATTTCAAGCA GCCTTTCCTA GAGTTGAATC GAATCCTGGA
 601 AGCCCTGCAC GAACAAGACC TGGGTCCTGC GTTGGAATGG GCCGTCTCCC
 651 ACAGGCAGCG CCTGCTGGAA CTCAACAGCT CCCTGGAGTT CAAGCTGCAC
 701 CGACTGCACT TCATCCGCCT CTTGGCAGGA GGCCCCGCGA AGCAGCTGGA
 751 GGCCCTCAGC TATGCTCGGC ACTTCCAGCC CTTTGCTCGG CTGCACCAGC
 801 GGGAGATCCA GGTGATGATG GGCAGCCTGG TGTACCTGCG GCTGGGCTTG
 851 GAGAAGTCAC CCTACTGCCA CCTGCTGGAC AGCAGCCACT GGGCAGAGAT
 901 CTGTGAGACC TTTACCCGGG ACGCCTGTTC CCTGCTGGGG CTTTCTGTGG
 951 AGTCCCCCCT TAGCGTCAGC TTTGCCTCTG GCTGTGTGGC GCTGCCTGTG
1001 TTGATGAACA TCAAGGCTGT GATTGAGCAG CGGCAGTGCA CTGGGGTCTG
1051 GAATCACAAG GACGAGTTAC CGATTGAGAT TGAACTAGGC ATGAAGTGCT
1101 GGTACCACTC CGTGTTCGCT TGCCCCATCC TCCGCCAGCA GACGTCAGAT
1151 TCCAACCCTC CCATCAAGCT CATCTGTGGC CATGTTATCT CCCGAGATGC
1201 ACTCAATAAG CTCATTAATG GAGGAAAGCT GAAGTGTCCC TACTGTCCCA
1251 TGGAGCAGAA CCCGGCAGAT GGGAAACGCA TCATATTCTG ATTCCTACCT
1301 GGAAGGAATT TTGTTGAAAG GGGTTTTCAC CTGTGAGCCT TGGTCTGTCT
1351 CGGTAGGGTG GTCAACTTCA GTGGACTGTG GTTGGTTTCA GAGCGCCTGG
1401 CTGAGGAGTT CCACTGAGGG GAGCACTGGA GCAGCCCTTT GGCAGAGGCT
1451 GAGGAGGGAG ATGGACCAGC CCACGCCTGG CACCTGGCTC CATGGCATAA
1501 GGAAAGGGAG ATGCTGGCCT CTGTGCTCCT GCTGTCTTTT CCTGTTTCTG
1551 TTTGCGTTTG ACTTAGTAGC AACCGACAGA GTGGCAAGGG ATTTGGTCTT
1601 CAGCAGTAGA CATCCTTCCA CCCCTGCCCT CAGCCAAGTC TCTTGCTGCC
1651 ATGCCAATGC TATGTCCACC CTTGCCCCTC GGCCCAAGAG TGTCCAGCGG
1701 TGGCCCACCT CTTCCTCCCA CTACAGCCTC AACAGTATGT ACCATCTCCC
1751 ACTGTAAATA GTCCCAGTTA GAACGGAATG CCGTTGTTTT ATAACTTTGA
1801 ACAAATGTAA AAAAAAAAA
```

BLAST Results

Entry HS579359 from database EMBL:
human STS WI-6350.
Score = 1027, P = 9.9e-40, identities = 207/209

Medline entries

No Medline entry

Peptide information for frame 2

ORF from 110 bp to 1288 bp; peptide length: 393
Category: similarity to unknown protein

```
  1 MEQCACVERE LDKVLQKFLT YGQHCERSLE ELLHYVGQLR AELASAALQG
 51 TPLSATLSLV MSQCCRKIKD TVQKLASDHK DIHSSVSRVG KAIDRNFDSE
101 ICGVVSDAVW DAREQQQQIL QMAIVEHLYQ QGMLSVAEEL CQESTLNVDL
151 DFKQPFLELN RILEALHEQD LGPALEWAVS HRQRLLELNS SLEFKLHRLH
201 FIRLLAGGPA KQLEALSYAR HFQPFARLHQ REIQVMMGSL VYLRLGLEKS
251 PYCHLLDSSH WAEICETFTR DACSLLGLSV ESPLSVSFAS GCVALPVLMN
301 IKAVIEQRQC TGVWNHKDEL PIEIELGMKC WYHSVFACPI LRQQTSDSNP
351 PIKLICGHVI SRDALNKLIN GGKLKCPYCP MEQNPADGKR IIF
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphmcf1_1a11, frame 2

TREMBL:SPBC29A3_3 gene: "SPBC29A3.03c"; product: "hypothetical protein"; S.pombe chromosome II cosmid c29A3., N = 2, Score = 302, P = 3.4e-42

PIR:S67312 probable membrane protein YDR255c - yeast (Saccharomyces cerevisiae), N = 1, Score = 271, P = 5.3e-22

TREMBL:CET07D1_2 gene: "T07D1.2"; Caenorhabditis elegans cosmid T07D1., N = 1, Score = 193, P = 5.6e-13

```
>TREMBL:SPBC29A3_3 gene: "SPBC29A3.03c"; product: "hypothetical protein";
     S.pombe chromosome II cosmid c29A3.
            Length = 398

  HSPs:

 Score = 302 (45.3 bits), Expect = 3.4e-42, Sum P(2) = 3.4e-42
 Identities = 55/142 (38%), Positives = 89/142 (62%)

Query:   252 YCHLLDSSHWAEICETFTRDACSLLGLSVESPLSVSFASGCVALPVLMNIKAVIEQRQCT 311
             Y +LD   W  +   F R+ C+ LG+S+ESPL +   +G +ALP+L+ + ++++++
Sbjct:   258 YIDVLDLD-WKSLELLFVREFCAALGMSLESPLDIVVNAGAIALPILLKMSSIMKKKHTE 316

Query:   312 GVWNHKDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLICGHVISRDALNKLING 371
               W  + ELP+EI L     +HSVF CP+ ++Q ++ NPP+ + CGHVI +++L +L
Sbjct:   317 --WTSQGELPVEIFLPSSYHFHSVFTCPVSKEQATEENPPMMMSCGHVIVKESLRQLSRN 374

Query:   372 G--KLKCPYCPMEQNPADGKRIIF 393
             G  + KCPYCP E   AD  R+ F
Sbjct:   375 GSQRFKCPYCPNENVAADAIRVYF 398

 Score = 161 (24.2 bits), Expect = 3.4e-42, Sum P(2) = 3.4e-42
 Identities = 51/221 (23%), Positives = 102/221 (46%)

Query:    22 GQHCERSLEELLHYVGQLRAELASAALQGTPLSATLSLVMSQCCRKIKDTVQKLASDHKD 81
             G C   L EL       + +   + L+  P ++   LV   C  K +      L    K
Sbjct:    15 GNKCLAKLNEL----ESILKDAKKSCLKD-PTTSMKELVA--CSEKTQQVFDDLKRTEKK 67

Query:    82 IHSSVSRVGKAIDRNFDSEICGVVSDAVWDAREQQQQILQMAIVEHLYQQGMLSVAEELC 141
             H+S++R GK +++ F+ ++  +    + +++++++   +  A+  H ++QG + +A   C
Sbjct:    68 FHTSLNRFGKTLEKKFNFDLEDIKLHSSFESKKRE---IDTALSLHFFRQGDVELAHLFC 124

Query:   142 QESTLNVDLDFKQPFLELNRILEALHEQDLGPALEWAVSHRQRLLELNSSLEFKLHRLHF 201
             +E+ +    +    F  L  I++ + ++DL   +EWA   R  L    SSLE+ L +
Sbjct:   125 KEAGIEEPSESLHVFTLLKSIVQGIRDKDLKLPIEWASQCRGYLERKGSSLEYTLQKYRL 184

Query:   202 IRLLAGGPAKQL-EALSYAR-HFQPFARLHQREIQVMMGSLVY 242
             +        K +  A+ Y R +   F + H  +IQ  M +L +
```

Sbjct: 185 VSNYL--TTKDIMAAIRYCRTNMAEFQKKHLADIQKTMIALFF 225

Pedant information for DKFZphmcf1_1a11, frame 2

Report for DKFZphmcf1_1a11.2

```
[LENGTH]        393
[MW]            44414.77
[pI]            6.15
[HOMOL]         TREMBL:SPBC29A3_3 gene: "SPBC29A3.03c"; product: "hypothetical protein";
S.pombe chromosome II cosmid c29A3. 2e-39
[FUNCAT]        99 unclassified proteins      [S. cerevisiae, YDR255c] 8e-23
[PIRKW]         transmembrane protein 2e-21
[PROSITE]       MYRISTYL        2
[PROSITE]       AMIDATION       1
[PROSITE]       CK2_PHOSPHO_SITE        3
[PROSITE]       PROKAR_LIPOPROTEIN      1
[PROSITE]       TYR_PHOSPHO_SITE        3
[PROSITE]       PKC_PHOSPHO_SITE        1
[PROSITE]       ASN_GLYCOSYLATION       1
[KW]            TRANSMEMBRANE  1

SEQ  MEQCACVERELDKVLQKFLTYGQHCERSLEELLHYVGQLRAELASAALQGTPLSATLSLV
PRD  ccceeehhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccccccchhhhh
MEM  ............................................................

SEQ  MSQCCRKIKDTVQKLASDHKDIHSSVSRVGKAIDRNFDSEICGVVSDAVWDAREQQQQIL
PRD  hhhhhhhhhhhhhhhhhhhhhhhccccccccchhhhhcccccceeeechhhhhhhhhhhhhh
MEM  ............................................................

SEQ  QMAIVEHLYQQGMLSVAEELCQESTLNVDLDFKQPFLELNRILEALHEQDLGPALEWAVS
PRD  hhhhhhhhhhhcccchhhhhhhhhhhcccccccccchhhhhhhhhhhhhhhcccccchhhhhhh
MEM  ............................................................

SEQ  HRQRLLELNSSLEFKLHRLHFIRLLAGGPAKQLEALSYARHFQPFARLHQREIQVMMGSL
PRD  hhhhhhhccccchhhhhhhhhhhhhhhcccccchhhhhhhhhhhhhhhhhhhhhhhhhhhhh
MEM  ............................................................

SEQ  VYLRLGLEKSPYCHLLDSSHWAEICETFTRDACSLLGLSVESPLSVSFASGCVALPVLMN
PRD  hhccccccccccccccchhhhhhhhhhhhhhhhhhhhcccccceeeecccccchhhhhh
MEM  .....................................MMMMMMMMMMMMMMMMMMMMMMM

SEQ  IKAVIEQRQCTGVWNHKDELPIEIELGMKCWYHSVFACPILRQQTSDSNPPIKLICGHVI
PRD  hhhhhhhhhhhcccccccccceeeeeccceeeeeeeeecchhhhhcccccccccccccceee
MEM  MMMMMM......................................................

SEQ  SRDALNKLINGGKLKCPYCPMEQNPADGKRIIF
PRD  eehhhhhhhccccccccccccccchhhhhcccc
MEM  .................................
```

Prosite for DKFZphmcf1_1a11.2

PS00001	189->193	ASN_GLYCOSYLATION	PDOC00001
PS00005	180->183	PKC_PHOSPHO_SITE	PDOC00005
PS00006	28->32	CK2_PHOSPHO_SITE	PDOC00006
PS00006	135->139	CK2_PHOSPHO_SITE	PDOC00006
PS00006	190->194	CK2_PHOSPHO_SITE	PDOC00006
PS00007	211->219	TYR_PHOSPHO_SITE	PDOC00007
PS00007	27->36	TYR_PHOSPHO_SITE	PDOC00007
PS00007	244->253	TYR_PHOSPHO_SITE	PDOC00007
PS00008	37->43	MYRISTYL	PDOC00008
PS00008	50->56	MYRISTYL	PDOC00008
PS00009	387->391	AMIDATION	PDOC00009
PS00013	282->293	PROKAR_LIPOPROTEIN	PDOC00013

(No Pfam data available for DKFZphmcf1_1a11.2)

DKFZphmcf1_1c23
----

group: mammary carcinoma derived

DKFZphmcf1_1c23.1 encodes a novel 311 amino acid proline rich protein.

No informative BLAST results; No predictive prosite, pfam or SCOP motife.

The new protein can find application in studying the expression profile of mamma carcinoma-specific genes.

unknown, proline rich protein

complete cDNA, complete cds? potential start at Bp 50, EST hits

Sequenced by DKFZ

Locus: unknown

Insert length: 3077 bp
Poly A stretch at pos. 3067, polyadenylation signal at pos. 3048

```
   1 AACTGGCCCC CTCCCCCACC CCCTGCCCCT GAGGAGCAGG ACCTGTCCAT
  51 GGCTGACTTC CCCCCACCAG AGGAGGCTTT TTTCTCTGTG GCCAGCCCTG
 101 AGCCTGCAGG CCCTTCAGGC TCCCCAGAGC TTGTCAGCTC CCCGGCTGCT
 151 TCGTCCTCCT CAGCTACTGC TTTGCAGATT CAGCCCCCGG GTAGCCCAGA
 201 CCCTCCTCCA GCTCCGCCAG CCCCAGCTCC TGCTAGTTCC GCCCCAGGGC
 251 ATGTGGCCAA GCTCCCTCAG AAGGAACCGG TGGGCTGTAG CAAGGGTGGT
 301 GGGCCTCCCA GGGAGGACGT AGGTGCGCCC CTGGTCACGC CCTCGCTCCT
 351 GCAGATGGTG CGGCTGCGCT CCGTGGGTGC TCCAGGAGGG GCTCCCACCC
 401 CAGCACTGGG GCCATCGGCC CCCCAGAAAC CACTGCGAAG GGCCCTGTCA
 451 GGGCGGGCCA GCCCAGTGCC TGCCCCCTCC TCAGGGCTCC ATGCTGCGGT
 501 CCGACTCAAG GCCTGCAGCC TGGCCGCCAG TGAAGGCCTC TCAAGTGCTC
 551 AGCCCAACGG ACCGCCTGAG GCAGAGCCAC GGCCTCCCCA GTCCCCTGCC
 601 TCAACGGCCA GTTTCATCTT CTCCAAGGGC TCTAGGAAGC TGCAGCTGGA
 651 GCGGCCCGTG TCCCCTGAGA CCCAGGCTGA CCTCCAGCGG AATCTGGTGG
 701 CAGAACTCCG GAGCATCTCA GAGCAGCGGC CACCCCAGGC CCCAAAGAAG
 751 TCACCTAAGG CTCCCCCACC TGTGGCCCGC AAGCCGTCTG TGGGAGTCCC
 801 CCCACCCGCC TCCCCCAGTT ACCCTCGAGC TGAGCCCCTT ACTGCTCCTC
 851 CCACCAATGG GCTCCCTCAC ACCCAGGACA GGACTAAGAG GGAGCTGGCG
 901 GAGAATGGAG GTGTCCTGCA GCTGGTGGGC CCAGAGGAGA AGATGGGCCT
 951 CCCGGGCTCA GACTCACAGA AAGAGCTGGC CTGACCACCA GGCACCTCAC
1001 TGGCACTGCT GACCCATCCC AGAAACACAA TCTCAGGGAC CCGAGCAGCT
1051 CCAAGGACGA GAGGATACAG CAGACACAAC CTAATAGAGA GGGCGCCTGC
1101 AGCCTTAACC TCCACGGCCT TCGATACTTA TGCAAGCCTG GTGTTGCTCC
1151 TGTCCTCAGA GTCATCCTGC GCTCATGCCT TTTCCCGAAT GGGTTCACCT
1201 CTGGCAGTTG CCGCTTCAGT CTTGGCCTTA GCCTCATCTT GAAGTGGGTA
1251 GCTGGCGGGA GAGGGTGGCT GCGCCCCCTG CTGGCCCTGA GGCTGCAGAG
1301 TTGGGAGCAG GACACCTCAC CTGAGTTTCA TTTTTTTTCA TGTCCAAACC
1351 ATGCACATAC TATAGTCCAG AATCAAAGCA CTTTTGAAAA GTGGCTGCAT
1401 GGCCATCCTC CAGGGCCCAG GAAGTTGCAT TCCAAGGGCC TGTTTACATG
1451 GCAGCAGAAT CCATCCCCGG CAGTCAGCCC ATAGCTTGGG ACCAGTCTGT
1501 GCCCTCCTGC CCAGTCCAGT TTACTCCTCT TGGTTCCTGA AGGTGGCCAA
1551 GTCATTGTGT TCCCACAGGC TTCTCTAGGC TGGGGGCAGG TGTGGGGCTG
1601 TGGAATTCCA AAGCACAAAA GGTGCAGAGG GGATTGGCCT TCCTGTGCCT
1651 CAACTCACCA ACCACCCTCC TGCCTTCCAG TTCTGCCAGG TGCTCCATGC
1701 TGGGGACAAG TAGGAGACTG CCAGGGCCCA AAGAAATGGG TGAGCAGTAG
1751 AGTCATCTCG GGGCACTTGG CAGTGTCAAG CACCTGCCCC TTGCCTCCTT
1801 GACCACACTG GGGTGGGTGG GCCCCCAGCA CTTCAGAGGC AGGAGCCTTT
1851 GGGCTGAGCA AGCACTGAGG AGGTGGATGG AAGGGAGCAT CTGGAGGGGG
1901 GGAGCTTCCT TGAGCAGTGG GCCCAGGCCT GGCCCTCCAC ACTTCATTCT
1951 CTGACCTTTC TCTCTCCTCA TTTCGGTGCA TGTCCTTTCT GCAGCTGCCT
2001 TTCAGCACAG GTGGTTCCAC TGGGGGCAGC TAACGCTGAG TGACAAGGAT
2051 GGGAAGCCAC AGGTGCATTT TACTCAAGTC TTCTCTAGTC AATGAGGGGC
2101 ACCCAGTGCT TCTAGGGCAG GCTGGGTGGT GGTCCCCTAG GTATCAGCCT
2151 CTCTTACTGT ACTCTCCGGG AATGTTAACC TTTCTATTTT CAGCCTGTGC
2201 CACCTGTCTA GGCAAGCTGG CTTCCCCATT GGCCCCTGTG GGTCCACAGC
2251 AGCGTGGCTG CCCCCCAGGG CCACCGCTTC TTTCTTGATC CTCTTTCCTT
2301 AACAGTGACT TGGGCTTGAG TCTGGCAAGG AACCTTGCTT TTAGCTTCAC
2351 CACCAAGGAG AGAGGTTGAC ATGACCTCCC CGCCCCCTCA CCAAGGCTGG
2401 GAACAGAGGG GATGTGGTGA GAGCCAGGTT CCTCTGGCCC TCTCCAGGGT
2451 GTTTTCCACT AGTCACTACT GTCTTCTCCT TGTAGCTAAT CAATCAATAT
2501 TCTTCCCTTG CCTGTGGGCA GTGGAGAGTG CTGCTGGGTG TACGCTGCAC
2551 CTGCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTTCTGCTC
2601 AGAGCTCCTG ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT
2651 GCATGAAACC AGGCCCTGGC AGCAACCTGG GAATGGCTGG AGGTGGGAGA
2701 GAACCTGACT TCTCTTTCCC TCTCCCTCCT CCAACATTAC TGGAACTCTA
```

```
2751 TCCTGTTAGG ATCTTCTGAG CTTGTTTCCC TGCTGGGTGG GACAGAGGAC
2801 AAAGGAGAAG GGAGGGTCTA GAAGAGGCAG CCCTTCTTTG TCCTCTGGGG
2851 TAAATGAGCT TGACCTAGAG TAAATGGAGA GACCAAAAGC CTCTGATTTT
2901 TAATTTCCAT AAAATGTTAG AAGTATATAT ATACATATAT ATATTTCTTT
2951 AAATTTTTGA GTCTTTGATA TGTCTAAAAA TCCATTCCCT CTGCCCTGAA
3001 GCCTGAGTGA GACACATGAA GAAAACTGTG TTTCATTTAA AGATGTTAAT
3051 TAAATGATTG AAACTTGAAA AAAAAAA
```

BLAST Results

No BLAST result

Medline entries

No Medline entry

Peptide information for frame 1

ORF from 49 bp to 981 bp; peptide length: 311
Category: putative protein
Classification: unset

```
  1 MADFPPPEEA FFSVASPEPA GPSGSPELVS SPAASSSSAT ALQIQPPGSP
 51 DPPPAPPAPA PASSAPGHVA KLPQKEPVGC SKGGGPPRED VGAPLVTPSL
101 LQMVRLRSVG APGGAPTPAL GPSAPQKPLR RALSGRASPV PAPSSGLHAA
151 VRLKACSLAA SEGLSSAQPN GPPEAEPRPP QSPASTASFI FSKGSRKLQL
201 ERPVSPETQA DLQRNLVAEL RSISEQRPPQ APKKSPKAPP PVARKPSVGV
251 PPPASPSYPR AEPLTAPPTN GLPHTQDRTK RELAENGGVL QLVGPEEKMG
301 LPGSDSQKEL A
```

BLASTP hits

No BLASTP hits available

Alert BLASTP hits for DKFZphmcf1_1c23, frame 1

PIR:S49915 extensin-like protein - maize, N = 1, Score = 215, P = 6.1e-15

PIR:A28996 proline-rich protein M14 precursor - mouse, N = 1, Score = 191, P = 3.8e-13

```
>PIR:S49915 extensin-like protein - maize
            Length = 1,188

  HSPs:

 Score = 215 (32.3 bits), Expect = 6.1e-15, P = 6.1e-15
 Identities = 81/269 (30%), Positives = 115/269 (42%)

Query:      5 PPPEEAFFS----VASPEPAGPSGSPELVSSPAASSSSATALQIQPPGSP--DPPP---A 55
              PPP     S    V SP P  P  SP      PA +SS   ++  PP +P    PPP    +
Sbjct:    598 PPPPAPVASPPPPVKSPPPPTPVASPP---PPAPVASSPPPMKSPPPPTPVSSPPPPEKS 654

Query:     56 PPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGA 115
              PP P PA S P    + P    P    K    PP + +  P + PS     +       P
Sbjct:    655 PPPPPPAKSTPPP-EEYPT--PPTSVKSSPPPEKSLPPPTLIPSPPPQEKPTPPSTPSKP 711

Query:    116 PTPALGPSAPQKPLRRA-LSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPE 174
              P+    PS P++P+      + ++SP PAP S             +LA       S + + PP
Sbjct:    712 PSSPEKPSPPKEPVSSPPQTPKSSPPPAPVSSPPPTPVSSPPALAPVSSPPSVKSSPPPA 771

Query:    175 AEPRPPQSPASTASFIFSKGSRKLQLERPV-SPETQADLQRNLVAELRSISEQRPPQAPK 233
                   PP +P   +S           +Q+  P  +P++    L    V+     + +  PP AP
Sbjct:    772 PLSSPPPAPQVKSS------PPPVQVSSPPPAPKSSPPLAP--VSSPPQVEKTSPPPAPL 823

Query:    234 KSPKAPPPVARKPSVGV--PPPASPSYPRAEPLTAPPTNGLP 273
              SP   P  +  P V V   PPP   S P   P+++PP    P
Sbjct:    824 SSPPLAPK-SSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKP 864

 Score = 206 (30.9 bits), Expect = 9.1e-14, P = 9.1e-14
```

```
 Identities = 82/261 (31%), Positives = 108/261 (41%)

Query:    17 PEPAG-PSGSPELVSSPAASS---SSATALQIQPPGSPDPPPAP---PAPAPASSAPGHV 69
             P P G P  SP +    PAAS+   S  T    + P   P+P P P    P P P    +P
Sbjct:   410 PTPGGGPPSSP-VPGKPAASAPMPSPHTPPDVSPEPLPEPSPVPAPAPMPMPTPHSPPAD 468

Query:    70 AKLPQKEPV-GCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTPALGPSAPQKP 128
              +P   PV G S       P    V  P  +      +V+L    AP G+P P +  ++P  P
Sbjct:   469 DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQAPVGSPPPPVKTTSPPAP 528

Query:   129 LRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSPASTAS 188
             +      G  SP P P S +     +K+     A  G     + P   PPE   P PP     AS
Sbjct:   529 I-----GSPSP-PPPVSVVSPPPPVKSPPPPAPVG---SPP--PPEKSPPPPAPVASPPP 577

Query:   189 FIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVARKPS- 247
             + S      L     P   P   ++        VA         + PP   P  SP   P PVA   P
Sbjct:   578 PVKSPPPPTLVASPP--PPVKSPPPPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPP 635

Query:   248 VGVPPP----ASPSYPRAEPLTAPPTNGLPHTQD 277
             +  PPP    +SP  P    P   PP    P  ++
Sbjct:   636 MKSPPPPTPVSSPPPPEKSPPPPPPAKSTPPPEE 669

 Score = 202 (30.3 bits), Expect = 2.9e-13, P = 2.9e-13
 Identities = 81/254 (31%), Positives = 110/254 (43%)

Query:    16 SPEPAGPSGSPELV--SSP--AASSSSATALQIQPPGSP-DPPPAPPAPAPASSAPGHVA 70
             SP PA P  SP L    SSP        SS     ++  PP +P     PP   P  PA   S P HV+
Sbjct:   817 SPPPA-PLSSPPLAPKSSPPHVVVSSPPPVVKSSPPPAPVSSPPLTPKPA---SPPAHVS 872

Query:    71 KLPQ----KEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTPALGPSAPQ 126
             P+       P     +       PP E    +P   TP   L     ++S     P      +P + P +
Sbjct:   873 SPPEVVKPSTPPAPTTVISPPSEPKSSPPPTPVSLPPPIVKSSPPPAMVSSPPMTPKSSP 932

Query:   127 KPLRRAL---SGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSP 183
             P+   +      + ++SP PAP S   A      K+     A     L       P   PPE  +  PP +P
Sbjct:   933 PPVVVSSPPPTVKSSPPPAPVSSPPATP--KSSPPPAPVNL----P--PPEVKSSPPPTP 984

Query:   184 ASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPVA 243
             S+                 +  P  PE  ++         V+          +  PP AP   SP    PPPV
Sbjct:   985 VSSPPPAPKSSPPPAPMSSPPPPEVKSPPPPAPVSSPPPPVKSPPPPAPVSSP--PPPVK 1042

Query:   244 RKPS---VGVPPPASPSYPRAEPLTAPP 268
             P     V   PPP      S P      P+++PP
Sbjct:  1043 SPPPPAPVSSPPPPVKSPPPPAPISSPP 1070

 Score = 190 (28.5 bits), Expect = 7.9e-12, P = 7.9e-12
 Identities = 74/264 (28%), Positives = 111/264 (42%)

Query:     5 PPPEEAFFSVASPEPAGPSGSPELVSSPAAS-SSSATALQIQPPGSPDPPPAPPAPAPAS 63
             PPP     S     PE + P     P    + P        +   T+++   PP         PP      P+P
Sbjct:   639 PPPPTPVSSPPPPEKSPPPPPPAKSTPPPEEYPTPPTSVKSSPPPEKSLPPPTLIPSPPP 698

Query:    64 SAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTPALGPS 123
                        P K P      K     PP+E V +P   TP               V +P     PTP     P
Sbjct:   699 QEKPTPPSTPSKPPSSPEKPS-PPKEPVSSPPQTPK--SSPPPAPVSSP--PPTPVSSPP 753

Query:   124 APQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSP 183
             A    P+     S ++SP PAP S     A ++K+     +     +   +     P   PP     +   PP  +P
Sbjct:   754 A-LAPVSSPPSVKSSPPPAPLSSPPPAPQVKS----SPPPVQVSSP--PPAPKSSPPLAP 806

Query:   184 ASTASFIFSKGSRKLQLERP-VSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPPPV 242
             S+    +                L   P ++P+++          +V+       +   +  PP AP    SP     P
Sbjct:   807 VSSPPQVEKTSPPPAPLSSPPLAPKSSPP--HVVVSSPPPVVKSSPPPAPVSSPPLTPKP 864

Query:   243 ARKPS-VGVPP----PASPSYPR------AEPLTAPP 268
             A  P+ V  PP    P++P  P            +EP ++PP
Sbjct:   865 ASPPAHVSSPPEVVKPSTPPAPTTVISPPSEPKSSPP 901

 Score = 189 (28.4 bits), Expect = 1.0e-11, P = 1.0e-11
 Identities = 86/271 (31%), Positives = 112/271 (41%)

Query:     5 PPPEEAFFSVASPEPAGPSGSPEL-VSSP--AASSSSATALQIQPPG--SPDPPPAP--- 56
             PPP   A   S      P P       S   P  + VSSP   A   SS     A        PP             PPPAP
Sbjct:   768 PPP--APLSSPPPAPQVKSSPPPVQVSSPPPAPKSSPPLAPVSSPPQVEKTSPPPAPLSS 825

Query:    57 PAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAP 116
             P   AP SS P   V     P     PV   S        PP     V  +P  +TP                V +P
Sbjct:   826 PPLAPKSSPPHVVVSSPP--PVVKSS---PPPAPVSSPPLTPKPASPPA--HVSSPPEVV 878

Query:   117 TPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKAC-SLAASEGL---SSAQP--- 169
             P+   P AP     +          ++SP P P S          V+          ++ +S   +      SS  P
```

```
Sbjct:  879 KPST-PPAPTTVISPPSEPKSSPPPTPVSLPPPIVKSSPPPAMVSSPPMTPKSSPPPVVV 937

Query:  170 -NGPPEAEPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRP 228
             + PP  +  PP +P S+             + P  PE ++       V+       + P
Sbjct:  938 SSPPPTVKSSPPPAPVSSPPATPKSSPPPAPVNLP-PPEVKSSPPPTPVSSPPPAPKSSP 996

Query:  229 PQAPKKSPKAPPPVARKPS----VGVPPPASPSYPRAEPLTAPP 268
            P AP  SP  PPP  + P      V  PPP   S P   P+++PP
Sbjct:  997 PPAPMSSP--PPPEVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP 1038

 Score = 181 (27.2 bits), Expect = 8.8e-11, P = 8.8e-11
 Identities = 73/277 (26%), Positives = 105/277 (37%)

Query:    3 DFPPPEEAFFSVASPEPAGPSGSPELVSSPAASSSSATALQIQPP----GSPDPP---PA 55
            D+ PP        V    P    S SP+ V   PAAS+   + +++ PP     GSP PP    +
Sbjct:  469 DYVPPTPP---VPGKSPPATSPSPQ-VQPPAASTPPPSLVKLSPPQAPVGSPPPPVKTTS 524

Query:   56 PPAPAPASSAPGHVAKL----PQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGA 111
            PPAP   + S  P  V+ +      P K P    + G PP  +    P   P       ++S
Sbjct:  525 PPAPIGSPSPPPPVSVVSPPPPVKSPPPPAPVGSPPPPEKSPPPPAPVASPPPPVKSPPP 584

Query:  112 PG--GAPTPALGPSAPQKPLRRA---LSGRASPVPAPSSGLHAAVRLKACSLAASEGLSS 166
            P     +P P +     P  P+       +       P P  S     A V      + +    +
Sbjct:  585 PTLVASPPPPVKSPPPPAPVASPPPPVKSPPPPTPVASPPPPAPVASSPPPMKSPPPPTP 644

Query:  167 AQPNGPPEAEPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQ 226
                  PPE  P PP  PA +           +     ++      PE            L+       +
Sbjct:  645 VSSPPPPEKSP-PPPPPAKSTPPPEEYPTPPTSVKSSPPPEKSLP-PPTLIPSPPPQEKP 702

Query:  227 RPPQAPKKSPKAPP-PVARKPSVGVPPPASPSYPRAEPLTAPP 268
             PP  P K P +P  P     K  V  PP      S P   P+++PP
Sbjct:  703 TPPSTPSKPPSSPEKPSPPKEPVSSPPQTPKSSPPPAPVSSPP 745

 Score = 177 (26.6 bits), Expect = 2.6e-10, P = 2.6e-10
 Identities = 78/264 (29%), Positives = 105/264 (39%)

Query:    5 PPPEEAFFSVASPEPAGP----SGSPELVSSPAASSSSATALQIQPPGSP--DPPPAP-- 56
            PPP          +P+PA P      S   PE+V  P++    +  T   I PP  P    PPP P
Sbjct:  850 PPPAPVSSPPLTPKPASPPAHVSSPPEVVK-PSTPPAPTTV--ISPPSEPKSSPPPTPVS 906

Query:   57 -PAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGA 115
             P P    SS P   +     P     P           PP    V +P   P+++             V +P
Sbjct:  907 LPPPIVKSSPPPAMVSSPPMTPKS-----SPPPVVVSSP--PPTVKSSPPPAPVSSPPAT 959

Query:  116 PTPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEA 175
            P   +   P+    P               ++SP  P P  S       A  +       S        +SS   P    PPE
Sbjct:  960 PKSSPPPAPVNLPPPEV---KSSPPPTPVSSPPPAPK----SSPPPAPMSSP-P--PPEV 1009

Query:  176 EPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKS 235
            +   PP +P S+             +   P  P    ++      V++       +  PP AP   S
Sbjct: 1010 KSPPPPAPVSSPPPPVKSPPPPAPVSSP-PPPVKSPPPPAPVSSPPPPVKSPPPPAPISS 1068

Query:  236 PKAPPPVARKPS---VGVPPPASPSYPRAEPLTAPP 268
            P  PPPV     P      V  PPP   S P   P+++PP
Sbjct: 1069 P--PPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSPP 1102

 Score = 177 (26.6 bits), Expect = 2.6e-10, P = 2.6e-10
 Identities = 82/267 (30%), Positives = 110/267 (41%)

Query:   17 PEPAG-PSGSPELVSSPAASS---SSATALQIQPPGSPDPPPAP---PAPAPASSAPGHV 69
            P P G P  SP +     PAAS+    S   T     + P   P+P P  P     P P P    +P
Sbjct:  410 PTPGGGPPSSP-VPGKPAASAPMPSPHTPPDVSPEPLPEPSPVPAPAPMPMPTPHSPPAD 468

Query:   70 AKLPQKEPV-GCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTPALGPSAPQKP 128
             +P    PV G S        P    V   P  +        +V+L      AP G+P P +    ++P  P
Sbjct:  469 DYVPPTPPVPGKSPPATSPSPQVQPPAASTPPPSLVKLSPPQAPVGSPPPPVKTTSPPAP 528

Query:  129 LRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPPQSPASTAS 188
            +     G  SP P P  S  +       +K+     A  G     + P  PPE    P PP    AS
Sbjct:  529 I-----GSPSP-PPPVSVVSPPPPVKSPPPPAPVG---SPP--PPEKSPPPPAPVASPPP 577

Query:  189 FIFSKGSRKLQLERPV---SPETQADLQRNLVAELRS------ISEQRPPQA------PK 233
             + S       L     P       SP   A +  +      ++S           ++      PP            P
Sbjct:  578 PVKSPPPPTLVASPPPPVKSPPPPAPVA-SPPPPVKSPPPPTPVASPPPPAPVASSPPPM 636

Query:  234 KSPKAPPPVARKP---SVGVPPPASPSYPRAEPLTAPPTN 270
            KSP  P PV+   P          PPP + S  P   E       PPT+
Sbjct:  637 KSPPPPTPVSSPPPPEKSPPPPPPAKSTPPPEEYPTPPTS 676

 Score = 170 (25.5 bits), Expect = 1.6e-09, P = 1.6e-09
 Identities = 78/279 (27%), Positives = 108/279 (38%)
```

```
Query:     5 PPPEEAFFSVASPEPAGPSGSPELVSSPAASSSSATALQIQPPGSPDPPPAPPAPAPASS 64
             PP      S  S   + P  +P  +  P   SS   A+   PP +P    +PP P   SS
Sbjct:   883 PPAPTTVISPPSEPKSSPPPTPVSLPPPIVKSSPPPAMVSSPPMTPKS--SPP-PVVVSS 939

Query:    65 APGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPG--GAPTPALGP 122
              P  V   P   PV       PP     +P   P  L    ++S   P    +P PA
Sbjct:   940 PPPTVKSSPPPAPVS-----SPPATPKSSPPPAPVNLPPPEVKSSPPPTPVSSPPPAPKS 994

Query:   123 SAPQKPLRRALSG--RASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEAEPRPP 180
             S P  P+        ++ P PAP S     V+    S      +SS  P  PP  +  PP
Sbjct:   995 SPPPAPMSSPPPPEVKSPPPPAPVSSPPPPVK----SPPPPAPVSS--P--PPPVKSPPP 1046

Query:   181 QSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKSPKAPP 240
              +P S+             +  P  P  ++      V+      +  PP AP  SP  PP
Sbjct:  1047 PAPVSSPPPPVKSPPPPAPISSP-PPPVKSPPPPAPVSSPPPPVKSPPPPAPVSSP--PP 1103

Query:   241 PVARKPS---VGVPPPAS---PSYPRAEPLTAPPTNGLPHTQDRTKREL 283
             P+   P    V  PPPA    PS P   P+++PP    P    + ++ L
Sbjct:  1104 PIKSPPPPAPVSSPPPAPVKPPSLPPPAPVSSPPPVVTPAPPKKEEQSL 1152

 Score = 169 (25.4 bits), Expect = 2.1e-09, P = 2.1e-09
 Identities = 75/266 (28%), Positives = 104/266 (39%)

Query:     3 DFPPPEEAFFSVASPEPAGPSGSPELVSSPAASSSSATALQIQPP----GSPDPP---PA 55
             D+ PP      V    P   S SP+ V  PAAS+   + +++ PP    GSP PP    +
Sbjct:   469 DYVPPTPP---VPGKSPPATSPSPQ-VQPPAASTPPPSLVKLSPPQAPVGSPPPPVKTTS 524

Query:    56 PPAPAPASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGA 115
             PPAP  + S P  V+ +    PV       PP   VG+P   P          V +P
Sbjct:   525 PPAPIGSPSPPPPVSVVSPPPPVKSP----PPPAPVGSP--PPPEKSPPPPAPVASP--- 575

Query:   116 PTPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSAQPNGPPEA 175
             P P   P  P          ++ P PAP +     V+    S      ++S  P  P  +
Sbjct:   576 PPPVKSPPPPTLVASPPPPVKSPPPPAPVASPPPPVK----SPPPPTPVASPPPPAPVAS 631

Query:   176 EPRPPQSPASTASFIFSKGSRKLQLERPVSPETQADLQRNLVAELRSISEQRPPQAPKKS 235
              P P +SP             K     P  P               S+    PP+
Sbjct:   632 SPPPMKSPPPPTPVSSPPPPEKSP--PPPPPAKSTPPPEEYPTPPTSVKSSPPPEKSLPP 689

Query:   236 PK---APPPVARK--PSVGVPPPASPSYPRA--EPLTAPP 268
             P    +PPP  +   PS    PP+SP  P    EP+++PP
Sbjct:   690 PTLIPSPPPQEKPTPPSTPSKPPSSPEKPSPPKEPVSSPP 729

 Score = 168 (25.2 bits), Expect = 2.7e-09, P = 2.7e-09
 Identities = 75/267 (28%), Positives = 102/267 (38%)

Query:     2 ADFPPPEEAFFSVASPE-PAGPSGSPELVSSPAASSSSATALQIQPPGSPDPP-PAPPAP 59
             A  PPP  +   ++ P+ P G    P   +SP A   S +        SP PP  +PP P
Sbjct:   496 ASTPPP--SLVKLSPPQAPVGSPPPPVKTTSPPAPIGSPSPPPPVSVVSPPPPVKSPPPP 553

Query:    60 APASSAPGHVAKLPQKEPVGCSKGGGPPREDVGAPLVTPSLLQMVRLRSVGAPGGAPTPA 119
             AP  S P      P   PV       PP +    P +  S    V+     AP  +P P
Sbjct:   554 APVGSPPPPEKSPPPPAPVASPP---PPVKSPPPPTLVASPPPPVKSPPPPAPVASPPPP 610

Query:   120 LGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSL-AASEGLSSAQPNGPPEAEPR 178
             +    P  P+       + P PAP +     ++        +S       P  PP A+
Sbjct:   611 VKSPPPPTPVA------SPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPPPAKST 664

Query:   179 PP--QSPASTASFIFSKGSRKLQLERPV---SPETQADLQRNLVAELRSISEQRPPQAPK 233
             PP  + P    S   S    K  L  P    SP  Q              S ++P  +P
Sbjct:   665 PPPEEYPTPPTSVKSSPPPEK-SLPPPTLIPSPPPQEKPTPPSTPSKPPSSPEKP--SPP 721

Query:   234 KSPKAPPPVARKPSVGVPPPASPSYPRAEPLTAPP 268
             K P + PP   K S   PPPA  S P   P+++PP
Sbjct:   722 KEPVSSPPQTPKSS---PPPAPVSSPPPTPVSSPP 753

 Score = 166 (24.9 bits), Expect = 4.6e-09, P = 4.6e-09
 Identities = 81/268 (30%), Positives = 108/268 (40%)

Query:     5 PPPEEAF---FSVASPEPAGPSGSPE-LVSSPAASSSS----ATALQIQPPGSPDPPP-- 54
             PPPE++      VASP P   S  P  LV+SP     S    A      PP    PPP
Sbjct:   560 PPPEKSPPPPAPVASPPPPVKSPPPPTLVASPPPPVKSPPPPAPVASPPPPVKSPPPPTP 619

Query:    55 --APPAPAPASSAPGHVAKLPQKEPVGC----SKGGGPPREDVGAPLVTPSLLQMVRLRS 108
               +PP PAP +S+P  +   P   PV       K   PP      P           ++S
Sbjct:   620 VASPPPPAPVASSPPPMKSPPPPTPVSSPPPPEKSPPPPPPAKSTPPPEEYPTPPTSVKS 679

Query:   109 VGAPGGA-PTPALGPSAPQKPLRRALSGRASPVPAPSSGLHAAVRLKACSLAASEGLSSA 167
                P  + P P L PS P  P  +  +  ++P   PSS    +   +  S       SS
Sbjct:   680 SPPPEKSLPPPTLIPSPP--PQEKP-TPPSTPSKPPSSPEKPSPPKEPVSSPPQTPKSSP 736
```

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: ______________________

IMAGES ARE BEST AVAILABLE COPY.
As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.